

999

CGTTGAGCCA AATGAAGCTG GAGAAACACG CTTTACCTAT GCCACTTATG GTGAGGGAAA	180
GCTTCCAGAA GGTCTGACCA TTCCTCCAA GGAGAGTGCA GAAACGAGTG ATTTATTAGG	240
GTCTTACTTG ATTGTATCAG GAAGTTTGGA TGGAGTGAGC TTACAGACCA CCTTGAAAGA	300
GCTTGGTTAT CAAGGCTTTG TTTCGAATGG AGAAGATCCA TTTTCGATAG TCTTACTATT	360
GACGGCCACC CCTATGGTGC TACTGAGTTT AGCTATTTT CTGCTGACCT TTATGAGTCT	420
GACCCTGATT TATCGGATCA AATCCCTTCG TCAGGCAGGG ATTCGCTTAA TAGCTGGTGA	480
GAGCTTGTTT GGAGTTGCTC TCAGACCAGT GTTAGAAGAT GTGAGACAGC TTATCTGCTC	540
AGTGCTGGTA TCCAGTCTTT TGGGATTGGG GATTCTCTGG TATCAAGGTG CCTTGTTTAT	600
GGCAACGGTG CAACTGGTCA TCATTGCTCT TCTACTTTAT GGATTGACCT TGGCAGGGAT	660
TTCTACCTTA CTAAGTGTG TCTATCTACT TGGTTTACAG GAAAATAGTC TGGTGGATCT	720
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AGCTGTATTG GTGGTCGGAT CGAGTGCGAC AGCTCTCCTA CCCCCTACC GTGAAATGCA	840
GGAAATGGAG AGAGCTAGCA ATAAATGGAG CCAGTCCTCA GACCGTTACC GTCTATCCTT	900
TGGTTGGTCT AGTGCATTTG CCGATGAAGA AGGAACGCGT AAGGATAATC GTGAGTGGCA	960
GACATTTACT GAAGAACGGT TAGCCAATAC AGACTCTTTT TATATTATGA GCAATGTGTA	1020
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GTCAGGGAAT GTTATCTATG TCTCACCGCG CTATCTGATA GAAGAAAAGA TTACCGTTTC	1140
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TGAGAGCTTG CGAGAGCAGT CTGTCTACTA CCAAGGATTG TTTACAGATT ACCTGCAAAA	1260
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TGTTGCGAGG ATGTTGTGGG GAACTACGGC TAATAGTGCC TTGAAACTAG ATCGATATGG	1500
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AAGCCAGCTA TTTTGTGCCA AGGTACTAAA TGACAAACGG GTGGAGTTT ACTCTCTCCT	1620
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TGAGCTTCAT GGCAAGTATT TACTGGCGCA AGGAGGAGTT CTCTTGCTTG GCCTAGTCCT	1800
ATCTAGTATT TTGACAAGAG ATGGTTTGAT TAGCGCTCTA GTTGTAGCTT TGTTTACGCT	1860

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GTGGAAGGGT TCTCTATCAG GGGAAAGATT TAAAAACCAT TCCCACTCGT GAGTATTTTC	2160
GAGACCAGAT GGGCTATCTC TTTCAAAATT TCGGCCTCTT AGAAAACCAA TCAATCAAAG	2220
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CTGCCGAGGA AAATTCAGAA GGCTATATCC TCAAAATTCA CGAACGGAAA AACAGTCTGG	4080
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5640					
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5940					
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6000					
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6060					
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6120					
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6300					
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6900					
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6960					
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7020					
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7140					
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7200					

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TCGAGAAAAT GTTCCTTTCA AAACGTAGTC TTAAGGCAGG CAGCCGTGTC TTGATTGTGG	9120
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TTGAACTGGG GACAGACATT ATGGACAATC CTGGGGAGGC TAAGTTTGGC ATGACCAAGG	9900
ACCAGCTCTT TGAAGCCTTT GCTATCTTGA AGGAAAAAGG AGCCAAGACT TTTGGGATTC	9960
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CAGTTAATCG CGAACTGCCT CATAAGAAA TCGGTGATTT GCTGGTCATT CATGATACAG	10500
GTGCCCACGG ATTTTCAATG GGCTACCACT ATAATGCCAA ATTACGTTCT GCGGAAATCC	10560
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GACAGAGGCC	TTGCGCTACC	GTGGTTTCTG	GGGAAATAAG	GGTGGGATTA	CAGTCAGTGG	11040
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CAACGAAGAA	CAGCACAAGA	TTGTCACCTAG	CCAAACCAAT	AAAAATATCT	TGGCTTGTGC	11280
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AATTCATAT	TCCCTCGAAG	GAGTCAAACC	ACCAACAGCA	GATCGCGTCA	AGAACGCTAA	11520
ACAATCATG	GATACCGAAA	GTTATCAAGA	TTATATGAAA	CGTGTACATG	GATAGAAAAG	11580
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AAGTGTGACA	CTAGCTGGTG	AGAAGAGGGA	GAAGACGACG	ATCATGAGTG	GGCTCATGTA	11940
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AGTAGTCGCT	TCTTTGAGAC	GCGTTTGGTG	TGGCTCAAGG	ACGTGCTTGA	GGGCGTTCAT	12300
CTTTTCAGAG	TGAAGCGTTG	CCTTCCATGA	TTGGTAGATA	CCAAGTGGTA	AGATAATCAA	12360
GCGTACGATA	ATGGTTACGA	TAATGATAGC	GACACCAAAG	CCTAGACCTT	TATCAGTAGC	12420
GAAGTACTTG	ATGGCTTCAG	CCATAGGCGC	TCCGATCGTA	TTCCAAATAA	ATCCTGTTGG	12480

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CTGACCTGTG GTTTTATCGA CATTGACACA GCCAGTCAAG ACAAGCAACA TAGCCACTCC	12540
CATAGCCGAG AGTGCAAAAT CGGGGT	12566

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TGACACTCTG TAGGATTGTC GTTAATTGAT TGCTCGTACT CTCTACAATA ACCACCAAAG	60
TAAAAACGAC ATAGAAAGAT AGCATCAGCT GTAGCCATAG CGCCTTTGAC ACCTTCTGGA	120
TGATTATGAG TTACCTCTGC AGAAAGACTC GTAAGTCCTC TAGATGATGG CCATATACCA	180
GTTTTTCGCAT AAAAACCACA GTCCATGATC CAAGCACATG GAGAAATACG CATAGCTGAT	240
CCATTCCCAA AGCTATTATA AGGCTCACGG TTATCGCTGT TTAGCCATGC ATTAAACCGA	300
GCACCGTAAT CAGCATTCGG ATACATTCTG CCATATTCTT TCATCGCGTC AATGAAGTCA	360
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ATTTTAAAAA TTTTCATTTT TTCAAAATAG GTTTTTACCA TTTCTTTCCA CCTAGCTCTA	660
TGAAAATTGA TTGATTTTAA AGGAGATAGG CCATAATTTT CCAATGCATA ACCATCATTT	720
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GGCGCATCTT TCCAACATGA TATCGCTTCA TCAATTACAC TTGCATCAA TTGTGCATGA	840
TAATCACCTG TATAGGTCG AACATCTAAT ACGCGACCAT CTAACACAAA ACAACGCCAT	900
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CCTATTAAAT CATGGGTTCC ATTAACAACCT CTTCCAGTAA AGACTTTTGA ACCAGCTTTA	1020
GGCTTAATAA ATTTTCCCA ATTATCAGGT ATATTCACAA TCTCTCCTAA AATACCAGCA	1080
TAAATCTTTC GACCATAAAA CTCTTTAAGC TCAATAGGAT AGTCATGAAC CGGAACGTTT	1140
AAGCCCATCA TTTTATAGTAA TGCTCTAGTC TCCATTATAT AATCTACAAC TATATCTTCA	1200
CTTGTTAACT CTTTTATTTC AGAAAAAGAT TGATATAAAA TAACTTCTTC TCCTTGTAAG	1260
TAGGCACCTA CTTGAGCATT GTATTTATTA ATTGAAACCT CACTTGGTAA TTTACTTTGT	1320

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CTAATATAAA CAACCATTTT ATCACTCCTA TATCACTAGT GTTACACCAA TTTGTAAAAA	1380
ATAATAGCAA TTTTGCTCTT ATTTTTTTGA GTAAATAGCC CCCATAATAT CATCGAAATA	1440
ATCAACGGTA TTTAGGAGTA ATTCAATAAC CTGGGACTTT GTTAGTCGCA TTCCCCTTCT	1500
ATCTCTAGCA TCTTCTACTA AATTTTCAAG TTTCTCTAGA TTTTATCAT CCAAGCTAAT	1560
CATTATTCTA TTTTATATCG TGCCATTTT CATCACCTCA AGTTAATTCT ATCACAGGTG	1620
TAACACTAGT GTCAACTGGC TTTTATAATA CATTAGTTTA AAAGTGAGG GGATTTTAA	1680
CACAGTAACT TTAAATCTTT GGTATTAAAA AATTTTCACA ATATTATAG AAATAAAATC	1740
TGTCTCAAA CAGTTATCAA ATCTAGTATA AATTATGAGC GGCTACTCTA ATACTTTCCC	1800
TCTAAACAAG AAAAAGACTT AACTCAAGG GTTTTCTTCC CCCCCTTCGT TATAACGTTT	1860
TGACTCTTTT ACTAGCAAAG GTATATACTC ACAAGGAAT TTGGTTGACT ATTGAATCTC	1920
TCCAACCTCT TCTTTAACAT ATCCTTCTAC ATCTTCAATC TCTACAAACA TTGGGTCTAA	1980
GTGACACAAG AAATGCCAAA CTTGATCCC TTTTCTCTG TAAAGAATCG CTTACCCGTC	2040
TTCACCTCCG AAAAAGCTTC TGTCGATTTT ATATCCGCGG CTTTCTAAGA AGTCTTTTGC	2100
TTTACGATAG TTCGTTTCTC TTGTTTCGAC ATAGGCTTTA ACTTCATGGT TGTTAACGAC	2160
ATATGCATCA ATTTTGAAT ATCCTTCGAT CACTCTATCA TTTTGTAGGG ATAAATTTGA	2220
AATCTCTTTC CAAATAATGT TTACATTTTC CTCAGGATCG AACATAAATT TAGATAAAGG	2280
AACAATATTT CCGTTAAAA TAATTTCAT ATAATCCGGT ATGTTTTTAG GATTAAAATA	2340
CTCCACTTCA AAACCATCTT CTGTTCCAG AGTGTATCCC GGGATTTGAG CTACAAAGGC	2400
TTTCCCATCT TCTATGGAAT CAAATGCTAC TAAATCTTTA GAATAATCAT TTTGGTACAA	2460
TTCCAATATA ACCATCGATA ATCTCTCCAT TTTCATTATC AGGCTAATGT AAATAAGCAC	2520
GTCACCTGAC CAATTCAGGC TCTCTGTATC ATCTCATCAT ATTTCTACT TACTTTACGA	2580
GTCTTATACC CAGAACACAC CTTATCGACC TTCGGTCTCA CCTCGTCGCA TTGGCTGAAC	2640
ATCTACTTTT ACTTTGCTGA TGCTTCAACT CGTACAAGCA GTGATACCGC CTCAGCGTGA	2700
TGCGTCAGTG GGAATCAAAA GGTTCGGGGA ACCTTTTGAG GATTAACTAC GTTCTCTAA	2760
TAAACTTACA CATTCAACTT GTTCATCATT GTCCAAACCT ATGTTGAGAT TTTCTTCTAT	2820
AATTGGTAGC TTAAAAGTAA TGGATTTTAG CCATTGTCCG TTAGATTGTT TTTCTTCATA	2880
AACTTGAATT TCAGAAATCA AAGCTGAAAT TAACTGCCTA CGCTCTACAT CATTATGAC	2940
TTTATAGAGC TTATCAAAAT AGATCAGAAC CTTATATATG TTATCTCCTG TAAGCTTTTC	3000
AGCTTCAATA GTCTGTTTCT TTGCTTTCGC ATCAATTAGT GATGATTCTA ATTCATCTAG	3060

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TTTGTACATAC ATACGATATA GTCTATCATC TAAATCCTGT TTCCTTCTCT TATAATGCTT	3120
ATCTTCAACA TCTAAATTAT CTATTTCTCT AATTAGCTTA AACTTTGTAG AATGACTCTT	3180
TCTCAATTCC TTTTGGTAAT TATCTATTTT TTTTCTATT TCAGAGGTAT CCACCTTCAT	3240
GTTGATTTTT TCTTGCATCA TAGAAGCAAA TTTCGGATTA CTTACTATCT TGACAATCAC	3300
CTCTGCAACA GCATCATCTA ACAATTCTTC TCTAATTGTC TTTACTGAATG TACACTTATT	3360
ACCTCTTATC ATCTGCCTAT GGTTACAACC ATAGTAATAA AAATCTTTAT ACTTTGTGCC	3420
ATCTTTCTTT TTCTTGATAC ACTTGTTCCC AAACATTCCC ACTCCACATA TCGGGCATTT	3480
TACAATTCCA GAAAGCAAGT GTGTGCGTGT ATCTTTTCCT TTATTACAT GCTCATATTT	3540
CTTTGCTTGA GATTTTAGCT TAACCTGAGC AGCTTGCCAA ACTTCATCGG AAACATAGC	3600
TTCATGTATC CCTTCAGATA TTAGATATTC ATCTTGTTCA ACCTGCTTAT ATTCATTTCT	3660
TGTACCATGA ACTTTTCTTA AAGTTCTTCT TCCAAATGCT ATTTTCCCAT TATATACAGG	3720
ATTCTTTAAT ATCTTTCTTA TAAGACCTGC ATCAAACAAA GGATTCTTAC CATTCTGTCT	3780
TGGGATTTTT CTAATTCAT GATTCTCTAA GTATTTAGAT ATCCCATGG CTCCTATCGT	3840
AGTATTTACA TACTGGTCGA AAATCGTTCT TATTGCAACT GCCTCTTCCT CATTTATAAA	3900
CAGCTTGCCG TCTTCAAGTT TATATCCATA CGGAGCAAAG CCACCATTC ATTTTCCTTC	3960
CCCTGCTTTT TGAATGCGAC CTTCCATTGT TTGAATACTG ATGTTTTCTC TTTCTATTTT	4020
AGCCACAGCT GATAAACAG AAATCATTAG TTTCCAGCA TCTTTAGATG AATCAATGCC	4080
ATCTTCAACG CAGATAAGAT TAACTCCATA ATCCTGCATT ATATGAAGTG TAGAAAGAAC	4140
ATCAGCGCA TTTCTTGCAA ATCTTGATAA CTTAAACACA AGAACAAAAG ATACTCCATC	4200
TTTTCCAGAT TTTATATCTT CCATCATTCG ATTGAAGTGT ATTCTACCTT CAATAGACTT	4260
GTCAGACTTC CCGGCATCTT CATACTCTCC AACAATTTCA TAATCGTTGT AAATAGCAAA	4320
AGCTTTCATT CGTGATTTTT GTGCCTCTAA CGAATACCCC TCTATCTGTA TTGACGTAGA	4380
TACTCGTGTA TAGAGGTATA CTTTTATTTT TTCTTTTGAC ATAGTATTAA CCTCAATATA	4440
ATTTTCTAT ATCATATATA ATTTTTTTAA TTTAAGTTTG GACTATCATT TCAAGTATAT	4500
TATAACACTT TTATTAGTCC GTCTCAATTT GTGTTTTGTC CATGTCAAAA CTATTTTCA	4560
TCTCTGATT TTTTGCTGGC GTTGATCGG GTAGATTATC TAAATCTAAA GCACCAGCAT	4620
ATTTTGCAAT CAGATTGCT ATTAATCAG CCAATCCATT CCAGTCATTG TCCAATATAT	4680
ACCTCCTCTA AAGTTTATA TCTAATAATT ATTTGTTTAA TTAAGTTTTT TGACATTGAC	4740
AAGTGCTTG GATTAGCAAC ATAGGAATCT CACTTCCGCC TCTATTCGG ATGAGCCGGC	4800
TTCAACCTTA GAAGTATCAT TACCCTCATT TTCTTCATAG CGGATAGGGT ATCCCTCCCT	4860

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ATATTCAAAC TCTTACTTAT CGCTCACTTT CTTTTTGCTT AGCAGAACTT TTTTGGCCGA	4920
ATTATTTCAGC CGAAAGATCT TGACGGATAG GTTATTACGC TCCAAAAATA ATTAACGTCT	4980
TGTCTTGGTC TATTCAATTG TTAAGGTTCA AAATTTATCG AGAGTTATTA ATCTTTTAA	5040
AATTTGACCA TCAGAAAATA TTTATCTTGA TGTAACAAAA TTCTATAAAT TACCCTCTTA	5100
TACTTAACAG TGAAAAGAAG TCTTTCTTGG TAACCAATTT TGAAATAGAA TTTGCTTATA	5160
TAAAAAGGTC CAATTCACAC TGCATAAATA GCAGTGAAAA TTAGACCCCTC TTGGTAACTG	5220
TCATCTAAAA GTCTTCTA	5238

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GACGATTTAC GAAGAATCGA ACAAGAACCT GCTCCTATCA ATTCCCAACC TCTATCTCTA	60
AAATCTTGCA GTTCATGCTT ATACTTTTTT AAGAAATCTA GAATCATAGA TACGGTAGAT	120
GACATCGTCT GGTGACATT GGTCAAAATA GAACAAACCA AAACGACTCG TTCTATACCT	180
CCAACCTTTC AAATGCATCT CATGTAAATG TTCTTCTTCC TTGTCCAAAT CAACAATGGT	240
GAAAATCCGA AATCTACTC TGCTATTTCAT TGTCTTACCC CAAAATTAGA AAACATGCCT	300
GGCGTTATTT ATTAGATAAT TCTTTCCACT TTTGACTCAA TCTCCAAAAA ATATAAGAAA	360
TCTGAATCGC AAAAATATC AATAAAACCC AATCTATTAT GAAAATCAA AACACTTTCC	420
AACTGAAAGA ACTACCTCCA GTGACAAACT TTGAGAAAA CGGTAGTAGA GCTAAAAAGA	480
GAAATAAAAT AGGAAGCATC CGCATGTGTA AAATCCGTTT GGCATAAAAA AATCTTTATT	540
TAAACGAAAA TATTATGGCA AAATTTACGC CAGTTTTTGA ACGGCTGATG TAGATATTTT	600
ATACTTTCAA AATGTTTAA TGTGATTATT TATTTTTGAA AAATAGATCA CCAGCCCGAC	660
TGAAAGTGCT TATAGAATGA TAATAAGTCG CCTGCCGAAA ACAGCGAAAA ATAGCGGTGT	720
TATGCGGAGA TAATCTGACG CGATGCGAAA GTATATTGCA TACTTATTTT CAACAATTTA	780
GCAGAGTATT TTTATAAGTG TGATATAATA GAAGTATAAT TTGTTCTGAT AGTTTATTTT	840
ATGGAGAAGT AGATTTTTAG AATGCGGAGG GTTCAATATG GTTGAGTTTA TAAAGTCTAA	900
GAAAGAAATG AGTGAGGAGG ATATTAAAGC AAATTTTCATC ACTCCTGCTA TTGTATCCAA	960

1010

AGGATGGAAA AATGGTGAGC ATATCGCTTA CGAAGAATAC TTCACTGATG GTCGAATTGA	1020
AGTTAGAGGA GATAAGGCTC GTCGTAAAGA AGGAAAAAAA TCAGACTATT CACTGTATTA	1080
CCAATTTGGA ACTCGAATTG CAATTGTTGA GGCAAAGGAT AATAAACACA GCGTTCGAGC	1140
AGGATTACAA CAAGCTATTG AATATGGAGA GATTTTAGAT GTTCCATTG TTTATTCTTC	1200
GAATGGTGAT GGCTTTTATG AACACGACCG TATCACGAGA GAAGAACGTG AGCTGGAGTT	1260
AGACGAATTC CCTACTCGTG AAGAATTATT TTCTCGTATG ACGAAGGAAA AAGGATTGAC	1320
GTACGAAATT ACAGAAGCTA TCTCAACTCC ATACTATACA GACGCCTTCT CAATGAAAAAC	1380
GCCACGCTAT TATCAGCAAA TAGCTATCAA CCGTACTATT GAAACAGTTG CCAGAGGACA	1440
AAAACGAGTA ATGTTTGTGA TGGCAACAGG AACGGGAAA ACGTTCATGG CTTTTCAAAT	1500
TATTCATCGC CTTGAAAAAG CTGGTTTGGC TAAACGAGTT TTATTCTTAG CAGATAGAAA	1560
CATCTTAGTA GACCAAACGA TGGCTGAAGA CTTTAGGCCA TTCGAAAAGG TAATGACGAA	1620
AATTACACCA AAACCTTTGA CTGCTCCTGA AAAATTAAAT TCTTTTGAAA TTTATCTAGG	1680
GCTTTATCAG CAACTAACTG GTGAAGATGG AACTGAAACA CATTATCAAA AATTTGACAA	1740
AGACTTCTTT GATTTAATCG TAATTGATGA AGCGCACCGT GGTTCAGCTA AGGAAAACAG	1800
TAAGTGGCGT AAGGTAATTG ATTATTTTCAG TTCTGCGACA CAGATTGGGA TGACCGCTAC	1860
TCTTAAAGAA ACCAAGAATG CTTCCAATAC GGAATACTTT GGTGAGCCAA TCTATACTTA	1920
TAGTTTAAAA CAGGGAATCG AGGATGGTTT TTTGGCTCCA TATCGTGTTA TGAGGGTTAA	1980
TTTAGATGTG GATGTGGATG GTTATCGTCC AGAAACTGGA AAAGTTGATG CTAACGGACA	2040
ATTAATAGAA GATAGGTACT ACGGCAGGAA AGATTTTGAT AAAACCATG TCATTGATGA	2100
TAGAACGCAA AGAGTTGCCA AGTTTGTTTC TGATTATATG AAGCAAAACA ATGCACGATT	2160
TGATAAAACA ATTGTTTTTT GTGTTGATAT TGACCATGCC GAGCGAATGC GTGCTGCACT	2220
TGTAAAAGAG AATCTAGACT TAGTCCAAGA AGACTATCGT TATGTCATGC AAGTAAGTGG	2280
TGACAACGCT GAAGGAAAAG CTCAACTGGA TAACTTTATG GATGTCAATT CTAATTTTCT	2340
CGCTATTGTA ACAACGTCTA AATTATTAAC GACAGGAGTT AATGCTAAAA CATGTCGTTT	2400
GATTGTTTTA GACTCTAATA TCCAATCCAT GACTGAATTT AAACAAATTA TTGGTCGTGG	2460
CACACGTCTT TATCCTCAAA AGGGGAAAGA ATTTTITACG ATTATTGATT TTCGAAATGT	2520
TACCAATTTG TTTGCTGACC CTGATTTTGA TGGTGATCCA GTGAAGGTGC TAGAAACAGG	2580
TGCGAAAACA GTCAGTGGTT CTACGCCCGG TTTCGTAGAT GAGGAAGGTG ACCCAGTAGA	2640
AAAATATATC GTTACAGACA AGCAGGTTAC CATTCTTAAT TCTACTGTTT AAGTATTGGA	2700
TGAAAACGGG AAAC TGATTA CCGAAAGCCT GACCGACTAC ACTCGAAAGA ATATCTTAGG	2760

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TAGCTACGCC	ACTTTGAACG	ATTTTATCAC	AGTTTGGCAT	ACGGCAGATA	AGAAGAAGCT	2820
TATCTTAGAC	GAACCTTATA	AAAAAGGAGT	TTATCTAGAT	GCTATTCGAG	AGTCGGAGGG	2880
AATATCAGAA	CAAGAAATCG	ATGATTTTGA	TTTACTCCTA	AAACTTGCCT	ATGGTCAAAA	2940
AGAATTAACC	AAAACGGAAC	GTATCAATAA	ACTCAAACAA	AGCGGATATT	TATATAAATA	3000
TAGTGAGGAA	GCGCGTGCTG	TTTTGGAAAT	TTTACTGAAC	AAATACATGG	ATAAAGGTAT	3060
TGGAGAACTC	GAAAGCATTG	AAACATTAAA	ACTTCCAGAA	TTTCAGATAT	ATGGTGGAAC	3120
CTTCAAAATC	ATCAATACTT	ATTTTGGAGA	TAAAAAACGA	TATTTACAAG	CAATTAAAGA	3180
ATTGGAGCAA	GAGCTATTTA	CAGTAGCTTA	ATGAAAGGAA	AGTATGTCAA	TTACATCATT	3240
TGTA AAAAGA	ATTCAAGATA	TCATCTCGAA	CGATGCTGGT	GTTAATGGTG	ATGCTCAACG	3300
TATTGAGCAA	ATGTCTTGCT	TATTATTCTT	AAAAATTTAT	GATAGCCGTG	AAATGGTTTG	3360
GGAATTAGAA	GAAGACGAGT	ATGAGTCAAT	TATCCCAGAG	GAATTAAAA'	GGCGAAATTG	3420
GGCTCATGCT	CAAAATGGGG	AACGGGTATT	GACAGGCGAT	GAATTACTTG	ATTTTGTCAA	3480
TAACAAGTTA	TTCAAAGAGT	TGAAAGAGCT	TGAAATAACT	TCAAATATGC	CTATTCGAAA	3540
AACGATTGTT	AAATCAGCTT	TTGAAGATGC	GAACAACTAT	ATGAAAAATG	GCGTCTTGTT	3600
ACGCCAAGTC	ATCAATGTTA	TTGATGAAGT	TGATTTCAAT	AGCCCTGAAG	ATCGTCATTC	3660
GTTTAATGAT	ATTTACGAAA	AAATTCTTAA	AGATATTCAA	AATGCTGGGA	ACTCAGGAGA	3720
ATTTTATACG	CCACGTGCAG	CGACTGATTT	TATTGCCGAA	GTTCTTGACC	CAAAACTTGG	3780
AGAATCAATG	GCAGACCTTG	CTTGCGGAAC	AGGAGGCTTC	TTGACTTCGA	CTCTGAACCG	3840
TTTAAGTAGT	CAACGTAAAA	CTAGTGAAGA	TACCAAAAAA	TATAATACAG	CTGTTTTTGG	3900
TATTGAAAAG	AAAGCATTTC	CTCATCTTTT	AGCAGTTACA	AATCTGTTTC	TTCACGAAAT	3960
TGATGACCCT	AAAATTGTTC	ATGGAAATAC	TTTGAGAGAA	AATGTTCCGTG	AATATACGGA	4020
TGATGAAAAA	TTTGACATTA	TTATGATGAA	TCCACCTTTT	GGAGGGTCAG	AATTAGAAAC	4080
AATAAAAAAT	AACTTTCCAG	CAGAATTACG	GAGTTC TGAA	ACAGCTGATT	TATTTATGGC	4140
TGTCATTATG	TATCGTTTGA	AAGAAAATGG	TCGTGTTGGA	GTTATTTTAC	CTGATGGTTT	4200
TCTATTTGGT	GAAGGTGTAA	AAACTCGCTT	GAAACAAAAA	CTGGTAGATG	AGTTCAACTT	4260
GCATACGATT	ATTAGGTTGC	CTCATAGTGT	CTTTGCACCG	TATACAGGAA	TCCATACGAA	4320
CATTCTTTTC	TTTGATAAAA	CAAAGAAAAC	AGAAGAAACT	TGGTTTTATC	GTTTAGATAT	4380
GCCAGATGGT	TATAAAAAAT	TCTCGAAAAC	TAAGCCGATG	AAGTCAGAAC	ACTTCAATCC	4440
TGTTCTGTAC	TGGTGGGAAA	ATCGTGAAGA	GATTCTGGAA	GGTAAGTTCT	ACAAATCTAA	4500

1012

ATCATTTACA CCTAGTGAAT TGGCTGAGTT GAATTATAAT TTAGACCAGT GTGACTTTCC	4560
AAAAGAGGAA GAGGAAATCT TAAATCCCTT TGAGTTGATT CAGAATTATC AAGCGGAAAG	4620
AGCAACTTTA AATCATAAGA TTGATAATGT ATTAGCTGAT ATTTTGCAGT TGTGGAGGA	4680
CAAATAATGA CACCAGAACA ACTTAAAGCA AGTATCTCTC AAAGAGCGAT GGAAGGGAAA	4740
TTAGTGCCGC AAAATCCCAA TGACGAACCT GCAAGTGAAT TATTAAAGAG AATTAAAGCT	4800
GAAAAAGAAA AACTTATCAG TGAAGGAAAA ATCAAACGAG ATAAAAAGGA AACTGAGATA	4860
TTTCGTGGTG ATGATGGGAA ACATTATGGG AAGTTTGCTG ATGGAAGCAC TCAAGAAATT	4920
GATGTTCCCTT ATGATATTCC TGATACTTGG GAGTGGGTGA GGTTTTCTAC ATTGGTTGAA	4980
ATTGTCAGAG GTGGCTCTCC ACGACCAATC AAaGATTATC TTAATTCTGA AGTAGATGGA	5040
ATAAATTGGA TAAAAATAGG TGATACTGAA AAGGGTGAAA AGTATATAAA TAATGTTAAA	5100
GAAAAAATCA AAAAATCAGG GCTTAACAAA ACTAGATTTG TAAAAAAGG TACATTTTGT	5160
TTAACTAATT CTATGAGTTT TGGTAGACCT TATATTTTGA ATGTTGATGG TGCAATACAC	5220
GATGGATGGT TGGCTATTTT GAACTATGAA AACTCATTA ATAAAGATTA CCTATCTAT	5280
ATTCTTTCAT CAAATGTAGT TTATTCTCAA TTTCTATCTC TAATTAGTGG AGCTGTTGTG	5340
AAAAACTTGA ATAGTGATAA AGTTGCTTCT ATTCTTATCC CTCTCCCCC ACTATCCGAA	5400
CAACAACGAA TAGTAGAAGC AATCGAATCA GCTTTAGAAA AAGTAGATGA ATATGCTGAA	5460
AGTTATAATA GACTAGAACA GCTAGATAAA GAATTTCAG ATAACTAAA AAAATCTATT	5520
CTTCAATATG CTATGCAAGG AAAATTAGTT GAACAAGACC CAAATGATGA ATCAGTCGAA	5580
GTTTTACTTG AAAAAATACG AGCAGAAAAA CAAAACTCT TTGAAGAAG CAAGATTAAA	5640
AAGAAAGATT TGGACATTTT TATTGTTTCC CAAGGAGATG ATAACCTTTA TTATGGGAAT	5700
ATACCTATGA ATTGGGTTGT TATAAAAATA AAAGATATTT TTTCAATAAA TACAGGTCTT	5760
TCTTACAAGA AGGCGGATTT AAGCATTAAT AATAAAGGTG TTAGAATTAT ACGTGGTGGT	5820
AATATTAAGC CTTTAGAATT TTCTCTGTTG GATAATGATT ACTACATTGA TACACAATTC	5880
ATCTCCTCTG AGCAAGTTTA TTTAAAACAT AATCAGCTAA TAACACCTGT ATCAACCTCT	5940
TTAGAACATA TTGAAAGTT TGCAAGAATC GATAAAGACT ATGATGGTGT TGTGGCTGGT	6000
GGATTTATTT TCCAATTAAC ACCATTTCGAA AGTTCAGAGA TTATTTCAA ATTTCTATTA	6060
TTTAACTTGT CCTCTCCGTT ATTTTATAAA CAATTGAAAG CAATAACTAA ACTATCAGGT	6120
CAAGCTTTAT ATAATATTCC TAAACTACA CTGAGCGAGC TATTAATTCC GTTAGCTCCT	6180
TTTGAGGAAC AGGAACCTAT TACTCAAAAA GTTGAGAAAC TTTTGAAGG AGTAAATCAA	6240
CTTTGAAAAT GATTCTTTTC ATCTCTTCAT GATTAGAAAT AGGGATTAAT AATTCGGAGA	6300

1013

TACTGGTACT ATTTAATGTT TTCCCTTTGA TAGCATCTTT TGAATCACCT AAAGTAGAGA	6360
TAAGTGGCAA AAATATCATT AAGTAATCTC TGATAATATT TTCTTTATTA GCATAGGGGA	6420
ATATCGATAT AATGGCTTCA TTATGAGTGG CAGGAATATC CAATATGGCA ACTTTTCCAA	6480
TAGATAATTT AAAACTCATT AATAAAGTTC CTTTAGGTGA AATGTCTATT TTCTTTGATT	6540
TTAATGCTAA TTTAGAAATA GATTCTCTCG CATTAGTTAC ATAACCAGAT ATAGGCATAT	6600
CTGATATAGA TACCCAAGGT ATTTCAGTTC CCCAAAAAGT AGCTTCACTG CGTGGAGGAG	6660
TTTTTCCTAT TCTGAAGTTA ACTAGGCTAG CAAATTTAAT ATATCTCCAT GCTTCTGGGA	6720
TTTCATATAT AGGATAAGAG GTTGTTTCGT CTTTGTTCCC ATAATAAGAG CCATAATCAC	6780
AAAAATAGCA GGTAGTCAGT TTGACCACCT GTTATTTTTT ACCAATTAAC AATTTTATCT	6840
ACAATATTTT GTTGTTTCAGT AGCTGTTTTT CTTAGATAAA TTCGAGTAGT TTCTATACTT	6900
TCGTGTCCCA TCAAATCTGC AAGCAAGGCA ATATCATTTAT ACTTCGCTAA AAAATTCTTA	6960
GCAAATAAAT GCCTAAAAGA ATGAGGGTAA ATTACGTTAG GATTCATTTT GTATTTATCA	7020
GCATAATTTT TTAAGTGTG AGCAACTCCT CTGCTGTAA TTGGTTCGTT AAATTTATTC	7080
AAAAATAAAT AACCACCTCG GCGATTTTCT GATTCTAACC AACTAAGACA ACTATTTCTT	7140
AATTTTTTAG GAATGTACAG TCTACGAATT TTACCACCTT TTGAGTAAAT GTCAAAATAA	7200
CCGATTTCTA CATGCTCTAC TTTTAGTTTA ATAAGTTCAC TTACACGAGC CCCAGTTGCA	7260
CCTAAAAACC AAACGACAAA ATGCCATTTT AAAATACCAT CTTTTTTCAA ACTACGTTTA	7320
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ACAAATTTTA ATTTCAAATC ATCATGACCA ATAAAAGCCA GATATTTATT TACTCCTTGT	7440
AGTCGCAAAAT TGACAGTTTT AGGTTTAAAA TTGTCTAATA AATATCCTTT GTATTCAAAT	7500
AAATCTTCCA TTTTGAGTTC GTAATTCCTC AAGAAAAATC GAACACCATA AAGGTACGAA	7560
CGCACAGTAT TTTCAGCTAA ACCAGCTTTC TTCAAATGTA ATTCAAAATC TTCAACGTA	7620
AAACTCCTAT CTTATGTTTG ATAGAAATTC CACCGCACGT AAAACTATTA TACTAAATTA	7680
GTGCGTCAAT ATGGGCGAAA AATTGTTCTGA TTTTATCAAC GATTCTGGAT TGTTACAGAA	7740
GGGGTGGGAG GGGGATTAAA TATTCTTTTA TAGTTTTCGT TAATAATTCT TTTTGTTTG	7800
TACTACCCGA CGCTTTTTCT TCAATAACTG ACTGAACAAT AGGAGAGGAA AGAAAATTAT	7860
AGATGAAATG GCAATTAATA ACCCCCGATA AGACTCTTAT AACTGTAACA TGGCTATCTG	7920
CAACAGCCCA GCCATAAGGA TTTTATTTTT CATGGTAAAT AGCTAATCGT CCTAACGTAC	7980
CTAGACCTGT TGAATCCAC ATTAAATCAC CATCTCTTAG TAATCTTTCT TTCTGGTAAC	8040

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TATGAACTGT	TTCGGGATCA	ATAAATCTTG	CTAAGTCAAT	AGAAAAGCCA	GACCATTGAT	8100
TACATTTCTG	AGCAATCACA	GGGTATATAG	GAATATTTGA	ATATTTTGGA	GACTTCCCTC	8160
TTTGAATGTA	GGAGGTTATA	TCGTTTAACC	TCACCCATTC	CCAACTTTCT	GGTATTTTCA	8220
AAGGTACTTC	CTCATAATAA	GAGTTATCAT	CTCCTTGCGA	AACAATAGAA	ATGTCCAAAT	8280
CTTTCTTTT	AATCTTGCCT	TCTTCAAAGA	GTTTTTGTTT	TTCTGCTCGT	ATTTTTTCAA	8340
GTAAAACTTC	GACTGATTCA	TCATTTGGGT	CTTGTTC AAC	TAATTTTCCT	TGCATAGCAT	8400
ATTGAAGAAT	AGATTTTTTT	AGTTTATCTG	GAAATCTTTT	ATCTAGCTGT	TCTAGTCTAT	8460
TATAACTTTC	AGCATATTCA	TCTACTTTTT	CTAAAGCTGA	TTGATTGCT	TCTACTATTC	8520
GTTGTTGTT	GGATAGTGGG	GGGAGAGCAA	TTAATAATAG	ATTAAAAATTA	TAATCATTTGA	8580
TTGCAGGATA	ACTTGTTCCT	GATAGTTTAT	TATTAACACG	ATTGATAAAA	TTATCTGATA	8640
ATAAATAATA	TTTCAAATAT	GTTTCGTTAA	GTAAGTATC	CAAAACAATA	AATGCTGTAC	8700
TAGCTATCAA	ATACTCTTTA	AGTCTCTTAA	CTACAGCAAT	ATTTTTTTAGA	TATGGTCTAA	8760
CTGTTGAAAA	TAAGACACTA	TTCTGCGAAA	CTAATTTTCT	AGCACGGGAA	GGCGCTTGTT	8820
CAGGTGAAAG	ATATTGTAGA	TTTTTGTTAGT	TGATTATGTT	CTTTTTTCTA	TCAATACTAG	8880
ACGTATCTAT	ATACCTAAAG	GATTTCTCTG	GCTTATTTTG	CCCAAAATTC	CAATAAATTG	8940
ATTTTATCCT	CACCCACTCC	CAAGTATCAG	GAATATCATA	AGGAACATCA	ATTTCTTGAG	9000
TGCTTCCATC	AGCAAACTTC	CCATAATGTT	TCTTATGTGC	TTCAAGTATA	TAAAAAGGCG	9060
TAAAAATACG	CCTATAGATA	ATGGGGTTGA	AATAGGTTTA	TTGTTGATGA	GATTGTAGAT	9120
AATTCAATTT	TTTACTTCCA	ATCGAATATT	CAAATCCTCC	ACCTTTTCTG	CCTGTAATTG	9180
TTTCATCATA	AATTCAATAT	CTTCAGGATT	TTCCCTTTGG	CAACCTCGGC	AGAAATATTC	9240
TTCCGCTCGA	TCAGGATTCA	AAAATCGACA	AGCACAAACA	AAACAGTCGC	CATCATCATT	9300
TATTGAGATA	ATATAGTAGA	TTGAAATAAG	ATGTAAACAA	ATCGATTAGG	AAAGTTAAAT	9360
TAGTTTCTAG	AAATTTT TAG	CAGATGTAGT	GTAATTTTCT	AGTCTCAATT	TACTATGGCT	9420
TCAAATATAT	CTTTCGAAAA	AATATTTACA	GATGTGTAAT	TTTGAAGCTT	GCAAAAAGTTA	9480
GTAAACTTGT	AGATTTTCGAT	TTGAAAGTAAC	TTGTTTCTCT	GCCCCGATATT	GTTTTTGAAA	9540
TTGAATTTTT	CCATAGTGAC	TCCTTAATTT	TCTTCTACAC	GTCTGATGAT	AAATCTAATT	9600
CGCAAAAGAG	TCAAGAGGAT	TTTTCGAAAA	ATAAATAGCG	ACCGAAATCG	CTATTTTAAAG	9660
GGTTATAGGT	ATTTGATGGC	TTAGACTGCT	GTGTGACTGT	TTACCCACAG	GCAATCTTTC	9720
TTCTATATTA	GTATTAGTAA	AGGTCTAAAT	AATTATCAAT	TTCCCATTTGT	GAAACGAAGG	9780
TTGCATAACT	TGCCCCATTCG	ATTTCGTTTG	CTTCAAGGAA	GCTAGTATAG	ATGTGATCTC	9840

1015

CGAGAGCAGC	TTTAACCACT	TCATCTTCTG	TCAAAGCTTT	CAAAGCGTTG	TGAAGAGTTG	9900
ATGGAAGGTC	TGTAATACCA	GCTTCCTTGC	GCTCTTCTGC	TGTCATGATG	TAGATATTTT	9960
CTTCGATAGG	AGCTGGTGCT	TCGATTTTAT	TTTCAATACC	ATACAAACCA	ACTTCCAAAA	10020
GAACAGCCAT	AGCAACGTAA	GGGTTCGCCA	TTGGATCCAC	TGAACGCAAC	TCAAGACGAG	10080
TTCCCATACC	ACGTGAAGCA	GGTACGCGCA	CAAGTGGCGA	ACGGTTACGA	CCAGCCCAAG	10140
CAATGTAAAC	AGGCGCTTCA	TAACCTGGAA	CCAAACGTTT	GTATGAGTTA	ACTGTTGGGT	10200
TCATGATGGC	AGTATAGTTG	TAAGCATGCT	TGATCAAACC	GCCTAGGAAA	TGGTAAGCTG	10260
TTTCTGACAA	CTGCATTCCCT	TTTGGATCAT	TTGGATCAAA	GAAGGCGTTA	TTTCCTTCTG	10320
CATCAAACAA	GGACATATTA	CAGTGCATAC	CTGATCCAGC	AATACCAAAT	TTTGGCTTCG	10380
CCATAAATGT	TGCGTAAAGT	CCGTGTTTGC	GAGCAATGGT	TTTAACAACA	AGCTTAAAGA	10440
TTTGAATCTT	ATCACAAGCA	CGGAGAACTT	CATCGTACTT	AAAGTCAATC	TCATGCTGTC	10500
CAACCGCAAC	CTCGTGGTGA	CTCGCTTCTA	CTTCAAATCC	CATTTTGGTC	AAGACATTCA	10560
CAATCTCACG	ACGTGTGTTG	TCCGCAAGGT	CAGTAGGTGC	CAAGTCAAAG	TAGCCACCCCT	10620
TGTCATTAC	TTCAAGTGTT	GGGTCCCAT	TTTCATCCAA	CTTAAATAGG	AAGAATTCTG	10680
GCTCTGGACC	AAGGTGAAG	GATTTGAATC	CAACTTCTTC	CATGTGACGA	AGAGCTCGTT	10740
TCAAATTACC	ACGAGGGTCA	CCCGCAAATG	GTTCACCTTC	TGTTGTATAG	ACATCACAGA	10800
TCAGACCTGC	AACACTTCCA	TTTTCATCTC	CCCAAGGGAA	GACTGTCCAT	GTATCCAAGT	10860
CCGGGTACAA	GTACATATCC	GACTCATTGA	TACGTACAAA	ACCTTCAATA	GAAGATCCAT	10920
CAAACATAAC	CTTGTTTCGAC	AAGACCTTAT	CTAACTGTTT	ATCTGTAGCA	GGAATTTCTGA	10980
CGTTTTTCAT	GGTTCCCAA	ATATCTGAGA	ACATAAGACG	AATAAAGGTA	ACATTTTTTTT	11040
CCTTGACTTC	ACGACGAATA	TCTGCAGCTG	TGATTGGCAT	AAGTTTTCTC	CTTAATCTAT	11100
GACTACTTGC	GGTTGCCTAA	CCGCGACCAA	AAGGTGACTG	TACTGAAGCA	AAACGCCCCCT	11160
GTGGAGGAG	TTCATTGTGA	AGTGCACGAC	GTACTTCAGT	CTGACTAACC	GCTTCTTGG	11220
ATTCGCTTC	ACGTTTCAGCA	TATTTTTTCT	TAATGGCAGC	GATATTATAA	CCTTCAGAGA	11280
TATAATCTTT	GATTTCAAGC	AGACGATCCA	TGTCATTCAA	GGAATACATG	CGACGATTTT	11340
CTTCGTTTCG	ATCGGGCTTG	ATCAACTCTT	GATCTTCATA	ATAACGAATC	TGACGCGCCG	11400
ATAGATCGGT	CAACTTCATA	ACACTGCCGA	TAGGAAAAAC	AGCCATATTT	CGGCGAAAT	11460
CTTTTCTCTT	CATTTACAAT	TTCCTTCTTT	CTGTCTATTA	TAGTCTAAAA	AAAGACAAAC	11520
GTCAATTGAT	AATGTTATAA	AATGTAACAT	TATTTTTCTT	TTTTCTCTAA	AAAGAGACGA	11580

1016

ATACGATCAA	TATCGTAATT	TACGATAAAT	GCGACAAAAA	CTCCCATAAA	CGTTTCTAAT	11640
ACACGCACAA	ACACGTACAA	AATTGTCTCA	CCACTTGGAA	TTGATAGGGT	AATGATTAAAC	11700
ATAGCTGCTA	CACCACCAAT	AACCCCTGCT	TTGTTATTCA	TGGCTACATT	TGTCATAATG	11760
GTTAACATGG	TGCAGATTGG	AACAAC TACC	AAGGTCACCC	AAAAGGCTTC	GTGGAAAAAG	11820
GTATTTAATA	AGAAGAAGAC	CAAGGCATAG	AGTCCACCGA	TACTATTTCC	TAGAATACGC	11880
GAAGTCCCAA	AATGAACACT	CTCATCAAAA	CTCTCCCTCA	GGCTAAAAAC	GGCTGTCAAA	11940
GCACCAATTT	GAAGACCTTT	CCAGCCAAAA	AAGCCAAAAA	TCAAGAGAAC	TAGAAAAACA	12000
GCAATACCTG	TTTTAAAGGT	TCGCATACCA	AGTTTGAAC T	GGGATTTATC	GAATTTATAT	12060
TTTTTAAAT	AATCATAAT	CTCAACTTTC	TATTTCCATT	TTATCATAAA	TCGGTGATTT	12120
TTATGAGTAA	TAGTTGAGAG	GAAGCGTTTT	TATTTTAAAGC	AAAAGAAAAG	AGGAAC TTTC	12180
ATCCCTCTCT	TCTTTGATTT	ATTTATAAAA	TCTTATTTTT	CTGTCAAGGC	TGCAAGTCCT	12240
GGAAGAACCT	TACCTTCAAG	AAGTTCATT	GATGCTCCAC	CACCCGTACT	AATCCATGAG	12300
AAC TTGTCTG	CACGGCCAAG	GTTAATCGCT	GCGGCAGCTG	AGTCACCACC	ACCGATGATT	12360
GATTTAACTC	CTGGTTGTTT	CACGATAGCG	TCCATCACAC	CGATTGTACC	AGCTTGGAAG	12420
TCTGGGTTTT	CAAATACACC	CATAGGTCCG	TTCCATACGA	CTGTTTTGGC	ACCAGTCAAA	12480
GCTTCGTCAA	ATTTGGCGAT	AGATTTTGGA	CCGATGTCAA	GACCAAGGAA	GCCTTCAGAA	12540
ACTGCTTCAC	CTTCAGTGTC	ACGCACTTCA	GTGTAACCAG	CAAATGCGTT	AGCTTC TTTT	12600
GAGTCAACTG	GCAAGATCAA	TTTACCATT	GCTTTTTCAA	GAAGAGCTTT	CGCAACATCC	12660
AATTTGTCTT	CTTCTACAAG	TGAGTTACCG	ATTTGATAC	CTTGTGCTTT	G TAGAATGTG	12720
TAAGTCATCC	CACCACCGAT	AAGGACGTTA	TCAGCTTTTT	CAAGCAAGTT	TTTCGATAACA	12780
CCGATCTTGT	CTGAAACTTT	TGAACCACCA	AGGATAGCCA	CGAATGGACG	TTCTGGAGTT	12840
TCAACTGCTT	CTTGGATGTA	GGCAATTTCG	TTTTCAAGAA	GGAAACCAGC	AACTGCTTTT	12900
TCAACGTTTG	CTGAGATACC	AACGTTAGAT	GCGTGTGCAC	GGTGAGCTGT	ACCGAATGCA	12960
TCGTTTACGA	AGATACCATC	TCCAAGTGAT	GCCCAGTATT	TACCAAGTTC	AGGATCGTTT	13020
TTAGATTCTT	TCTTGCCGTC	AACATCTTCG	TAACGAGTGT	TTTCAACCAA	GAGAACTTGT	13080
CCATCTTCAA	GAGCGTTGAT	TGCCGCTTCT	AATTCAGCAC	CACGAGTGAC	ACCTGGGAAA	13140
ACAACATCTT	GACCAAGTTT	TGCTGCCAAG	TCAGCTGCTA	CAGGAGCAAG	TGATTTACCA	13200
GCTTTATCAG	CTTCTCTTTT	CACACGTCCA	AGGTGAGAGA	AAAGAATTGC	ACGTCCACCT	13260
TGTTTCGATG	TGTACTTAAT	AGTTGGAAGA	GCTGCTGTGA	TACGGTTATC	GTTAGTGATT	13320
ACGCCATCTT	TCAATGGTAC	GTTGAAGTCA	ACACGAACGA	GGACTTTTTT	ACCTTTCAAG	13380

1017

TCAACGTCTT TAACAGTAAG TTTTGCCATG TTACAAAAAC TCCGG

13425

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 905 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

GATTATCCTT ACCGnGAAT TTCCGAGGG GTTCTAGCAG CAATCTTAGG AATCTATGAA	60
CGAATGATTG GCTTTCTGGC CCATCCCTTT AAAGACTTTA AAGAAAATGT TTTGTACTTT	120
ATTCCAGTTG CCATCGGTAT GCTTCTGGGA ATCGGCTTAT TTTCTACCC GATTGAATAC	180
CTGCTTGAAA ATTATCAGGT TTTGTATTA TGGAGCTTTG CGGGAGCTAT TATCGGTACA	240
GTTCTTAGCC TCCTCAAAGA ATCAACTCGA GAATCTGACC GAGACAAGAT TGATTTAGCT	300
TGGTTATGGA CAACCTTTAT CATTTCTGGA TTAGGACTCT ATGCCTTAAA TTTTGTTCGT	360
GGAACCTTAA GCGCCAGCTT TCTTAACCTC GTCCTAGCAG GCGCACTATT GGCCCTTGGC	420
GTCTTGCTC CTGGCCTCAG CCCATCAAAT TACTTTTGA TTTTGGGACT CTATGCTCCT	480
ATGTTGACTG GTTTTAAAC TTTTGATTTC TTGGGAACCT TCTTTCCGAT TGGAATTGGT	540
GCAGGTGCAA CTCTCATCGT TTTTCAAAA TTGATAGATT ATGCCTTAAA CAACTACCAC	600
TCACGCGTCT ATCATTTCAT CATCGGTATC GTCCTATCAA GTACCCTTTT GATCTTAATT	660
CCAAATGCAG GAAACGCTGA AAGTATCCAA TACACAGGAC TTTCACCTGT CGGTTATGTC	720
ATCATCGCCT TCTTCTTTGC GCTGGGAATC TGGCTTGGTA TTTGGATGAG TCAATTGGAG	780
GATAAATATA AATAATGGCA AAAAAAGTTA AAATCAAAAA AACATTGGTG GAACAAATCC	840
TATCTAAAGC AGCTATCCCT CATCAGGGGA TTCAAATCAA TGCCCTAGAA GGAGAGCTTC	900
CTCAA	905

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

1018

CTTGAATTAA ATAAAAACG TCATGCGACT AAGCATTTTA CTGATAAGCT TGTGATCCC	60
AAAGATGTGC GTACGGCTAT CGAAATTGCA ACCTTAGCGC CAAGCGCCCA CAACAGCCAG	120
CCTTGGAAT TTGTGGTGGT ACGTGAGAAA AATGCTGAAC TGGCAAAGTT AGCTTATGGT	180
TCCAATTTTG AACAGGTATC ATCAGCGCCT GTAACCATG CCTTGTTTAC AGATACGGAC	240
TTAGCCAAAC GTGCTCGTAA GATTGCCCGT GTTGGTGGTG CTAATAACTT TTCTGAAGAG	300
CAACTTCAAT ATTTTATGAA AAATCTGCCA GCTGAGTTTG CCCGTACAG TGAGCAACAA	360
GTCAGCGACT ACCTAGCTCT CAATGCAGGT TTGGTTGCCA TGAAGTTGGT TCTTGCATTG	420
ACAGACCAAG GAATTGGTTC TAACATTATT CTTGGTTTTG ACAAATCAAA AGTTAATGAA	480
GTTTTGAAA TCGAAGACCG TTCCGCCCA GAAGCTTGA TCACAGTGGG TTATACAGAC	540
GAAAAATTGG AACCAAGCTA CCGCTTGCCA GTAGATGAAA TCATCGAGAA AAGATAGAAA	600
GAAGAAAAA TGACAGCAAT TGATTTTACA GCAGAAGTAG AAAACGCAA AGAAGACCTC	660
TTGGCTGACT TGTTAGCCT TTTGAAATC AATTCAGAAC GTGATGACAG CAAGGCTGAT	720
GCCCAGCATC CATTTGGGCC TGGTCCAGTA AAGCCTTGG AGAAATTCCT TGAAATCGCA	780
GACCGCGATG GCTACCCAAC TAAGAATGTT GATAACTATG CAGGACATTT TGAGTTTGGT	840
GATGGAGAAG AAGTTCTCGG AATCTTTGCC CATATGGATG TGGTGCCTGC TGGTAGCGGT	900
TGGGACACAG ACCCTTACAC ACCAACTATC AAAGATGGTC GCCTTTATGC GCGCGGGGCT	960
TCGGACGATA AGGGTCCTAC AACAGCTTGT TACTATGGTT TGAAATCAT CAAAGAATTG	1020
GGTCTTCCAA CTTCTAAGAA AGTTCGCTTC ATCGTTGGAA CAGACGAAGA ATCAGGCTGG	1080
GCAGACATGG ACTACTACTT TGAGCACGTA GGACTTGCCA AACCAGATTT CGGTTTCTCA	1140
CCAGATGCTG AATTTCCAAT CATCAATGGT GAAAAAGGAA ATATCACGGA ATACCTCCAC	1200
TTTGCAAGGAG AAAATACAGG TGTTGCCCGT CTTACAGCT TTACAGGTGG TTTACGTGAA	1260
AATATGGTAC CAGAATCAGC AACAGCAGTC GTTTCAGGTG ACTTGGCTGA CTTGCAAGCT	1320
AAACTAGATG CCTTTGTGTC AGAACACAAA CTTAGAGGAG AACTCCAAGA AGAAGCTGGC	1380
AAATACAAGG TGACGATCAT TGGTAAATCA GCCCACGGTG CTATGCCTGC TTCAGGTGTC	1440
AATGGCGCAA CTTACCTTGC CCTCTCCTC AGCCAGTTTG GCTTTGCTGG TCCAGCCAAA	1500
GACTACCTTG ACATCGCAGG TAAAATTCTC TTGAACGATC ATGAGGGTGA AAATCTTAAG	1560
ATTGCTCATG TGGATGAAAA GATGGGTGCT CTTTCTATGA ATGCCGGCGT CTTCCACTTC	1620
GATGAAACAA GTGCTGATAA TACCATTGCC CTCAACATCC GCTATCCAAA AGGAACAAGT	1680
CCAGAACAAA TCAAGTCAAT CCTTGAAAAC TTGCCAGTTG TTTCTGTTAG CCTGTCTGAA	1740
CACGGTCACA CGCCTCACTA TGTGCCAATG GAAGATCCAC TTGTGCAAAC CTTGTTGAAT	1800

1019

ATCTATGAAA AACAACTGG CTTTAAAGGT CATGAACAAG TCATCGGTGG TGGAACTTTT	1860
GGTCGCTTGC TAGAACGCGG AGTTGCCTAC GGTGCTATGT TCCCAGACTC GATTGATACC	1920
ATGCACCAAG CCAATGAATT TATCGCCTTG GATGATCTTT TCCGAGCAGC AGCAATTTAT	1980
GCCGAAGCTA TTTACGAATT GATCAAATAA AACGATAGAA GTCTGAGATC TTATGCTTGG	2040
ACTTCTTTTT GGAGGGAAAG TAGATGTCTC AAATCGAAAG AATCAAACAG GCTATCATGG	2100
CGGATTTCGA GAATGCCAGC TATACAGAGC GTGGCATTGA GCCTCTCTTT GCAGCGCCAA	2160
AAACTGCTCG CATCAATATC ATCGGTCAGG CTCCGGGACT TAAAACTCAA GAAGCAGGCC	2220
TTTACTGGAA AGATAAAAGT GGTGACCGCT TCGGGGACTG GCTAGGTGTG GATGAAGATA	2280
CCTTTTACAA TTCAGGTAT TTTGCTGTTT TGCCTATGGA TTTCTACTTT CCAGGACATG	2340
GCAAGTCGGG TGATCTTCCG CCTCGTACAG GTTTTGCAGA AAAATGGCAT CCGCAGGTCT	2400
TACAGGAATT GCCTGATATT CAGTTAACCC TCTTGATTGG GCAATATGCC CAAGCCTACT	2460
ATTTACAGGA GAAAATCAGT GGGAAAGTAA CGGAGAGGGT GAAACACTAT AAAGACTATC	2520
TGCCAGCCTA TTTTCCGCTA GTTCACCCAT CACCACGAAA TCAAATCTGG ATGGCCAAAA	2580
ATCCTTG GTT TGAGGCAGAA GTAGTGCCAG ATTTGAAAAA AAGAATTAAA ACCATTTTAT	2640
AGTCAATGAA AATCAAAGAG CAAACTAGGA AGCTAGTCGT AGGCTGCTCA AAGTACAGCT	2700
TTGAAGTTGC AGATAAACT GACGAAGTCG GTAACATACG CACGGTAAGG CGACGCTGAC	2760
GTGGTTTGAA GAGATTTTCG AAGAGTATTA GAAGAAAAAG AATGAAAGAA ATAGCCTTTG	2820
ACGCATTTTA CCAGCTTTAC CAAAACGACC AGCTTTCTTT AGTGGATGTG AGAGAAGTGG	2880
ATGAGTTTGC AGCTCTTCAT TTAGAAGGTG CCCACAACCT ACCGCTTAGT CAATTGGCTG	2940
ATAGTTATGA TTAATTGGAC AAAGATCGCT TGCATTATAT TATTTGCAAA TCTGGAATGA	3000
GATCGGCGCG TGCTTGCCAA TTCCTATTAG AACAAGGTTA TAATGTTATC AATGTCCAGG	3060
GTGGCATGTT AGCCTTTGAA GAACTTTAAA ATTTTGCATT TCTCCTACTT GGTGTGGACT	3120
GGGTAGGAGA GTTTTATTTT TAGATAATTC TTATTTTTAA GAAAATTGAA AACATTTAAT	3180
ATTTGCCTCG TGATGCTTTT TTCAGACTCC TAATCGTGGT ATACTAGGTC AGTATTTTAT	3240
AAATATGAAG GAGATTTTTA TGGCTAAAAA AGGTACCCTA ACAGGTTTGC TCCTGTTTGG	3300
AATATTTTTT GGTGCGGGGA ACTTGATTTT TCCGCCTTCT CTAGGTGCTC TATCTGGAGA	3360
ACATTTTCTT CCTGCCATCG CAGGTTTGT CTTTTCAGGC GTTGGTATCG CCGTCTTGAC	3420
CCTTATTATT GGAACGCTAA ATCCTAAAGG ATATATCTAC GAGATTTCAA CGAAGATAGC	3480
GCCTTGGTTT GCGACTCTTT ACCTCTCAGT TCTTTACTTG TCAATCGGTC CATTCTTTGC	3540

1020

TACCCACG	ACTGCTACAA	CAGCTTACGA	AGTAGGGATT	AGCCCCCTTT	TGTCGGATGC	3600
AAATAAAGGA	CTTGGCTTGA	TTGTATTTAC	GGTTCTGTAT	TTTGCGGCAG	CCTATTTGAT	3660
TTTCGCTTAAT	CCATCAAAAA	TCTTAGACCG	CATTGGACGT	ATTTTAACGC	CAGTCTTTGC	3720
AATTTTGATT	GTATCTTGG	TCGTCTGGG	AGCTATCAAA	TATGGTGGAA	CAAGTCCTCA	3780
AGCTGCTTCA	CTGCTTATCA	AGCTTCTGCC	TTTGGTACAG	GTTTCCTAGA	AGGTTACAAT	3840
ACCTTGGACG	CCCTTGCCTC	AGTGGCCTTT	AGCGTAATCG	CAGTTCAAAC	CTTGAAACAA	3900
CTTGATTTT	CAAGTAAGAA	AGAATACATT	TCAACTATTT	GGGTGTTGG	TATCGTTGTT	3960
GCCCTTGCCT	TCAGCGCTCT	TTACATCGGT	TTAGGTTTTT	TTGGAAATCA	TTTCCCAGTA	4020
CCAGCTGAAG	CGATGAAGGG	TGGAACACCA	GGTGTTTACA	TCTGTGCACA	AGCCACTCAA	4080
GAAATCTTTG	GCTCAACAGC	TCAACTCTTC	CTTGCAGCTA	TGGTTACCGT	AACCTGCTTC	4140
ACAACGACTG	TTGGTTTGAT	TGTGTCAACA	GCTGAGTTCT	TTAATGAGCG	CTTCCCACAA	4200
ATCAGCTACA	AGGTTTATGC	GACAGCCTTT	ACCTTGATTG	GATTTGCTAT	TGCCAATTTG	4260
GGTCTTGATG	CGATTATC					4278

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1953 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

ACCCGATCAA	ATGACAAAAG	CTAACTTTGG	TGTCGTAGGT	ATGGCCGTAA	TGGGTCGTAA	60
CCTTGCCCTT	AATATTGAAT	CTCGTGGTTA	CACAGTTGCT	ATCTACAACC	GTAGTAAAGA	120
AAAAACGGAA	GATGTGATTG	CTTGCCATCC	TGAAAAGAAC	TTTGTAACCA	GCTATGACGT	180
TGAAAGTTT	GTAAACTCAA	TCGAAAACC	TCGTCGTATC	ATGCTGATGG	TTCAAGCTGG	240
ACCTGGTACA	GATGCTACTA	TCCAAGCCCT	TCTTCCACAC	CTTGACAAGG	GTGATATCTT	300
GATTGACGGA	GGAAATACTT	TCTACAAAGA	TACCATCCGT	CGTAATGAAG	AATTGGCAAA	360
CTCTGGTATC	AACTTTATCG	GTACTGGGGT	TTCTGGTGGT	GAAAAAGGTG	CCCTTGAAGG	420
TCCTTCTATC	ATGCCTGGTG	GACAAAAGA	AGCCTACGAA	TTGGTTGCGG	ATGTTCTTGA	480
AGAAATCTCA	GCTAAAGCAC	CAGAAGATGG	CAAACCATGT	GTGACTTACA	TCGGTCTCTGA	540
TGGAGCTGGT	CACTATGTGA	AAATGGTTCA	CAATGGTATT	GAGTACGGTG	ATATGCAATT	600
GATCGCAGAA	AGCTATGACT	TGATGCAACA	CTTGCTAGGC	CTTTCTGCAG	AAGATATGGC	660

1021

TGAAATCTTT ACTGAGTGGG ACAAGGGTGA ATTAGACAGC TACTTGATTG AAATCACAGC 720
 TGATATCTTG AGCCGTAAAG ACGATGAAGG CCAAGATGGA CCAATCGTAG ACTACATCCT 780
 TGATGCTGCA GGTAACAAGG GAACTGGTAA ATGGACTAGC CAATCATCTC TTGACCTTGG 840
 TGTACCATTG TCACTGATTA CTGAGTCAGT GTTTGCACGC TACATTTCAA CTTACAAAGA 900
 AGAACGTGTA CATGCTAGCA AGGTGCTTCC AAAACCAGCT GCCTTCAACT TTGAAGGAGA 960
 CAAGGCTGAA TTGATTGAAA AGATCCGTCA AGCCCTTTAC TTCTCAAAAA TCATTTTCATA 1020
 CGCACAAGGA TTTGCTCAAT TGCGTGTAGC CTCTAAAGAA AACAACTGGA ACTTGCCATT 1080
 TGCAGATATC GCATCTATCT GGCCTGATGG CTGTATCATC CGTTCTCGTT TCTTGCAAAA 1140
 GATTACAGAT GCTTACAACC GCGATGCAGA TCTTGCCAAC CTTCTTTTGG ACGAGTACTT 1200
 CTTGGATGTT ACTGCTAAGT ACCAACAAGC AGTACGTGAT ATCGTAGCTC TTGCGGTTCA 1260
 AGCAGGTGTG CCAGTGCCAA CTTTCTCAGC AGCTATTACT TACTTTGATA GCTACCGTTC 1320
 AGCTGACCTT CCAGCTAACT TGATCCAAGC ACAACGTGAC TACTTTGGTG CTCACACTTA 1380
 CCAACGTAAA GACAAAGAAG GAACCTTCCA CTACTCTTGG TATGACGAAA AATAAGTAGG 1440
 TCAGCCATGG GGAAACGGAT TTTATTACTT GAGAAAGAAC GAAATCTAGC TCATTTTTTA 1500
 AGTTTGGAAC TCCAGAAAGA GCAGTATCGG GTTGATCTGG TAGAGGAGGG GCAAAAAGCC 1560
 CTCTCCATGG CTCTTCAGAC AGACTATGAT TTGATGTTAT TGAACGTTAA TCTGGGAGAT 1620
 ATGATGGCTC AGGATTTTGC AGAAAAATTG AGCCGAAC TAACCTGCCTC AGTCATCATG 1680
 ATTTTAGATC ATTGGGAAGA CTTGCAAGAA GAGCTGGAAG TTGTTTCAGCG TTTTGCAGTT 1740
 TCATACATCT ATAAGCCAGT CCTTATCGAA AATCTGGTAG CGCGTATTTC GCGATCTTC 1800
 CGAGGTCGGG ACTTCATTGA TCAACACTGC AGTCTGATGA AAGTTCCAAG GACCTACCGC 1860
 AATCTTAGGA TAGATGTTGA ACATCACACG GTTTATCGTG GTGAAGAGAT GATTGCTCTG 1920
 ACACGCCGTG AGTATGACCT TTTGGCGACA CGG 1953

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

CCGGCAGTAC ACGAGCTTGG GGAACAGCCA CTGGAACGAT GAGGTGTGAG CTCAAAATAT 60

1022

CCTCCAGTTA TGTTTTTCCT AATAGTATAC CGGAAGAGTG AAAGGATTTT ATAATGGAGC	120
GGTTACAAAG AACCTACTTT CTATTAAACA GTATACTATG AAAATGTGAA AATTTAACAT	180
TTTTTTGTAC AAATTTTATA AATTATTGCC TTTTAAATAT CAATAGTTAA TCTCTTATCC	240
AGATCCCCCT TGTGTAACT TTATCTTTAT AAGCTTCAAG GCCCCTATCC CATCTATTTG	300
CAACAATTAG ATCACTTTGT TTTGTAAATA GTTCAAAAT CTTTCAATA ATTACGTTAT	360
CTATACTAAC GTTTAAATTT GGTTCATATA CTAAAATTTT TATACCGACA ATCAATAGTT	420
CATTAATTAT ACTTAAATA GCTGACTCTT TGAATTATC TGAATTATAT TTCATCCCCA	480
ATTTATATAT TCCTACTATC TTTGGCTTTC GTTCCAATAT TTGTTTAACT ATGAACTGTT	540
TTCTATTTGT GTTTGAAATA TCAATCGCTT CTATCACTGG GGCATTTATT TCTATAAATT	600
CTTTTTTTTAA TTGTTTAGTA TCTTTGGGAA GACAATATCC TCCAAATCCA AAAGAAGGAT	660
TATTATAAAA ATTTCCAATT CTTGGATCTA AACAAACACC TTTTATTACA ACTTCAGCAT	720
TTAAGCTTCT CCTCTCAGCA AAAGAATCTA GTTCATTAAA AAAGCAACAC GGAGAGCTAA	780
GAATGTGTTA GAAAAAAGCT TAATTGCTTC TGCTTCAGTA GGAGAACTA ACATAACATT	840
TTTAATATTG GCAGTACTAT GAGTACTAAT CGAAAGGAAC AACTCTGCAA TTTTCTTCC	900
TTCAACTGTC TCATCTCCAA CAACTATGCG ACTTGATAT AAATTATCAT ATATAGAACA	960
ACCTTCTCTC AAAAATTCAG GGACAAAAAT GATATTTTTT GTATCAAACA GCCTTTTTTAA	1020
TTTGTTTTGA AAGCCGATCG GAACTGTTGA CTTTAAATA ATCTTTCCAT TAGGTTTTAC	1080
CCTCAGAATC TTCGATACCG TTTGTTGAT TTCATATGTA TTAAACTAC CAATTTTCTC	1140
ATCATAATCT GTCGGAAGCG CAATAATATA ATAATCAATA TTATTTTTTAA TTTCAGAAAA	1200
TGTATCAAAA AAAGTAATAT TTAAGTTATT CTCGCAAAAA AACTTCATAA GCTCTTCATT	1260
TTTAGATGGA AGAATGCCCT TTTTAAATT ATTTATTTTT ACAGAATCTA TATCATATGC	1320
AACAACTTA TATTTAGATG CAAATAGTAA CGCGTAGGCC AGCCCAACAT GCCCCAAACC	1380
AATTACTGCT ATATTCATAA AACTACTTCC TTATTTCTTA ATCCAAAATC TAATAGAAAT	1440
AGCTGCCCCA TTCCTTAAAT ACAACTCTTT AATATTGTTT AAAAGTTTTT CAACTGATTT	1500
CCAGATTATC AAAATCTGAG ATTTATAGCA CAATATTGAT GATATTCTAT CAATATAATT	1560
TTTTTCATCA AGTTCCTCTT GATACATTTT TAATCTTTA GTTTTCCCA TATAACTAAC	1620
CATACTACTA TCACCTACAT ATGGGAAGTC CTCATAATAT ATTACTTTAT AACGCATAAA	1680
TTCAAGCGCC CTTCCAATAC TATTACAAA AACATGAGCA ACATGGTCAC CAAGTGAAAG	1740
CGGACAATAT ACGACACATT TGTCGTCTAA ATGCATTAAC AGCTCTTTTA TGATATCATT	1800
CTTAATGTG TCCTCATTTT TTAATTCATT ATAGATATGA CGGTATAGAA AATTGCCATT	1860

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TCTATCTTTC CTATAGAGAC ATTCATAGTA CGATAAGTGT CTAAAATCAC ATTGTAGACG	1920
TTCACAAGCT AACCTGTCTT CTTTCTTCCT TTCTTCAATC GGATATTTCC CAAGGTTACA	1980
CAACTTATGA AATTGCTTAG CAGAGGGCTG TAGCTGTTGG CTCAAAGGGT AACCAGAAAA	2040
TATAGTAATA ACAAGTACAA TTTCTCCTTC TGAAGTTAAT TTTGAAATAT AATCACCACA	2100
GGAAAAAATT GCGTCATCTA AATGTGGAGA TAAAAAGATA TACTTAGTAT TGTTACTCAT	2160
AACCATTCCC TCTACAATTT ATCTAAAAAC TCACTAAGTG TCTGATTAAA TTCCACATCA	2220
TCAAAAAAAT TCACCTTATT CTTAATAATG AATATTTTCGT TAAATAAACA TATATATAAA	2280
TATTTCAATA TCCTTTCAAT ATCATCCTCT AAATTCCTCT CAATATTTTG TATCAGCCCA	2340
TTTACAATCT TATTAAAAAA GATAAGCTCT TTATCTCTAA AATTAAATAT TTTCATACAA	2400
CTGTTGTATC GAAAAATATA TAAAAAATTT TTTACTAATG TTTGAATATT TAAACAACCTA	2460
AATAAATGAG TTGTACCCGG GACACTATTT ATGTTATCAA GAACACTATC TTGAAACCTC	2520
AACTCACAGT TCTTTTGTG AAATCTTTTT TTATCGTTTA GATCTGATAT TTTTGTAGAC	2580
ATTTCAACAA TCTCAGACAT TTTATATGGA TATCTAGGAT GAATGCCAAA ACTATGCAAA	2640
ATGAACTGCA CCCCAAAAGT TAGACAGAAT AAATCTAACT TTTGGGGTGC AGTTCATAAG	2700
ATTGGGATAT TTTTTTTGTAG CTAGAACTAG TAGAAATATA TAGTCAAATA ACAGATACCT	2760
TAAGGGTTTC TCATCTACAT AAAAAATGA TACTTTTTTC TCTTCAGTAA TTACCTCATA	2820
AGCTTCACAA TAGAATCTCA TGTTTCCCTC CCCTATATTC TTAAATAAAA TCCTTTGGAA	2880
ATTGATATAT CTTAGTAAAA TATTGTTTAA GTTCCGGATG CGGAGCATGG GTAACAATAA	2940
TGACAGTCAA ATCCTCTCTA TCTAATATCT TACGTTCAAT CGCTAACGAA GTTCTCCTAT	3000
CGATAGCAGA AGTTCCTCG TCAATTAATA CTATTTTCTT ATTTCTAATT AGCCCTCTAG	3060
CTAAAGTAAT TTTTGTGTTT TGCCCTCCTG ACAGTAATCT CCCATCATCA CCAACATAAT	3120
AATCTAAAT GTTATTAGGA AAATCTTTTA CACTCAAACC AACTTGCTCT AAAGACTGTA	3180
GTATTCTTTC ATCAGTATAA TTTTCTTCCA ATAAAAATTT ATCTCTAATC GTACCTTCAA	3240
ACAAATAAGC TTTTGTATCT ACATATAGAA CATTGGAAC CATATTTAAA TAGGAGGTTT	3300
TTTTTATATC ATCCCCGAG AATCGCAATT CTCCACTATA ATCTCTCAA AAGCCATTCA	3360
ATAATTTTAA TAATGTAGAT TTCCCGCTTC CACTTTCACC TAAATTTAAA TACTTTTCAT	3420
TACGTTGAAA AAAAAATTT AAGTTTTTTA ATATTTCTTT ATCTCCATAC TTATAGCAAA	3480
TATTTTTTGC TTCATATAAC GGAAATCTC TATTCACCTC ATTTGGTTCG ATATCATTC	3540
TTTTTATTGA CTCAATTGGA TTAATTGAAT ACAATTTTAA AAAAATAGGC TTCGTACCAA	3600

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TAATAGAGGA TAATTGACCT CCTAATTCAC CTAGCGCTGT AAAAATAACA CCTGTTAGTG	3660
CTCCTATTGC TTCAATAGTA CCAATTTTCA CTATTCCTTT TATTGCAAGA TAGCCTGTTA	3720
AAAAACGAG AGATATCTGA AAAAAATAT TGAGAAAGAA GCTAATAGCG CCTGCTAACG	3780
TTTCTACAGT TGTCTTTCTT TGTATAACCA TCTTTAATAA AATTCCTGCT TCTTTAATTT	3840
TCTTAGGCAA TACATATAAA AGATTCAAGG ACGCTAACAC ATCAAATCCA TTCAATATAG	3900
TCTCACTAGA TTTTAAAAA GCTTCATTTT GGTAGTTAA ATTTAGACTA ACTTCTCGCA	3960
TTTTCGATGC AAAGATTTT GGTACAAGTA GCATAATCAT TAATGAAAAC AAGGTGGCTA	4020
CAGTCAATGA CCAATGATAG TGATTAAGAG TCACAACGTC AAATATAGTA CCAGAAATTC	4080
CTTTTATTAC TAAAAAAGT TGTTTAAACG CCTGATCATT TAAAGTCTGA ACATCATTAT	4140
TTAGCCACGA AAGATATGTT CCTGATGATT TACTATGAAA TTCTTGATAG GTAGAGTTAG	4200
AGATGTCTGT GGCAACTCTA TTTCGAATCT CTAGATTAAA CTCTTGATC ACTTCAACCT	4260
GATAATTTTT CACTACCCAG TCAAGGAATA TTATCCCACA CCAGACAATC ATTTGGTAGA	4320
TTGACAATTT CAAAAACCGC TCTAAATTCA TCGCAATTAA TTCATTCAAC ACCAGAGCAT	4380
TAATAGTTGC TGCATAAATT AGCAATAATT GACCAGCAAC AATAAATATC GTTAATAAAC	4440
TAAATTTTTT TATATTTGAT TTTATAATAG TATACACAAT AGTTTCTCAC TTTCTAAATT	4500
TTAATTGAAC ATAGTTTTCA TATATACAAT AGAAAAAACC AAAATGATAT AATAACATAT	4560
ATTTCAAAA AGAAATTCGT TAAAAATTTT TTCTTCTCTT GCCTTCTTGA TTACTTTTAA	4620
AGCCTTGCAAT TTGTCTCCTA TTAATAGTAA CCGCTTTATG TTTAAAGAAT AATATTTCTT	4680
TGTAACCAAT ATTCTCTCGT TGAAACTCAA TAAATTAAAA TATTTCCCTAC AGTAATTATA	4740
ATATTCTTCA TCTGCATTAA TTGTTTTTTG TGTCACTCCA GTGATACCGT TTTCTTTACT	4800
GTGAGCGTAG TAATTCACCA AGAATTCTCG CACTATATCA ATTTGGTATC CTTGAACAAG	4860
TAGTTTTAAT AAAACAACAC CGTCCTGATG TGAATCTATT TTCTCAAAAC CATTAATTAA	4920
TTCTAGCACC TCTTTTTTAC ACAACCAAAA TGACGTACCT GCTATATTGT GAACCATTTG	4980
AACAAACAAG GGATTTCCAA CAAAATCGGT CTTCTCCTCT TCTCGGTGAC CATTTGGATA	5040
AATTATTATT CCATACTAC AACTAAAGC TAAATTCTTC ATTCTACTCT TTTTAAAACA	5100
AGCCATCAAC TTTAAAATTC GATCTGGCAT ATATTCATCA TCATCGTCTA AAAATGATAT	5160
ATACTTACCT CTAGAATTTT TGATACCTAT GTTTCTGGCA TTAGTTGCAC CTAAATCTTC	5220
ATTACTTAAA ATTAACCTAA TTCTATGATT GGTATAGCCA AATTGATGGA TAATTTTATT	5280
TCTTAAATTT ACATTACTAT AATTATCATC AATAATTATA ACTTCGATAT TTTTATAACT	5340
TTGATGTAAA CAACTTTTCA CAGCTCTAAT CAGAGATTCA TACCTATTAT GTGTTGGTAT	5400

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TATAATACTT ACTAATTCTT GATCTATATT CCTATCCATG ACTACTCTTC TCTAATAATT	5460
CATCATATAC TCTCATGGTT TCTACAAACA TTTTTTGCAC AGAAAAATGT TTTCTTATTT	5520
TTGATTTACT ATTCTCACCT ATATATTTCA AATACTCAGA ATCATTGAGT AAAAAATTAG	5580
CACAAGCACA CACTCCCTCA ACATCTTCCT TCTCAAATAA AAATCCATCA ACCCTATGTT	5640
CAATAATTC ACTTAACCCG CCAACATTAC TAGCTAAAAC CGGAGTTCCT TGTGACATTG	5700
ACTCTAAAAC ACACATAGGT ATTCCTTCTG TATCAGAAGG AATATACAAT AAATCCGATA	5760
TTTGGTAAAC TATAGTAGCT GGATAGATTT CACCAAGTAA CCTGAAATTA TCTCTACATT	5820
TCAAATGGCA AATTTTTTCT TTCAAAGCAG CCCACATACT ACCATTTCCA GCCATAATAA	5880
AAATCACATC TTCTCTGACT AAAAATAATT TTTCTGCAAA TTCAAGGAAT CTATCCGGCC	5940
TTTTTTCTGG ATCCAACCTT CCAACATAAC AAATGATTTT TTGTTATTTG GAATACAAAA	6000
TTCTTTTTTA AAGTCTTGAA CACCTACTAC ATCTAAATCG CTATTTGATA CATTAATTCC	6060
GTTATTTATT GCAACTATCT TCTTATTTT TATTATACTC TCCAATCTTT TTTTTCATAG	6120
TTTCAGATAC ACAAATAAAA GCATCTCCCA TAGAATATGT CCAAAAATCA AAATAAGTCA	6180
AGAATTTCTT TTTTAAGTTA TATTCAACCC ATCCATGGCA TGTATCACT GTCTTAACCT	6240
TTCCAAATCC ATTCTTGTCA AGTTTTTTTA ACATATATAA AAAATAATTA GTTGAGTAGC	6300
CATGACAGTG TATAAGTTGG ATTTTTAATA ATTTTAAAT ATTTTAAACG TGTAAGGCAG	6360
TTTCAAAATT ATTTGAACAT TGAGTACAAT CAACATAGGC AATATCTAAA TTTTATAAT	6420
CATCAATAAC CTTTGAATCT CTAGATACAA TTATCAAAAT AGGGAATAGA GACA	6474

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

TATTTAACGA TTTTTTTCAT GTCATTTCCCT CCAAAATAGA ATACCTTATA ATCTTAACAG	60
AAAAAGAGCA TTTACGCCAT TATATGATAT CTATCTCTGT GATAAGTTTT TTTTATGGGT	120
AATTTAAAAG ACCAAACGCA AGATGGCAAT CAAGACCACT CCAAAGAGAA CTGTTCCGAC	180
TAGATTGCGG TAGCGAAAG CTACCCAAGC TGTTGGAAAG ACGGCTAAGA AGTCCAGTCA	240
TTTGATTTGA GGAAGACTGC CAACCTTACC TGTCCTACG CTTGAAAGAA TCAGGGCAAA	300

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GATAATGGAA	ACAGGCCAAAA	ACTTCAAAAA	ACGCTCAACA	ATCGCAGGCA	GGCCCTTATA	360
CTTGACCAAG	ATGAAGGGAA	TCATACGGGG	AATCCAAGTC	ACCAAGCCAG	AGAAAATAAC	420
TGCTAATAAA	AGATACTTAC	TGACCATCTA	AAACCACCCC	CATGCTACAA	CCAAGTAGCG	480
TCGCAACAG	AACAGCTAGT	GACTGAGACA	TCACTGTCAA	GAGCAAAAAG	AAGGACACCG	540
CAACAACCTGC	TAGGATAATG	AGCAGATTGC	GGACAGGAAT	CCGTCTTTGC	ATAATCTGAA	600
ATTGCGAAGC	AAAATACCAA	TAAACATCCC	AACCAGGGCA	AAATCCAAGC	CAAAGATTTC	660
TGGATTTGGT	AGCAGGCCAC	CCAGAGCCGT	TCCGACTACT	GTCCCCACAA	ACCAAGCCAC	720
ATAGCTGTTA	AGATTGTTTC	CGTGCAATCA	CATAGGATTT	ACCTTGTCCTG	TATGGGCCAA	780
TTCACCCATC	AAAACGCCAT	AGGTCTCATC	TGTCAAGATA	CTAGACATAC	CGATATTGTA	840
CCAAAGACTG	GTATGACGGA	AATAAGTCGA	TGCGTGTAAA	CTCAACAAAA	AGAGACGCAA	900
GTTGATTAGA	AAAACCGTCA	TAGCAATAGC	TGCCACAGGA	GCTTGAACCA	CAATCAGTGC	960
CAACATGGCA	AACTGGGCAC	TCCCAGCATA	AACAAAGAGA	CTCATCAAGC	CCATCTCAAC	1020
AGGTGTCACA	TAGGGCGCAC	CGATAATTCC	ACAGGCCAGG	CCGATACTGA	CATAGCCAAG	1080
AGCCGTTGGC	ATGGCTGCCT	GCGCCCCCTC	CTAAAATCCT	TTTTCTTTCA	TCTTCTCTCT	1140
CATATTGTCT	TAATAATACT	CAATGAAAAT	CAAAGAGCAA	ACTAGGAAAC	TAGCCGCAGG	1200
TTGCTCAAAA	CACTGTTTTG	AGGTTGCAGA	TAGAACTGAT	GAAGTCAGCT	CAAAACACTG	1260
TTTTGAGGTT	GTGGATAGAA	CTGACGAAGT	CAGCTCAAAA	CACCGTTTTG	AGGTTGTGGA	1320
TAGAAGTGAC	GAAGTCAGTA	ACCATACCTA	CGGCAAAGTG	AAGCTGACGT	GGTTTGAAGA	1380
GAGTTTCGAA	GAGTACAAGT	AGGCTGAAAA	GAATCCAACC	ACAGCATGGA	CTATTATATA	1440
GCAGATTGAA	ATAAGATGAG	AACAAATCGA	TTGGGAAAGT	AAAATTAATT	TCTATAAATG	1500
TTTTAGCAAT	TGTTTCGTAC	TATTTTAGAT	TCAGTCTATT	ATAACACATT	CAGAAAAGAG	1560
AAAAAAGTCT	GTTGATTTTG	ACCATCATAA	AAAGACTGGC	AATCCAGTCT	CAAACATATA	1620
TTATAGAAAT	TCTCCACTAA	ATACTTTCAC	GAATATTCAG	AAGCATAACA	AAGGCAACTA	1680
GAAGAAATAG	CAATAAAACA	AAGCTAACTG	CCAGAGTTCC	AAAGCTAGTA	GCAATGGTTA	1740
CCAAAGCTAT	TGTAAATAAG	CTAGGTAAAA	CAACCGTAAT	GGCACCGATA	GAGGATTGAA	1800
CTGCTCCCAT	TGACTCCTCA	GGTATTTGTT	TAAAAACGAG	TTCTTGCAAT	CTAGGAGAGA	1860
GAACACCTGC	GAAAAAGGCA	TCCAAGGTAC	TAAAGATGAG	AATCCAGTCA	AAACGAACTG	1920
TGGCAAATCC	TACTAGAAGA	AGCAACTGGA	TGACAAGTGA	GGCATAGAGA	GCTGTTTTTA	1980
TGGAAATGGT	ATGTTGCAGA	TAGCCACTTA	CAAGGCTTCC	GACAATCAGG	GCTGATAATT	2040
CTAGTGTGGC	TAACAAGGCA	AGAGATTGAC	CAGTTTGTA	ATTCAAAAAG	GGCTGGTTCC	2100

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TTAAAAATAG AGTGGAATA GGAACCGTAA CATTTATCAC TGCTTGACTA GTAGAGATAA	2160
TAAACAAAAC CAAGAGCACC TTATTCATAT TCCATATCAA TTTCGATGAT TGGAGCAAAT	2220
GCTGGCAAAA GGATTTTACA GAGAGTCCTT CTTGATAGCT AATCGTTTTT TCTACTTTCA	2280
AGAGGTCAGT TTTTATGAAG AGGATACCTA AAAATGCGAT TAAAAAGGTA AGAGCGTTCA	2340
GTAAGGAAAT AAAGTGGATG GATAGAATGC CTAGTAAGAC TCCTCCTAGG ATATTACTGA	2400
TTGTTTTTAC TAAACTAACA GTTGACTGTT TAAAGCCAAT AGCTTCTGCC AGATGGTCTT	2460
GCCCAATAAT TCTAATGAAA ATCGGAGTGA GCATGGCGCC TGAAAAATAA CTCAATGTGT	2520
CAGACAAGAG GTTAATCAGA CAAATAAATG CTAAGTAGCA CAAGGAGAAA GACTGCCCTG	2580
AAAGTGATAA AGACACTATA GAGTAAAGCA AAAATTTTGC AAAACTAATG ACTGTGTATT	2640
TCAAGACACG ATGATGTTGA AAATCCGCCA AAAGTCCAG AAAGATTGTG AGAACTTGGG	2700
GCAGGGTTTC TGAAATCGTG ATGAGTAAAA TCGCCAAAGG GGCAAAAGAT GCATCTGCCA	2760
CATAATTCAG GAAGGCCAGA TAAAAAATCG TATCCCCAAG CGTTGAAATC CACTGGTTGA	2820
TAGTTAATTG CCTAAAATCT CTATTTTGAA GAAATACTTT CATCACAACCT CTTCTTAAG	2880
TTCAAATGGG AATCTTTCCC CAAGGATAGA CCGCGATACT ACTAACAACC AAAATTACAG	2940
TAACATCAA AGCTGACCAA TGCCATTGTA GACTATATGC AGTCCAATAG GCCAATAAAT	3000
TGACTTTGTC ATTCTAAATA AGACTGCAA TATAAGACCT CCACCCATAT AGAAGACAAA	3060
GTCTGTCAAG ACCCAACCGT GATTACTAAT GTGCGAGACC CCAAATAAAA CAGCGGAACC	3120
AAGTACATCT AGCCCCATT TCTTTCCTTT TTCCAGAGCA GTCATCACTA ATCCACGATA	3180
AATCATGTCT TCAAAAATGG GACCTGCAAT CACAGGATAA AAAAAATACA TCAAAAATGC	3240
TGTAGCCCCT GTAAAAGTCG GAGCAGCATG TTGATAAGAA ATTTCAATTTC GAGTAGGTGG	3300
GAAAAGAAAA AAGGTAACGA AATTCCAAAC AACAAAAGCA AGCAGAGCTA GGAAGGAATA	3360
GAAAAGATAG GATCCTTTAA ACTTTCTACT ATTGATTTTC TGCCATTTC CCGACCAAAT	3420
CATAGCAATA AGAGCAAATA AAACCACAAG AAAATTCAAC ATCATATCCG ACAGATAATA	3480
GGCAAAGTCA GATAGCCCAG TAACAAGGTC GCTGCGTAAA ACTAGAACAC TGAACCTCTG	3540
GTCAGCAATA ACTAGTAGAA AAAGTATAAT AAAGTAGCGG TGTGAGATTA TCTTTTTCAT	3600
ATATCACCTT TCTAATATCC AAATACCAAT AAAGTAACAA TGAGTAAGAA ACTATTCCAT	3660
GAAGCATGCA GAGCTATAGC CCAATAGATG GATCGGGTGT AGCGAAACAT CATACAAAAT	3720
ATCAAGCCCA TTCCAAAATA CTTTATGAAA TCTGTCTGTTA TCCAACCATA CTGCAAAACA	3780
TGCATAGCGC CAAATATGGC AGCGGAAACA AGAACATCAA GATAGTATCT CTTAACTTTA	3840

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GATAAACTTG TCATCAAAAG ACCACGACAA ACAACCTCTT CTGATACAGG TGCGATAATA	3900
CTAGTATAAA GTATTGCGGT AACAAAATAG CTAATTCCTG TTAAATTGGT GGCTACTTCT	3960
ACGACTGTAC TTCCATTCTG GGTACGAGGA AAGATATAGG TTGTTAGATT TGCCACACG	4020
AACAATAAGA AAAAAGAAAG AAGGAAAACA CCCAGGTAAG ACCAACGAAA CTGGAAACGA	4080
CCCACTCTT TCCAATGTC ACTTTTGACA AAAGCAATTG TAGCTATAGT TCCCAGAATA	4140
AGTACCAATA AAAGTTGGAA CACATAGTAC ATATTATCAG ACAAAGCAAC CATAAAATCT	4200
AAGTCTGATG TGACATTAAA AATGAGGTAA TAAGTCAAAA TCAACAAGCC AGTTGCTAGG	4260
TGAAATTTCA CTTCTTTCAT TTTCTTCATC CTATTATCTC CTATAAGAGC CTATCTTCTA	4320
CGGCGGCCAA ACAATCCATC TGCTAAATCT ATAGTCCAAT CAAAAGCTCC ACGATTAGGA	4380
CTCATCCCTT GATTGCCCCA ACCAGGGTAA ATTCTGGGA CGCCCCAACC AGATATACCA	4440
CTTCTCCAC CACCTCCCAT AGAATTTACG AGGTTGCCTC CTCTAACATC TTGCAACTCA	4500
GCTTCTGTCA ATTCCATTGT TTCTGCAAAT TGTAATTTA ACATCTTTTA CACTCCTTCA	4560
ATTATCTTCA TTTGTAAACC ACTTCTGCGA CCTAGGATTT GCTTCAAGTG CTTTACAAGT	4620
ACAGTATAAC ACGAACATTG GCTTATTTTA GAAATCGCA TATTTGATAT TTTTCTTAT	4680
AGAAATTTCA GATTTGCGAT TTTGGTGAAT TTGATTACTT CTCTGGTATA ATAAAGTTAC	4740
TACTAATGAG GAGTGGAGAA ATATGAAGAA ACAAATTTTA ACATTATGA AA	4792

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CCGTTCTCGG CGACGGCCAT CTGATGAAGC TATTTATGAG GGAAACTGGC AAGCTGGAGA	60
GTCAGAGTAT CTAGTCTTTC ACCGATTGCT GTGGCAGCAG ATGTGCAGGG AAAAGGAGTT	120
GCTCAAACCT TCTTAGAGGG CTTGATTGAA GGTTTTGATT ATCTTGATTT TCGCTCAGAT	180
ACGCATGCTG AAAACAAGGT TATGCAACAT ATTTTGTAAA AACTTGTTT TAAACAAGTC	240
GGTAAGATGC CAGTAGATGG CGAACGCTTG GCCTATCAAG AATTAAAGAA ATAATGCAA	300
AGAAGTATGT AAAATCCTC TACTCCTCAC CAATTGGTAT TCTATCACTT GTAGCTGATG	360
ACCATTATTT GTATGGAATT TGGGTCAGG AGCAGAAGCA TTTTGAGAGG GGAAGTAGG	420
ATGAAACGAT AGAAGAAGTT GTTAGTCATC CTATTTTAGA CCCAGTTATT GCTTGCTTAG	480

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ATGATTACTT TAAAGGCAAG CCTCAGGATT TATCCAACCTT GCTCTTGGCG CCAATCGGAA	540
CGAATTTTGA AAAGAGAGTT TGGGACTATT TACAGGGCAT TCCTTATGGT CAGACAGTGA	600
CCTATGGACA AATTGCTCAA GACCTGCAAG TGGCTTCTGC TCAAGCAATT GGTGGAGCAG	660
TGGGACGCAA TCCTTGGTCT ATCCTAGTAC CTTGTCATCG TGTGTTGGGA GCAGGCAAGC	720
GTCTGACAGG TTATGCTGCA GGAGTGGAAG AGAAAGCTTG GCTCTTGGAG CATGAAGGAG	780
TAGATTTTAA AGATAGAAGC AATAGAAGGA GAAGCACATG TTAGAATTTA TCGAATACCC	840
CAAAATGTTCA ACTTGTAATA AAGCAAAACA AGAATTAAT CAATTAGGTG TGGACTATAA	900
AGCCGTCCAT ATCGTGGAAG AAACACCTAG CCAAGAAGTC ATTTTGAATT GGCTAGAAAC	960
CTCAGGATTT GAATTGAAGC AATTTTTCOA CACCAGTGGT ATCAAATACC GTGAATTAGG	1020
GCTAAAAGAT AAGGTAGGAA GTTTGTCAAA CCAAGAAGCG GCTGAGTTGC TAGCAAGTGA	1080
CGGTATGTTG TTAACACGGC CCATTTTAGT AGAAAATGGA ACTGTTAAGC AAATCGGTTA	1140
TCGAAAATCT TATGAGGAAC TGGGACTGAA ATAGTTTTTA TCTATCTCTT TGATAGATAA	1200
AATATATAAC TTCCCTGTTT CAAAGTATGA TAAACTAGTA GGTAACAAA GTCTGTATCT	1260
GACCGTAGCA AATAATTTCA TTGACGGCAG AAGCATGGTA GCATGAATCA TTATCAGAAG	1320
AGGATGTTTT TATGAATGTT ACAACGATTT TAGCATCAGA TTGGTACCAA AACTTGATGC	1380
AATTGATTCC GGATGGCAAG CTGTTTAGCC TACGTTCCGT CTTTGATGGA ATCCCTAGAA	1440
TTGTCCAACA ACTTCCAACA ACAATTATGT TGACAATTGG TGGTGCCCTT TTTGGCTTGG	1500
TTTTTGGCGT TCTTTTGGC ATTGTGAAGA TCAATCGTGT CAAGATTTTA TATCCCTTGC	1560
AGGCCTTCTT TGTTAGTTTC TTAAGAGGA CACcGATTTT GTTGCAACTC ATGTTGACCT	1620
ACTACGGAAT CCCTTTGGCT TTGAAAGCCC TCAATCAGCA ATGGGGAACCT GTCTCAATA	1680
TCAATGCGAT TCCAGTGCA GCTTTTGCGA TTGTGCGCTT TGCCTTTAAT GAGGCAGCTT	1740
ATGCTAGTGA AACCATTCTG GCAGCCATTC TCTCAGTTAA TCCTGGTGAG ATTGAGGCGG	1800
CACGCAGTCT GGGTATGACC CGAGCGCAAG TTTATCGACG AGTGATTATT CTAATGCAG	1860
CGGTGGTAGC TACTCCAACC TTGATTAATT CCCTCATCGG TTTGACCAAG GGAACATCTC	1920
TAGCTTTTAG TGCGGGTGTG GTGGAAGTCT TTGCCCAAGC TCAGATTCTA GGTGGAGCTG	1980
ATTATCGCTA TTTTGAACGC TTCATCTCCG TTGCCCTTGT TTATTGGGTA GTCAATATCG	2040
GAATTGAAAG CCTCGGTCGT TTCATCGAGA GAAAAATGGC TATTTCTGCA CCTGATACAG	2100
TGCAACAGAT GTGAAAGGAG ACCTTCGTTA ATGATTAAGA TTTCAATTT AAGCAA	2156

(2) INFORMATION FOR SEQ ID NO: 158:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GTATCTCTAC ACATGTCTTC AATCGATTTT GTTGTCCTCC AATTAAATC CTTATATGCT	60
TTGTCTGCAT TTGCATAACA AGTTGCAACG TCTCCTGAAC GTCTTGGAAC TATTTTATAA	120
GGAATAGGGA TCTTATTAAC ACTTTCAAAT GTATTTACAA GTTGTAATAC ACTAGTGCCT	180
TCTCCCGAGC CTAGGTTATA GATATAAACA TCTGTTTTTT CAGATACTTT TTCTAAAGCT	240
TTTATATGTC CTATTGCTAA ATCTACTACA TGGATATAAT CACGCACACC AGTACCATCA	300
AGCGTATCAT AATCATTTCC GAACACACTT AGCTCTGATA GCTTACCTAC CGCTACTTGT	360
GCAATATAAG GCATCAAGTT GTTAGGAATT CCTGAGGGAT CTTCCCCAAT CAAACCAGAC	420
TCATGAGCAC CAATTGGATT GAAATAACGA AGCAACGCAA TACTCCATTC TGAATCTGCC	480
ACATGAACAT CTTTTAAAT TTGCTCAAGC ATCACTTTTCG TATACCCATA AGGATTTGTC	540
GCACTTGTTC GCATCGTCTC AATTAGAGGT GACTGATTGT TAATTCCATA TACAGTCGCA	600
CTTGAAGAAA AGACAATCTT TTTAACATTA AATTCTGACA TCACTTCAAC AAGTGCCAAT	660
GTACTCATAA TATTATTTTT GTAGTACATC ACAGGCTTTT GCACGGATTC TCCGACAGCT	720
TTATAACCTG CAAAATGAAT TGCAGCATCA ATCGATTCTT GTTCAAATAC CTTTCTCAAT	780
GCTTGTTTAT CACAAACATC TAATTCGTAA AACACGGGAC GTATTCCCTGT AATTGCTTCA	840
ATACGGTCTA GCACCAAGAT GCTAGAGTTC GAAAGGTTGT CGACAATGAT AACTTCCTTT	900
CCTAAATTTA GTAATTCTAC TACGGTATGG CTACCAATAT AACCAGCTCC GCCTGTTACC	960
AATATTGCCA TCTGGGTTC CTCCTAATTA ATTCCAACCG ACTTAACAAA TCTCATAAAC	1020
GCTTCATGCC CAGACGGTGT ATTCTTATAA ACTCCTGCAT CTTCCAGAAC TCTCGCAAAC	1080
ACTTGTCCTG CTTCTGTGTTG AACTACGCTA TTAACCTCTT CTTTATTAAT GCGAGGATAT	1140
TTTTCTTTCA ATTGGTCGGC CCATTCTAAA TGATAATCCG CAATTGCATT ATCCTCTCCT	1200
AAAAGATATT TTCCAACCTC TTCTAACTCT GGTTTCAAAC GAGGTGGTAA TATCGCAAGT	1260
CCCATCACTT CGATTAAACC GATATTTTCC TTTTAAATAT GTTGATACATC TTGATGAGGA	1320
TGGAAAACAC CATCTGGGTA TTGTTCACTA GTATGATTAT CTCTTAGAAC AATATCTAAT	1380
TCGTATCTCC CGTCCACTTT ACGAGCAATA GGAGTCACCG TATGGTGTGG GACATCTTCA	1440
GTCATAGCAA TGATGTCTAC TTCTAAATCT GAATATTCTC TCCACTTATT TAGAATTTTA	1500

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GTAGCTAAAT	CTAACAAGCG	ATTTTTATTT	TCACCTTGTA	ACCTAATTAC	TGACATTGGC	1560
CATTTTACAA	TACCAGCATT	AACATCCTCA	AAGTCTTTAA	AACAAAATTC	ACTCTCAAAT	1620
TTTGCTTTTT	CCATTGGGAA	AATATGTTTC	CCTCCCTGGT	AGTGGTTATG	ACTAAGAATG	1680
GAGCCTCCTG	AGATAGGAAG	ATCAGAATTT	GAACCAGCAA	AATATCCTGG	CAAAATATCA	1740
ACAATCTCCA	ATAATTGTTC	AAATGTTTTA	GAGGTAATAG	CCATTGGTAC	ATGTTGACTA	1800
TTCAAAAATA	TCGCATGCTC	ATTAAAGTAT	GAGTAGGGAG	AATACTGGAA	TCCCCATACT	1860
TCGTCACCAA	GTTTCAACCG	AATAATTCTA	TGATTGGAAC	GTGCTGGATA	ATTTATTCGC	1920
CCCTGATATC	CTTCATTTTC	CATACATAGT	AAACATTGCG	GATAATTAGT	TGCTTTTACT	1980
AATTTTTCAG	CAGCAATTGT	TTTTGGATCT	TTTTCGGGTT	TTGACAAATT	TATCGTAATC	2040
TCTAGCTCTC	CGTATTTAGT	TGATGCTCGA	AACTCAATAT	TCTTAGCAAT	AGCAGAAGTT	2100
TTAATATAAT	CACTATCTTT	ACTTAACTTA	TAAACTCTT	CAACTGCTTC	TTGAGGTGAT	2160
ATATCATATG	AACTCCAAAA	AATATCATTT	AATCGACTAG	GTAAAGGAAC	TATGAAATTC	2220
ATTAACCTCG	CTCCTAAACA	TTCTTTTCC	TCGATTAAAT	CTTTAATTTT	ACCGTTTTTT	2280
AAGGCGATTT	CCACTAAGTA	ATCTTTTATT	TGTTTCAGGT	CATTTTCATC	GGAAATGCGA	2340
TCAATTCCCT	CCTCACCTAT	TAACGCTAGT	ACTCTATTTT	TCACATATAT	TTTGTCAATT	2400
TCATTATACA	TTCCGTATTC	AATTACTCTA	TCAACAAAAT	TATCAATAAT	TGTTTTTCATA	2460
TATTTTCTTT	TCTAATTTAT	GTTCCCATAT	TTTCTATACA	TTATCCATTT	ATAAATGCT	2520
TGCGTAGTAT	GAGCAATTTT	ATCAAGGTGA	TGAATAATAT	CTAAAGCACT	AATTACTTCA	2580
GAAACGTTCC	CATCATCTTC	AAATATGTAA	TTCATTATTT	TCTTTTCCAT	ATTTATACTA	2640
AGCTCTTCTA	TCTCATTTCTG	TTTTTGTATA	ACAACCATAT	CTAAACATCC	AGATTGTTCC	2700
TCTCTATAAC	AAGATATAGC	CCTATTCATA	TGCAGTCCGA	TAACTTCATG	AAGTATTTTT	2760
ATTTTGTGAA	TAATTTTCTT	CAAAATTTCA	TTATTTTGAA	GAATCTGTAG	ATTTTTTAAA	2820
ATTTCAACAA	TTCTATCCCC	AATACGTTCA	ATGTCAGTTG	ATATTTTAT	TACACTAATA	2880
ATTCTTCTTA	AGTCATATGA	AACAGGATGT	TGTAAACAAA	TTAACTCATA	TCCTTTTTTA	2940
TCAATATTTA	GAACGACTC	ATTTATGATT	AAATCTTCTT	TAATCAATTC	TACTCGTTCT	3000
TCATTTGATA	AATATTCAAA	TAACTTCTCA	TATTTATCAA	GCACAGATAC	CCAAATGGTC	3060
TCTAAATTAT	TTGATAATTC	TATAATTTCA	TTTTCTAAAT	ATAACCTTAA	CATTTAGGTA	3120
CCTCTTCTTA	ACAAAGTTTCG					3140

(2) INFORMATION FOR SEQ ID NO: 159:

1032

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9048 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

CCGGATGATT TCCTGGTCAG ATAGGGGGAA AGTGACTTCC TCAGCAATCG CGCGTAGAGT	60
AGGATTCCCT TCACGGATAA TATCGTTCAT ATCAATTAAG TGAGCAGCTT TTGTAATACG	120
TTCTATTGCA GACATTTTCT CTCCTTATAT TATGTTTAGT GCAGTTAGCT ACTGCCAAAG	180
CCCAAGTGGT ATACTTGGA TAAGCCACTG TGGATTAGT CATTTTCTTT CATTACCTCT	240
ACATGATATC ACAAAATGAC AAGAATTGAA AGCATTATGG CATTTAGGAT TTATAGAAAA	300
TAGATAGGAA GTTCAATTCA ATTGTGAAAG AAATACTTAT CTGTGATATA ATAAAAAGAA	360
AAGGCTTGCA TAAGAAAGTA GGGAGAACGA AGATACAAAG AAGACAAAAT CGAAATCAGG	420
GTGGTTTAGC TTTTCGTTTT ATGAAGGGCT TGGTAACTT TTTAGGAGTT ATCGCAAGTG	480
GAGCAATAAG GGATTTGTGG CGATACTCTT GCTAGCAGTT GGTTTATCAA TGGGCTTGGT	540
CTTGTTGTTT GAAAGCTTCC AAGGAATCCC TTGACTAGTC AAAAACGAGA TACTATTTCT	600
CAAGAGGGGA CTAAGCAAAA GTCTCAGGAG TAGGAAGAGG AAAAACTGC CAGAATTATG	660
GCCCACGGGG ATTTGCTCTA CCACGATGGA CTTTCTTTT CAGCTAAAAA AGAAGACGGT	720
ACCTATGACT TTCATGAAAA TTTTGAGTAT GTGACTCCTT GGCTCAAGCA AGGGGACTAA	780
GCAGCAGATT TAGCTATTGG TGATTTTGAA GGAACCATTA ATAAGGATCA TTATTTAGCG	840
GGTTATCTTC TCTTTAATGC TCCTGTTGAA GTTATGGATG CTATTAAGGA GGCAGGTTAT	900
CATGTGCTGG ATTTAGCTCA TAATCATATT TTGGATTCGC AAATTGAGGG AGTTATTTCA	960
ACGGCCGATA TTATTGAGAA AGCTGGAATC ACTCCAATCG GAGTTTATAC GCACGAACCA	1020
CGTGATCAGG CTCCGCTGGT CATTAAGGAA GTGAATGGTA TCAAGGTGTC ATTGTTAGCC	1080
TATTCCATATG GTTTCATG AATTGAGCAG TATATTTCTC AGGAAGACTA TAATCGTTAT	1140
CTTTCAGATT TAAACGAAGA TAAGATGAAG GTTGAAATTG AACGGGCAGA GAAGGAAGCA	1200
GATATCACCA TTATCATGCT TCAGATGGGT GTTGAGTATC GATTGGAACC AACTGAAGAA	1260
CAAAAAGCTC TTTATCACAA GATGATCGAT TTGGGAGCGG ATATTATCTT TGGAGGGCAT	1320
CCTCACGTTG TTGAACCATC TGAAACGGTT GAAAAAGATG GAGATAAGAA ACTCATTATC	1380
TATTAAATGG GGAAC TTCAT TTCCAATCAA CGAATTGAAT CTATGGGAGA TGAAGAGAAT	1440
GCTAAGTGGA CTGAACGTGG TGTTCATG GATGTCACCA TCAAGAAGAA GGATGGAAAA	1500

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ACAACATATCG GAACAGCTAA AGCTCATCCT ACTTGGGTCA ATCGAACACC AAAGGGAACC	1560
TTTTTACCAG AAGGATATCC CTTGTATCAT TACCAAACCT ATATTTTGGA AGATTTTATA	1620
GAGGATGGCA GTCATCGTGA CCAGTTAGAT GAAGCGACTA AGGAACGAAT TGATACAGCC	1680
TATAAAGAAA TGAATGAACA TGTGGGATTG AAGTGGTATT AGCTTGAATC CAGAGGAAAAG	1740
TAAATGATGA TTAAGGTAAT TGCGACAGAT ATGGATGGGA CCTTGCTGGA TGCTAGAGGT	1800
CAGCTTGATC TCCCACGATT GGAAAAGATT TTAGATCAGT TGGATCAAAG GGGCATTTCGT	1860
TTTGTTCATTG CGACGGGCAA TGAAATTCAC CGCATGAGAC AACTACTGAG TCCCTTGGTG	1920
GATCGAGTGG TTTCTGGTTGT TGCTAATGGC GCTCGTATTT TTGAAAACAA TGAATTGATT	1980
CAGGCTCAGA CATGGGATGA CGCCATTGTC AACAAGGCTT TGACTCATTT CAAGGGTCGA	2040
GCGTGTCCAG ACCAGTTTGT TGTAACGGGG ATGAAGGGTG ATTTTGTCAA GGAAGGTACG	2100
ATTTTACAG ATCTTGAAAG TTTTATGACT CCAGAAATGA TTGAAAAATT CTACCAACGG	2160
ATGCAATTG TGGATGAATT AACATCTGAC CTCTTGGTG GTGTGCTCAA GATGAGCATG	2220
GTTGTTGGTG AGGAACGTTT GAGTTCGGTT TTGGAAGAAA TCAATGCTCT CTTTGATGGC	2280
CGTGTCCGAG CTGTATCCAG TGGCTATGGT TGCATTGATA TCCTCCAAGC TGGGATTTCAT	2340
AAAGCATGGG GCTTGGAGGA ATTACTCAAG CGCTGGGACT TGAAATCCCA AGAAATCATG	2400
GCTTTTGGTG ATAGTGAAAA TGATGTTGAA ATGCTTGAAA TGGCTGGAAT TGCCTATGCG	2460
ATGGAAAATG CTGATGAGAA AGCCAAAGCT GTGGCGACTG CTCTAGCACC AGCCAACAGC	2520
CAAGGAGGAG TTTATCAAGT CTTGGAAAAC TGTTAGAAA AAGGAGAATG AAGTGGCAGT	2580
ACAGTTATTA GAAAATTGGC TCCTAAAGGA ACAAGAAAAA ATTCAAATA AGTATCGTCA	2640
CCTAAATCAC ATTTCTGTTG TAGAACCAAA CATTCCTTTT ATTGGGGATT CCATTGTCTGA	2700
GTATTATCCT CTACAGGAGC TATTTGGGAC TTCAAAGACG ATTGTCAATC GAGGAATTCG	2760
TGGCTATCAG ACAGGACTGT TACTAGAGAA CCTTGATGCT CATCTATATG GTGGAGCAGT	2820
AGATAAAATT TTTCTTCTGA TTGGGACAAA TGATATCGGA AAGGATGTTC CTGTGAATGA	2880
GGCTCTCAAT AATCTCGAAG CTATCATTCA ATCCGTTGCT CGCGATTATC CATTGACAGA	2940
GATTAAATTG CTTTCCATTT TGCCTGTCAA TGAGAGAGAG GAGTACCAGC AGGCAGTCTA	3000
TATCCGCTCG AATGAAAAA TTCAGAACTG GAATCAAGCC TATCAAGAGC TTGCATCTGC	3060
CTATATGCAG GTGGAATTTG TGCCAGTATT TGATTGTTTG ACAGACCAAG CAGGCCAACT	3120
CAAAAAAGAA TATACAACTG ATGGACTGCA CCTCAGTATT GCTGGTTATC AGGCTTTGTC	3180
AAAATCCTTG AAAGACTATC TTTACTAAAT AGCTAAATAA TGTTAAATTT GAGCATAATA	3240

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TCTTGTA	AAAA	AATTC	AAAA	TCCTT	AAAA	TAAAA	AGTGA	CGGAG	GAATT	TATGA	ATGTA	3300
AATCAG	ATTG	TACGG	ATTAT	TCCTA	CTTTA	AAAGC	TAATA	ATAGAA	AATT	AAATG	AAACA	3360
TTTTAT	ATTG	AAACC	CTTGG	AATGA	AGGCC	TTGTT	AGAAG	AATCG	GCCTT	TCTGT	CACTA	3420
GGTGAC	CAAA	CGGGT	CCTGA	AAAGC	TGGTT	TTAGA	AAGAAG	CTCCC	AGTAT	GCGTA	CTCGT	3480
AAGGT	AGAG	GAAGAA	AAAA	ACTAG	CTAGA	TTGAT	TGTCA	AGGTG	GAAAA	TCCCT	TAGAA	3540
ATTGA	AGGAA	TCTTA	TCTAA	AACAG	ATTCG	ATTCAT	CGAT	TATAT	AAAG	TCAAA	ATGGC	3600
TACGCT	TTTTG	AAATTT	TCCTC	ACCAG	AAGAT	GATTT	GATTT	TGATT	CATGC	GGAAG	ATGAC	3660
ATAGCA	AGTC	TAGTA	GAAGT	AGGAG	AAAAG	CCTGA	ATTTT	AAACAG	ATTT	GGCAT	CAATT	3720
TCTTT	AAGTA	AATTT	GAGAT	TTCTA	TGGAA	TTACAT	CTCC	CAACT	GATAT	CGAA	AGTTTC	3780
TTGGA	ATCAT	CTGAA	ATTGG	GGCAT	CCCTT	GATTT	TATTC	CAGCT	CAGGG	GCAGG	ATTTG	3840
ACTGT	GGACA	ATACG	GTTAC	CTGGG	ACTTA	TCTAT	GCTCA	AGTTCT	TGGT	CAATG	AATTA	3900
GACAT	AGCAA	GTCTT	CGCCA	GAAGT	TTGAG	TCTAC	TGAAT	ATTTT	ATTTC	TAAGT	CTGAA	3960
AAATT	CTTCC	TTGGT	AAGA	TAGAA	ATAAT	GTTGA	ATTGT	GGTTT	GAGA	AGTAT	GAGT	4020
GGACCA	AGAT	TATTA	AAAAA	ATAGA	AGAAC	AAATC	GAGGC	AGGGAT	TTAT	CCCGG	AGCCT	4080
CTTTT	GCGTA	TTTTA	AGGAC	AATCA	ATGGA	CAGAG	TTCTA	TTTAG	GCCAG	AGTG	ACCCAG	4140
AGCAT	GGCTT	GCAG	ACTGAG	GCAGG	ACTAG	TTTAT	GACCT	AGCTA	GTGTC	AGCA	AGGTTG	4200
TTGGG	GTTGG	CACAG	TTTGT	ACCTT	CTTGT	GGGAA	ATAG	TCAAT	TAGAT	ATTGA	TAGAC	4260
TGGTA	ATAGA	TTTTT	TACCT	GAGAG	TGATT	ATCC	AGACAT	CACTA	TTTCGC	CAGCT	CCTGA	4320
CTCAT	GCAAC	AGACC	TTGAT	CCTTT	TATTC	CTAAT	CGTGA	TCTTT	TAAAC	GCCCC	TGAAT	4380
TAAAG	GAAGC	GATGT	TTTCAT	CTCA	ACAGAC	GAAGT	CAGCC	AGCCT	TTTCTT	TATTC	GATG	4440
TCCAT	TTTTT	GCTGT	TGGGC	TTTAT	TTTGG	AAAGA	ATTTT	TAATC	AAGAT	TTGG	ATGTGA	4500
TTTTT	AAAGGA	TCAAG	TCTGG	AAACCT	TGGG	GAATG	ACGGA	AACTA	AGTTT	GGGCC	AGTTG	4560
AGCTT	GCTGT	TCCA	ACAGTT	AGAGG	TGTAG	AGGC	AGGCAT	AGTGC	ATGAT	CCCA	AGGCTC	4620
GTCTC	CTGGG	TAGAC	ATGCT	GGGAG	TGCTG	GTTT	ATTTTC	GACTA	TAAAG	GATTT	TACAAA	4680
TCTTT	TTTAGA	ACACT	ATTTA	GCAG	ATGATT	TTGCA	AGAGA	CTTAA	ATCAA	AATTT	TTCTC	4740
CTTTG	GATGA	CAAGG	AACGT	TCTTT	AGCAT	GGAAT	TTGGA	AGGAG	ATTGG	CTAG	ACCATA	4800
CGGGC	TATAC	AGGT	ACCTTT	ATCAT	GTGGA	ATCGT	CAGAA	GCAAG	AAGCC	ACTAT	TTTTC	4860
TATCG	AATCG	TACCT	ATGAA	AAGG	ACGAGA	GAGCT	CAATG	GATAT	TAGAC	CGCA	ATCAAG	4920
TGATG	AACTT	GATTC	GCAAA	GAAG	AGTAAG	GAGAG	ACATG	TCAA	ATAGTT	TAAA	AGGGAC	4980
TTTAC	TAAACA	GTGTG	GGCTG	GTATT	GCCTTG	GGGTT	GTCA	GGAAC	GAGTG	GCCA	ATACCT	5040

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AATGGCACAC	GGAATTTTCGG	CTCTGGTCTT	GACTAACTTG	CGTCTTTTAA	TCGCTGGTGG	5100
AATTCTCATG	CTCTTGGCTT	ATGCTACTGC	AAAGGATAAA	ATACTGGTCT	TTTTAAAGGA	5160
TAGAAAGAGT	TTGCTGTCTC	TTCTTATTTT	TGCTCTGATT	GGTCTTTTTC	TCAACCAATT	5220
CGCCTATCTG	TCTGCTATTC	AGGAGACCAA	TGCGGGAACA	GCGACGGTGC	TTCACTATGT	5280
TTGTCTGTG	GGAATTTTAA	TTTATAGCTG	TATCAAGGAT	AGGGTGGCAC	CGACACTGGG	5340
AGAGATAGTT	TCCATCATAT	TCGCCATCGG	AGGAACCTTC	CTGATCGCAA	CACATGGGCA	5400
GTGGACCAG	TTATCCATGA	CACCTGCTGG	TCTGTTCTGG	GGTCTCTTTT	CTGCCTTGAC	5460
TTATGCTCTG	TATATCATTT	TACCCATAGC	CTTGATTAAA	AAGTGGGGGA	GCAGCTTGGT	5520
CATTGGTGTG	GGAATGGTCA	TAGCAGGTTT	GGTCGCCCTT	CCTTTTACAG	GGGTTCTACA	5580
GGCCGATATC	CCGACTAGTC	TTGATTTTCT	CCTGCGTTT	GCAGGCATTA	TCCTTATCGG	5640
GACTGTCTTT	GCCTATACAG	CTTTCCTTAA	AGGAGCCAGT	CTGATAGGAC	CGGTCAAGTC	5700
AAGCTTGTTG	GCTTCAATTG	AGCCAATATC	GGCGATTTPC	TTTGCCTTCT	TAATAATGAA	5760
TGAACAATTT	TATCCCATTG	ATTTTCTTGG	TATGGCAATG	ATATTGTTTG	CTGTAACTTT	5820
GATTTCTTTG	AAAGATTAT	TCTTAGAAAA	ATAAAAAAGA	CTCTTTGTCC	GTGACAGAGA	5880
GTTTTTCGCT	GGTAATCTAA	TTATTTTCAA	GATAAAATTC	AAAGCGTTCG	CCTACATATT	5940
GACTTTTAC	GTATTCAAAA	GCAGTACCAT	CTTCTAGGTA	GGAAACCTGG	GTCAATCCAA	6000
GAATAGCATG	TCCTTTTCA	ACTTCCAAAT	AGTGGGCAAT	CTTTTCTTTA	GCAAGGCGAG	6060
CATAGATGGT	CTGTTGAGAT	TTGCCGATAC	GATAGCCATG	TTTTTGAAG	GTTTGAAGA	6120
AATGACTGGT	GATTTCTTCT	TTTTTAAAGT	CCTTAATGAA	TTTTTCAGGA	ATAGAAGCAA	6180
CTTCATAAAC	TAGGGGAAC	TGGTCGGCAT	AGCGGACCCG	CTCCATTTCG	ATAATATTGT	6240
CCGTGGA	AATTCCTAGC	TTGGCAACTT	CTTGCTCATT	GGGAATGGTT	TTTTTGTAGG	6300
AAATGAGCTG	GCTAGAGGGA	ACTTTACCTT	GGGATTTGAC	AATTTAGTA	AAACTGGTTG	6360
TCCCTCGCAT	CTTTTCTTGT	ACTCGAGTAC	TGGAAACAAA	GGTGCCGCTT	CCTACACGGC	6420
GCTCTAAGAC	GCCTTCTTCG	ACTAATAGAG	ATACGGCTTG	GCGGAGGGTC	ATGCGACTGA	6480
CCGCAAACTG	CTCAGCTAAA	TCTCTTTCAC	TGGGAAGCCT	CTCACCAATA	GCCCAACGGT	6540
ACTCGTCAAT	ATCCTTTTTT	ATCTGATCAT	GGATTTTAT	ATAAGCAGGT	AGCATATTTT	6600
TCACTTCATT	TCTATCTTTT	CTCTATTGTA	CCCCAATAAA	CTAGAAAAAG	TCAAACCTCG	6660
CCTTGTTTAG	TTGGTAATTC	GCCCTTATTT	GTGATAGAAT	ATTGAGAAAA	GATATTTCTT	6720
TTGAGAAAGG	AAAAAGATGA	GCAACATTTT	AACTGATTTG	CAAGATGTAG	AAAAAATCAT	6780

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CGTATTGGAC	TATGGTAGCC	AGTACAACCA	GCTGATTTC	CGCCGTATCC	GTGAGATTGG	6840
TGTTTTTTTCA	GAACATAAAA	GCCATAAAAT	TTCAGCTGCT	GAAGTTCGTG	AAGTCAATCC	6900
TGTAGGAATT	ATTCTATCAG	GTGGTCCAAA	TTCTGTATAT	GAAGATGGTT	CATTTGATAT	6960
TGACCCAGAA	ATCTTCGAAC	TCGGAATTCC	AATTTTGGGA	ATCTGTTATG	GTATGCAGTT	7020
ATTGACCCAT	AAACTTGGAG	GAAAAGTTGT	TCCTGCAGGT	GATGCTGGAA	ATCGTGAATA	7080
CGGTCAATCA	ACCCTAACTC	ACACACCATC	AGCGCTTTTT	GAATCAACAC	CTGATGAACA	7140
GACTGTTTTG	ATGAGCCATG	GTGATGCGGT	TACTGAGATT	CCTGCTGACT	TTGTTTCGTAC	7200
AGGTACATCA	GCTGACTGCC	CATACGCAGC	CATCGAAAAC	CCAGATAAAC	ACATTTACGG	7260
TATCCAATTC	CACCCAGAAG	TTCGTCATTC	TGTATACGGA	AATGATATCC	TTCGTAACCT	7320
TGCCCTTAAC	ATTTGTAAGG	CTAAAGGTGA	CTGGTCAATG	GATAATTTC	TTGACATGCA	7380
GATCAAAAAA	ATTCGTGAAA	CCGTCGGTGA	TAAACGTGTC	CTTCTTGGTC	TATCAGGTGG	7440
TGTTGACTCA	TCTGTCGTTG	GGGTCTTCT	CCAAAAAGCG	ATTGGCGATC	AATTGATCTG	7500
TATCTTCGTA	GACCACGGTC	TTCTTCGTAA	AGGCGAAGCT	GATCAAGTTA	TGGACATGCT	7560
CGGTGGTAAG	TTTGGTTTGA	ATATCGTCAA	AGCAGACGCT	GCTAAACGTT	TCCTTGACAA	7620
ACTTGCTGGC	GTCTCTGACC	CTGAACAAAA	ACGTAAAAATC	ATCGGTAACG	AGTTTGCTTA	7680
TGTATTCGAT	GACGAAGCAA	GCAAGCTCAA	AGATGTGAAA	TTCTTGCTC	AAGGTACTTT	7740
ATATACAGAT	GTTATCGAGT	CTGGTACGGA	TACAGCTCAA	ACTATCAAGT	CACACCACAA	7800
CGTGGTGGTC	TTCAGAAGA	TATGCAGTTT	GAATTGATTG	AACCACTCAA	TACTCTTTAC	7860
AAGGATGAAG	TTCGTGCTCT	TGGTACAGAG	CTTGGTATGC	CAGACCATAT	CGTATGGCGC	7920
CAACCATTCC	CAGGACCAGG	ACTTGCTATC	CGTGTCTATG	GTGAAATCAC	TGAAGAGAAA	7980
CTTGAAACCG	TTCGTGAATC	AGACGCTATT	CTTCGTGAAG	AAATCGCTAA	AGCTGGACTT	8040
GACCGCGATA	TTTGGCAATA	CTTCACTGTT	AACACAGGCG	TTCGTTTCAGT	CGGTGTTATG	8100
GGTGACGGTC	GTACGTATGA	CTACACGATT	GCAATCCGTG	CTATCACTTC	TATCGATGGT	8160
ATGACTGCTG	ATTTTGCCAA	AATTCCATGG	GAAGTACTTC	AAAAAATCTC	AGTACGTATC	8220
GTAAATGAAG	TGGATCATGT	TAACCGTATC	GTCTACGATA	TTACAAGTAA	ACCACCTGCA	8280
ACAGTTGAGT	GGGAATAATC	GCAAAAAAAT	TAAAAGCTTT	GTAAAATCAA	CGGTTACAGA	8340
GGATTAAAAA	CTGTAACCTG	GATTAAAACG	GGAACATTTG	CTAAAAAGAA	TAAATTGAAT	8400
AATAGTTCCA	AGTGGTTTAC	ATTTGGACAA	AAAATTAGAC	CGTAGTTTTC	AAGCTGCGGT	8460
CTTTTGATAT	ATATAATGAG	AATTAATGGC	TCTTTGTCAA	CTGTAGTGGG	TTGAAGTCAG	8520
CTAAGCTCGA	GAAAGGACAA	ATTTTGTCTT	TTCTTTTTTG	ATATTCAGAG	CGATAAAAAAT	8580

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CCGTTTTTTG AAGTTTTC	AGTTCGAAA ACCAAAGGCA	TTGCGCTTGA TAAGTTTGAT	8640
GAGATTATG GTCGCTTCCA	ATTTGGCGTT AGAATAGTGT	AGTTGAAGGG CGTTGACGAT	8700
TTTCTCTTTG TCCTTTAGAA	AGGTTTTTAAA GACAGTCTGA	AAAAGAGGAT GAACCTGCTT	8760
TAGATTGTCC TCAATGAGTC	CGAAAAATTT CTCCGGTTCC	TTATTCTGAA AGTGAAACAG	8820
CAAGAGTTGA TAGAGCTGAT	AGTGATGTTT CAAGTCTTGT	GAATAGCTCA AAAGCTTGTT	8880
TAAAATCTCT TTATTGGTTA	AATGCATACG AAAAGTAGGG	CGATAAAAAAT GTTTATCGCT	8940
GAGTTTACGA CTATCCTGTT	GTATGAGCTT CCAGTAGCGC	TTGATAGCCT TGTATTCATG	9000
AGACTTTCGA TCCAATTGAT	TCATGATTTG AACACGCACA	CGACTCGG	9048

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

GTACCTTTAT TGATGAATGG	ACTGTTTAAA TCAGTAGCAC	GCCAACCAGA TATGCTTTCT	60
GAGTTTCGTA GTTTGATGTT	TTTAGGTGTT GCCTTTATTG	AAGGAACTTT CTTTGTAAC	120
CTTGTCTTCT CATTTATTAT	CAAATAAATA CATGGAACGA	GAAGAAAAGG GAGGATTTTA	180
GATGGAAGAA AGTATTAATC	CAATCATCTC TATTGGTCCT	GTTATCTTCA ATCTGACTAT	240
GTTAGCCATG ACTTTGTTGA	TTGTGGGAGT TATTTTGTG	TTTATTTATT GGGCAAGCCG	300
CAATATGACC TTGAAACCCA	AAGGAAAGCA AAATGTACTT	GAGTATGTCT ATGACTTTGT	360
TATTGGATTT ACAGAACCTA	ACATTGGTTC GCGCTACATG	AAAGATTACT CACTCTTTT	420
CCTTTGTTTA TTCCTTTTCA	TGGTGATTGC CAATAACCTT	GGCTTAATGA CAAAGCTTCA	480
AACGATCGAT GGGACTAACT	GGTGGAGTTC GCCAACCGCT	AATTTACAGT ATGACTTAAC	540
CTTATCTTTT CTGTGCATTT	TGTTGACACA TATAGAAAGC	GTTCGTCGTC GTGGATTTAA	600
AAAAAGTATA AAATCTTTTA	TGAGTCCTGT TTTTGTGATA	CCGATGAATA TCTTGGAAGA	660
ATTTACAAAC TTCTTATCTT	TGGCTTTGCG GATTTTGGG	AATATCTTTG CAGGAGAGGT	720
CATGACGAGT TTGTTACTTC	TTCTTTCCCA CCAAGCTATT	TATTGGTATC CAGTAGCCTT	780
TGGAGCTAAT TTGGCTTGGA	CTGCATTTTC TGCTTTTATT	TCCTGCATCC AAGCTTATGT	840
TTTACTCTT TTGACATCTG	TGTATTTAGG GAATAAGATT	AATATTGAAG AGGAATAGAA	900

1038

AGGAGTAACT	GATGCACGTA	ACAGTAGGTG	AATTAATTGG	TAATTTTATT	TTAATCACTG	960
GCTCTTTTAT	TCTTTTGCTA	GTCTTGATTA	AAAAATTTGC	ATGGTCTAAT	ATTACAGGCA	1020
TTTTCGAAGA	AAGAGCTGAA	AAAATTGCTT	CAGATATTGA	CAGAGCTGAA	GAAGCCCGTC	1080
AAAAAGCAGA	AGTATTGGCT	CAAAAACGCG	AAGATGAATT	GGCTGGTAGC	CGTAAAGAAG	1140
CTAAGACAAT	CATTGAAAAT	GCAAAGGAAA	CAGCTGAGCA	AAGTAAGGCT	AATATCTTAG	1200
CAGATGCTAA	ACTAGAAGCA	GGACACTTAA	AAGAAAAAGC	CAATCAAGAA	ATTGCTCAAA	1260
ATAAAGTAGA	AGCTTTACAG	AGTGTTAAGG	GTGAGGTCGC	AGATTTGACC	ATCAGCTTAG	1320
CTGGTAAAAT	CATCTCACAA	AACCTTGACA	GTCATGCCCA	TAAAGCACTC	ATTGATCAGT	1380
ATATCGATCA	GCTAGGAGAA	GCTTAATGGA	CAAGAAAACA	GTAAAGGTAA	TTGAAAAATA	1440
CAGCATGCCT	TTTGTCCAAT	TGGTACTTGA	AAAAGGAGAA	GAAGACCGTA	TCTTTTCAGA	1500
CTTGACTCAA	ATCAAGCAAG	TTGTTGAAAA	AACAGGTCTG	CCTTCTTTT	TAAAACAAGT	1560
GGCAGTAGAC	GAGTCGGATA	AGGAAAAAAC	AATTGCTTTT	TTCCAAGATT	CTGTGTCGCC	1620
TTTATTACAA	AACCTTATCC	AGGTCTTGGC	CTACAATCAC	AGAGCAAATC	TTTTTTATGA	1680
TGTGCTTGTA	GATTGCTTGA	ACCGACTTGA	AAAAGAAACA	AATCGATTTG	AAGTGACGAT	1740
TACGTCTGCT	CATCCTCTAA	CTGATGAACA	GAAGACTCGT	TTGCTCCCTT	TGATTGAGAA	1800
AAAAATGTCT	CTGAAAGTAA	GGAGTGTAAG	AGAACAAATC	GATGAAAGTC	TCATTGGTGG	1860
TTTTGTCAAT	TTTGCCAATC	ACAAGACAAT	TGATGTGAGT	ATTAAACAAC	AACTTAAAGT	1920
TGTTAAAGAA	AATTTGAAAT	AGAAAGTGGT	GTTCTTTTGG	CAATTAACGC	ACAAGAAATC	1980
AGCGCTTTAA	TTAAGCAACA	AATTGAAAAT	TTCAAACCCA	ATTTTGATGT	GACTGAAACA	2040
GGTGTGTGTA	CCTATATCGG	GGACGGTATC	GCGCGTGCTC	ACGGCCTTGA	AAATGTCATG	2100
AGTGGAGAGT	TGTTGAATTT	TGAAAACGGC	TCTTATGGTA	TGGCTCAAAA	CTTGGAGTCA	2160
ACAGACGTTG	GTATTATCAT	CCTAGGTGAC	TTTACAGATA	TCCGTGAAGG	CGATACAATC	2220
CGCCGTACAG	GGAAAATCAT	GGAAGTCCCT	GTAGGTGAAA	GTCTGATTGG	TCGTGTTGTG	2280
GATCCGCTTG	GTCGTCCAGT	TGACGGTCTT	GGAGAAATCC	ACACTGATAA	AACTCGTCCA	2340
GTAGAAGCAC	CAGCTCCTGG	TGTTATGCAA	CGTAAGTCTG	TTTCAGAAC	ATTGCAAACT	2400
GGTTTGAAAG	CTATTGACGC	CCTTGTACCG	ATTGGTCGTG	GTCAACGTGA	GTTGATTATC	2460
GGTGACCGTC	AGACAGGGAA	AACAACCATT	GCGATTGATA	CAATCTTGAA	CCAAAAAGAT	2520
CAAGATATGA	TCTGTATCTA	CGTCGCGATT	GGACAAAAAG	AATCAACAGT	TCGTACGCAA	2580
GTAGAAACAC	TTTCGTCAGTA	CGGTGCCTTG	GACTACACAA	TCGTTGTGAC	AGCCTCTGCT	2640
TCACAACCAT	CTCCATTGCT	CTTCCTAGCT	CCTTATGCTG	GGGTTGCTAT	GGCGGAAGAA	2700

1039

TTTATGTATC AAGGTAAGCA TGTTTTGATT GTATACGATG ATCTATCAAA ACAAGCGGTA	2760
GCTTATCGTG AACTGTCGCT CTTGCTTCGT CGTCCTCCAG GTCGTGAAGC CTTCCCAGGG	2820
GATGTTTTCT ATCTCCACAG CCGTTTGCTT GAGCGCTCAG CTAAAGTTTC TGATGAACTT	2880
GGTGGTGGAT CAATTACAGC CCTACCATT TATCGAGACAC AAGCAGGAGA TATCTCAGCC	2940
TATATCGCAA CCAACGTGAT TTCTATCACT GATGGACAAA TCTTCCTTGG CGATGGCCTC	3000
TTCAATGCAG GTATTCGTCC AGCCATCGAT GCGGGTTCAT CTGTATCTCG TGTAGGTGGT	3060
TCTGCACAAA TCAAAGCCAT GAAGAAGGTT GCTGGTACAC TTCGTATCGA CCTTGCTTCA	3120
TACCGTGAGT TGGAAAGCCTT TACTAAGTTT GGTTCGACT TGGACGCAGC AACACAGGCT	3180
AAGTTGAACC GTGGACGTCG TACCGTTGAG GTCTTGAAAC AACCTGTTCA CAAACCATTA	3240
CCTGTTGAGA AACAAGTAAC CATTCCTTAT GCTTTGACAC ATGGTTTCTT GGATACTGTT	3300
CCAGTAGATG ATATTGTTTCG TTTCGAGGAA GAGTCCATG CCTTCTTTGA TGCTCAACAT	3360
CCAGAGATTT TGGAAACCAT TCGTGATACA AAAGACTTGC CAGAAGAAGC AGTCTTGGAT	3420
GCTGCGATTA CAGAGTTTCT CAATCAATCT AGCTTCCAAT AAGAATAGAG GTGTCAGATG	3480
GCAGTATCTC TAAATGATAT TAAAACAAAA ATCGCCTCAA CAAAAATAC GAGTCAAATC	3540
ACTAATGCCA TGCAAATGGT ATCGGCTGCT AAGCTAGGTC GTTCTGAAGA AGCTGCTCGC	3600
AACTTCCAAG TTTACGCTCA GAAAGTGCCT AAACTTTGA CAGATATCCT TCATGGTAAT	3660
GGAGCTGGTG CTTCAACTAA TCCGATGTTG ATTAGCCGTT CTGTGAAGAA GACAGGCTAT	3720
ATCGTTATCA CTTCAGACCG CGGTTTGTT GGAGGTTATA ATTCCTCTAT TTTGAAAGCT	3780
GTTATGGAGT TGAAAGAAGA ATACCACCCA GACGGTAAAG GTTTTGAAAT GATCTGTATC	3840
GGTGGGATGG GAGCTGATTT CTTTAAGGCT CGCGGTATTC AACCACCTTA TGAATTACGT	3900
GGCTTGTCAG ACCAACCTAG CTTTGATCAA GTTCGTAAGA TTATTTCAAA AACTGTTGAA	3960
ATGTACCAAA ATGAACTCTT TGATGAGCTT TATGTTTGCT ACAACCACCA TGTCATACG	4020
CTAACCAGTC AAATGCGTGT GGAACAAATG CTTCGATTG TTGACTTGGA TCCAAATGAA	4080
GCGGATGAAG AGTACAGCTT GACTTTTGAA TTGGAAACCA GCCGAGAAGA AATCTGGAG	4140
CAGTTGTTGC CTCAGTTTGC AGAAAGTATG ATTTACGGTG CCATTATCGA TGCCAAGACA	4200
GCTGAGAATG CTGCGGGCAT GACAGCCATG CAAACAGCGA CAGATAATGC TAAGAAAGTC	4260
ATCAATGATT TGACAATTCA GTATAACCGT GCCAGACAGG CGGCGATTAC ACAAGAAATT	4320
ACAGAAATCG TAGCAGGTGC TAGTGCCTTA GAATAGGCTC TAGTCCAGCT CGTATGAAAA	4380
TGAACTTAGG ACCTAGTTGA GCTAGGAACC GACAGTATCT TATATAGAAT AGGAGAAGGA	4440

1040

GATGAGTTCA	GGTAAATG	CTCAGGTAT	CGGTCCCGTT	GTAGACGTTT	TGTTTGCAGC	4500
AGGGGAAAAA	CTTCCTGAGA	TTAACAATGC	ACTTGTCGTC	TACAAAAATG	ACGAAAGAAA	4560
AACAAAAATC	GTCCTTGAAG	TAGCCTTGGA	GTTAGGAGAT	GGTATGGTTC	GTA CTATCGC	4620
CATGGAATCA	ACAGATGGGT	TGACTCGTGG	AATGGAAGTA	TTGGACACAG	GTCGTCCAAT	4680
CTCTGTACCA	GTAGGTAAAG	AACTTTTGGG	ACGTGTCTTC	AACGTTTGG	GAGATACCAT	4740
TGACTTGGA	GCTCCTTTTA	CAGAAGACGC	AGAGCGTCAG	CCAATTCATA	AAAAAGCTCC	4800
AACTTTTGAT	GAGTTGTCTA	CCTCTTCTGA	AATCCTTGAA	ACAGGGATCA	AGGTTATTGA	4860
CCTTCTTGCC	CCTTACCTTA	AAGGTGGTAA	AGTTGGACTT	TTCGGTGGTG	CCGGAGTTGG	4920
TAAAACTGTC	TTAATCCAAG	AATTGATTCA	CAACATTGCC	CAAGAGCACG	GTGGTATTTT	4980
AGTATTTGCT	GGTGTGGGG	AACGTACTCG	TGAGGGGAAT	GACCTTTACT	GGGAAATGAA	5040
AGAATCAGGC	GTTATCGAGA	AAACAGCCAT	GGTCTTTGGT	CAGATGAATG	AGCCACCAGG	5100
AGCACGTATG	CGTGTGCCC	TTACTGGTTT	GACAATCGCT	GAATACTTCC	GTGATGTGGA	5160
AGGCCAAGAC	GTGCTTCTCT	TTATCGATAA	TATCTTCCGT	TTCCTCAGG	CTGGTTCAGA	5220
AGTATCTGCC	CTTTTGGGTC	GTATGCCATC	AGCCGTTGGT	TACCAACCAA	CACTTGCTAC	5280
GGAAATGGGT	CAATTGCAAG	AACGTATCAC	ATCAACCAAG	AAGGGTTCTG	TAACCTCTAT	5340
CCAGGCTATC	TATGTGCCAG	CGGATGACTA	TACTGACCCA	GCGCCAGCAA	CAGCCTTCGC	5400
TCACTTGGA	TCAACAACAA	ACTTGGAACG	TAAGTTGGTA	CAATTGGGTA	TCTACCCAGC	5460
CGTTGACCCA	CTTGCTTCAA	GCTCACGTGC	CTTGGCACCT	GAAATCGTTG	GAGAAGAGCA	5520
CTATGCAGTT	GCTGCTGAAG	TAAAACGTGT	CCTTCAACGT	TACCATGAAT	TGCAAGATAT	5580
CATTGCTATC	CTTGGTATGG	ATGAGCTTTC	TGATGAAGAA	AAGACCTTGG	TTGCTCGCGC	5640
CCGTCGTATC	CAGTTCTTCT	TGTCACAAAA	CTTCAACGTT	GCGGAACAAT	TTACTGGTCA	5700
GCCAGGTTCT	TATGTTCCAG	TTGCTGAAAC	TGTACGTGGC	TTTAAGGAAA	TCCTTGATGG	5760
TAAATACGAC	CACTTGCCAG	AAGATGCCTT	CCGTGGTGTA	GGTTCATATG	AAGATGTGAT	5820
TGCAAAAGCT	GAAAAAATGG	GATTTTAAGA	GGTGATCTAT	GGCTCAGTTA	ACTGTCCAGA	5880
TCGTGACACC	AGATGGTCTC	GTCTATGATC	ACCATGCCAG	CTATGTATCG	GTTGCAACTC	5940
TGGATGGTGA	GATGGGGATC	TTGCCACGAC	ATGAAAATAT	GATTGCGGTT	TTAGCAGTTG	6000
ATGAAGTAAA	GGTAAAACGT	ATCGATGATA	AAGATCACGT	GAAGTGGATT	GCAGTAAACG	6060
GTGGCGTTAT	TGAAATGCC	AATGATATGA	TCACAATCGT	CGCTGACTCT	GCAGAACGTG	6120
CTCGTGATAT	CGATATCAGT	CGTGCAGAAC	GTGCCAAACT	TCGTGCAGAA	CGTGCAATTG	6180
AAGAAGCACA	AGACAAACAT	TTGATTGACC	AAGAACGTCG	TGCTAAGATT	GCTTTGCAAC	6240

1041

GTGCTATTAA CCGTATTAAAT GTCGGAAATA GACTATAAGA AAAAATGAAC TTGAAAATAC	6300
CAAGTTCATT TTTTATGGTG TTTTAAGGAG CAAAACGGAT GCAGACTGCT TCGGGAACAT	6360
GGAAGTCGTT GGAGAGTTCT GCTAGACGAC CATTGTCACA ATTACGTTTA AAGACAGTTG	6420
CATTGTCAGA GTCTTGATGG ACAACAATGA GAAATTTTGT GTCGGGTGTC AAATCAAAAT	6480
CACGTGGAGT CTGACCATGC GTTGGAACGA TTTCTAATAA CTCTAAGCTA CCGTCCGCAA	6540
GGATGGTATA TACTGCGATA GAATCATGGC CACGGTTAGA AGCGTAGAGG TATTTACCGT	6600
CTTTAGAGAG ATGAATAGCA GCGGTTCCAT TAAAGCCTTC GTAAGCTTCC GGTAAAGTTG	6660
AAATGACCTG CATACTGTTCA AATTCGCCAA CGCCATCGTA GATTAAAACT TCGATAGTAC	6720
TATTGAGTTC ACAAATGAGA TAAGCGATTT TATAGTGGTT ATGGAAAATG ATATGGCGTG	6780
AGCCTGCTCC TGGCTTGCTG TGATAGGTAT AGAGCTTAGA TAATTTTCCT TCTTGATCGA	6840
GGTCATAGGT GATGACTTGG TCAGTTCCCA AGTCGCAGGT CACTAGATAG TGGTCAGGTG	6900
TTAAATCTGT ATAGTGAAACA TGGGGGGAAG CTGATTTTC ATGTGGACCT TGGCCACTGT	6960
GTTGATCCAT ATCACTAAGT AGAAGACTAC CATCTTCTG GCGTTTATAA ACAAGGACTT	7020
GTCCCTTGTG ATAGTTAGCT GCGTAAACCA AATCACGCTT TTCATCGACA GCAACATAAC	7080
AGTGGGGAGC TCCTTCTTCA ACAACATGAT TTAACACAGT CCCGTCAGTT TGATAGGCTG	7140
CAATTCCCC CTTATCGTCT TGGCTACCAA CAGTGATATA ATGTTGGTGC TGGTCAAAGG	7200
CAAGGTAGGT TGGACTTGGC TCAGCTGCAA AAAGTTCTAG ATTTGAAAGC TGACCAGTTT	7260
CTGTATCAAA GTCTGCCTTG TAAATCCCTT GAGAAGTACG ACGTGATATA GTTCCAAAAT	7320
AAACAGTTTC TTTCATTACT ATACCTCTGT GTAAAGATAA GACTATTATA TCACAAAAAC	7380
AAGTAAATTA AAGATATCCA ATTAGATGTA AGCACTTTAA AAAAGAGTTA TTTTGTTCAT	7440
AAAATGGTAT AATGAGAGAA CAATAGAAAG GAAGTATTTA TGGAGCAAAA AGAGAAACAT	7500
TTTAGCCTAT CTTGGTTTTT CAAGTGGTTT TTAGATAACA AGGCAATTAC GGTATTTTTA	7560
GTAACCTTAT TATTGGGACT GAATCTTTTT ATTTTAAGTA AGATTAGTTT TCTATTTTCA	7620
CCTGTTTATG ACTTTTATAG AGTTGTGATG TTGCCAGTCA TTTTGTCTGG TTGTTATAT	7680
TATTTGTTGA ATCCTATTGT TGATTGGATG GAGAAGCATA AGGTTAATCG TGTATAGCT	7740
ATCACTATTG TCTTTGTTAT CATCGCTCTC TTTATCATT GGGGCTTGGC AGTCGCCATT	7800
CCAAATCTGC AACGTCAGGT TTTGACCTTT GCAAGAAACG TTCCTGTTTA CTAGAAGAT	7860
ATAGATAGGA TTGTTAATGG ATTGGTAGCC CAGCACCTGC CAGATGATTT CAGACCTCAA	7920
TTAGAGCAAG TTTTGACCAA TTTTCTAGC CAGGCTACAG TTTTGGCAAG TAAGGTTTCA	7980

1042

TCTCAGGCAG	TCAACTGGGT	GAGTGCCTTT	ATTAGCGGGG	CTTCTCAAGT	GATTGTTGCC	8040
TTGATTATCG	TTCCCTTTCAT	GCTCTTTTAT	CTCTTGCGTG	ATGGGAAAGG	CTTGCGTAAC	8100
TATTTGACCC	AATTCATTCC	AAGAAAATTG	AAGGAACCTG	TTGGACAAGT	TTTATCAGAT	8160
GTGAATCAAC	AGTTGTCCAA	CTATGTTCTGA	GGGCAAGTGA	CAGTGGCTAT	TATTGTAGCA	8220
GTAATGTTTA	TCATCTTCTT	CAAGATTATT	GGTCTACGCT	ATGCGGTTAC	GCTGGGGGTT	8280
ACTGCTGGTA	TTTTAAATCT	GGTCCCTTAT	CTTGGTAGCT	TTCTAGCCAT	GCTTCCTGCT	8340
CTAGTATTGG	GTTTGATTGC	TGGTCCAGTC	ATGCTTTTGA	AAGTAGTGAT	TGTCTTTATC	8400
GTAGAACAAA	CTATTGAAGG	CCGTTTTGTC	TCTCCATTGA	TTTTGGGAAG	TCAATTAAAC	8460
ATCCACCCTA	TTAATGTTCT	CTTGTTTTTG	TTAACTTCAG	GATCTATGTT	TGGTATCTGG	8520
GGAGTTTAC	TTGGTATTCC	GGTTTATGCC	TCTGCTAAGG	TTGTCATTTC	AGCCATTTTC	8580
GAATGGTATA	AGGTAGTCAG	TGGTCTATAT	GAATTAGAGG	GTGAGGAAGT	CAAGAGTGAA	8640
CAATAGTCAA	CAGATGTAC	AGGCTTTGGA	GGAGCAAGAT	TTAACTAAGG	CTGAGCATT	8700
TTTCGCCAAA	GCTTTAGAAA	ATGATTCAAG	TGATCTTCTG	TATGAATTGG	CAACTTATCT	8760
TGAAGGGATT	GGTTTCTATC	CTCAGGCCAA	GGAATTTTAC	CTGAAAATTG	TAGAGGATTT	8820
TCCAGAGGTT	CATCTTAATC	TAGCTGCAAT	TGCTAGCGAG	GATGGTCAAA	TAGAAGAAGC	8880
CTTTACCTAT	CTTGAGGAAA	TCCAAGCTGA	CAGTGAAGT	TATGTCTCGT	CTTTGGCTCT	8940
GAAGGCAGAC	CTTTACCAGC	TGGAAGGTTT	GACAGATGTG	GCACGTGAGA	AATTATTGGA	9000
GGCCTTGACC	TACTCAGAGG	ATTCTCTCTT	GATATTGGGT	TTGGCAGAGT	TGGATAGTGA	9060
GTTGGAAAA	TACCAAGCGG	CTATTCAAGC	CTATGCCCAG	TTAGATAATC	GCTCGATTTA	9120
TGAGCAAACG	GGCATTTCCT	CCTATCAACG	AATTGGCTTT	GCCTATGCTC	AGTTAGGGAA	9180
ATTTGAAACG	GCTACTGAGT	TTTTAGAAAA	AGCCCTGGAG	TTAGAATACG	ATGACTTAAC	9240
AGCTTTTGAG	TTGGCCAGTC	TTTATTTTGA	TCAAGAAGAA	TATCAAAAAG	CCACCCTCTA	9300
CTTTAAGCAG	CTTGATACCA	TTTCTCCTGA	CTTTGAAGGC	TATGAGTATG	GGTACAGTCA	9360
GGCTTTACAT	AAGGAACATC	AAGTTCAAGA	AGCCCTGCGT	ATCGCTAAGC	AAGGATTAGA	9420
GAAAAATCCC	TTTGAAACTC	GCCTCTTGCT	AGCTGCTTCA	CAATTTTCTT	ATGAATTGCA	9480
TGATGCTAGT	GGTGCAGAAA	ATTATCTCCT	TACTGCAAAA	GAAGACGCTG	AGGATACAGA	9540
AGAAATCTTG	CTTCGTTTAG	CCACTATTTA	TCTGGAGCAG	GAGCGTTATG	AGGATATTCT	9600
AGAATTGCAG	AGTGAGGAGC	CAGAAAATCT	TTTGACCAAG	TGGATGATTG	CTCGTTCTTA	9660
TCAAGAAATG	GACGATTTGG	ATACTGCTTA	TGAGTATTAT	CAAGAGTTGA	CAGGAGATTT	9720
GAAGGACAAT	CCAGAATTTC	TGGAACACTA	TATCTATCTC	TTGCGTGAAT	TGGGACATTT	9780

1043

TGAAGAAGCA AAAGTCCATG CTCACACTTA CTTAAAACTG GTTCCAGATG ATGTGCAAAT	9840
GCAAGAAGCTG TTTGAGAGAT TGTAAGAATG TTTAACCCAA ATCATTCATA CCTCTCTCAA	9900
CTAGATGTAA CTTACAAAAC CCCTGACCTC ATGAGCCACT TTCTTCCTCC TCATGAGGTC	9960
AGTTTTACTT TCTGCTGTTC CAGTATCGTT TTTCTCGCT AGATTTCCTC AAAAGGGCAG	10020
ACTCCTCCCT TGGTGCGTCA CACGATTTTT TCATCTCGAC TGTTCCTTAA TGCATCATTA	10080
ACGACGCTTT TCTTCTAGGT GGTTCATAAG GAACAGGAAG ATTCAGGTTG ACTTTTCTAA	10140
TCCTAGAATA AAGTGCTGAA AACAATTCCG AATAGGCATA GAGACTAGAC AATTTGAGGA	10200
GCTGCTTGCG TCCTGTTCGA ACACATTTTC CCACCACGTG AAGAAAAAGA TGGCGGAAGC	10260
GTTTGATTGT TAAAGTTTGG AAGTCACCTC CAGCTAGATG TTTGAGAAAA AGATAGAGAT	10320
TGTAGGCGAT ACAGCTCATC ATCATACGAA TTCGTTTTTG ATTAAGGTTG AACATATCCGT	10380
TTTATCGCCA AAAAATCGG	10399

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

GATAAGATTA AGTTAGAAAA GAAAGAACTA GGACATATCT ACCAGATTCA GGTTTTTAAT	60
AGCTATGGGC AGGAAGAAAT CTATCGTGTG ATTTTGATGG AGACCAATAT TAGTTCGGTT	120
TCAACCAATA TCAAGTATGC TGCTGTCTTG ATTAATACCA GTCAGTTGGA ACAGGCTAGT	180
CAAAAGCATG AGCAATTGAT TGTGGTCGTG ATGGCTAGTT TCTGGATTTT GTCTTTACTT	240
GCCAGTCTCT ATCTAGCTAG GGTCAGTGTT AGGCCCTGC TTGAGAGTAT GCAGAAGCAA	300
CAGTCTTTTG TGGAAAATGC CAGTCATGAG TTACGAACTC CACTCGCAGT TTTGCAAAAT	360
CGCTTAGAGA CCCTTTTTCG TAAGCCAGAA GCTACCATTA TGGATGTGAG CGAAAGCATT	420
GCATCGAGTT TGGAAGAAGT CCGAAATATG CGTTTTTTAA CGACAAGCTT GCTGAACTTA	480
GCTCGGAGAG ATGATGGGAT TAAGCCGGAG CTTGCAGAAG TTCCAAC TAG CTTTTTTAAT	540
ACAACTTTCA CAACTACGA GATGATTGCT TCGGAAAATA ATCGTGTCTT CCGTTTTGAA	600
AATCGTATCC ATCGAACAAT TGTCACAGAT CAGCTTCTTC TGAAACAACAT GATGACCATT	660
CTTTTCGATA ATGCCGTCAA GTATACTGAG GAGGATGGTG AAATTGATTT TCTTATCTCG	720

1044					
GCGACCGATC	GCAATCTTTA	TTTACTTGTT	TCTGATAATG	GAATCGGTAT	TTGACAGAA 780
GATAAAAAGA	AAATTTTGA	CCGTTTTTAT	CGAGTAGACA	AGGCTAGAAC	CCGGCAAAAA 840
GGTGGTTTTG	GTTTAGGATT	ATCCCTAGCC	AAGCAAATTG	TAGATGCTCT	AAAAGGAACT 900
GTTACTGTCA	AAGATAATAA	ACCCAAGGGA	ACAATCTTTG	AAGTGAAGAT	TGCCATTTCAG 960
ACACCATCTA	AAAAGAAAAA	ATAAAAATAT	CGCTCCAATT	GGGGCGATAT	TTTGGATTTA 1020
TCTTCTACGT	TTTCGTTTGA	TAATAGACCG	TTGAACTTT	AAAACAAGTA	AGCTGAATCC 1080
GATTGCTGCG	GCAAAGGCAA	GAGCAGTTGA	TAATTTTAAT	GCTAAAAAGA	TAAAACATAA 1140
GATAGCAATA	CAGATACAAA	AAACAGCGAT	ATTAATAAAA	AATAGGATTT	CCTTGAGATT 1200
GGCATCAGAT	TGCGCTTCAG	GTGTATAAGC	TTGGTAATGA	GGAAGCTGCT	GGTTTAATTC 1260
TTCTTGATAG	TCTACCTCAT	AGGATTGTAA	TTTCTTACG	GGCATGATTC	TCTCCTTAAC 1320
AGTACATACC	TATTTTATCA	TTTTTTCGGC	AGAGAATTAT	TACAGAAAAG	TTACAAAAAG 1380
AATAAAGTCC	CTTTTCATTT	TCAAAGCATG	GCTGATTTTG	GAGAAATGTG	GTATAATTTT 1440
TCTTATGGAA	AAGATTGTCA	TTACAGCAAC	TGCTGAAAGT	ATTGAACAAG	TTGAACAACT 1500
ACTCGAAGCT	GGCGTAGACC	GTATCTATGT	CGGTGAGAAA	GATTTTGCTC	TTGCTCTGCC 1560
AACGACCTTT	AGTTATGACC	AATTACGTGA	AATCGCTAAG	TTGGTTCATG	ATGCTGGTAA 1620
GGAATTGATC	GTTGCGGTCA	ATGCTCTCAT	GCACCAAGAT	ATGATGGACC	GTATCAAGCC 1680
TTTCTTAAAC	TTCTTGGAAG	AAATCAAGAC	AGACTATATT	ACGATTGGGG	ATGCAGGCGT 1740
CTTTTACGTA	GTTAACCGCG	ATGGTTATTC	ATTTAAGACC	ATCTACGATG	CTTCAACCAT 1800
GGTAACTAGC	AGTCGTCAGA	TTAACTTCTG	GGGACAAAAG	GCTGGCGCAT	CTGAGGCTGT 1860
TTTGCGCGGT	GAAATTCCAT	CAGCTGAACT	TTTCAAAATG	CCAGAGATTT	TGGAAATTCC 1920
TGCTGAAGTT	TTGGTTTACG	GTGCTAGCGT	CATCCATCAT	TCTAAACGTC	CACTCTTGCA 1980
AAACTACTAT	AACTTTACAC	ATATCGATGA	TGAAAAGACG	CATAAACGTG	ACCTCTTCTT 2040
GGCTGAGCCA	AGTGATCCAG	AGAGCCACTA	TTCCATTTTT	GAAGATAATC	ATGGGACCCA 2100
TATCTTTGCC	AACAATGACC	TTGATTTGAT	GATCAAATTA	ACAGAATTGG	TGGAGCATGG 2160
CTTTACTCGC	TGGAAACTAG	AAGGGCTCTA	CACTCCTGGT	CAGAACTTTG	TTGAGATTGC 2220
AAAACCTCTT	ATCCAAGCGC	GTAGCTTGAT	TCAAGAGGGC	AACTTTAGTC	ATGCTCAAGC 2280
CTTCTTGCTG	GATGAAGAAG	TCGTAAACT	TCACCCTAAA	AACCGTTTCC	TTGATACAGG 2340
ATTTTATGAC	TACGATCCTG	ACATGGTTAG	ATAAAATACA	TGATTCGTTG	AGAGAAGGAA 2400
GATGCAAACA	TTTCTTCTCT	CAATTTTTCG	TATTTCTTCA	CTATTTTACA	AAAATCAGCA 2460
GGCTAGAATG	CTCTATTCGA	TGGGATTTTT	AAGAAAAGTA	GTGTTCTTGA	GTTTGAAAAT 2520

1045

TATCCTATGT	TTGCAGGTGC	CAAATGGCCC	TTTTTTTGGT	ATAATTTTTT	ATAATGAAAA	2580
CGATTGGTAA	TCGCTATGTT	GTGGTGGATT	TAGAGGCAAC	TAGCACAGGT	AGTAAGGCTA	2640
AAATTATCCA	AGTGGGAATT	GTCGTGATTG	AGGACGGAGA	AATCGTCGAT	CACTATACGA	2700
CGGATGTCAA	TCCACATGAA	CCCTTGGATG	CTCATATCAA	AGAACTGACA	GGATTGACAG	2760
ACCAACGTCT	GGCGCAAGCA	CCTGATTTTT	CGCAAGTTGC	CAGAAAAATA	TTTGACTTGG	2820
TGGAGGATGG	GATTTTGTGA	GCCCATAATG	TTCAGTTTGA	TGCTAATCTC	TTGGCGGAAA	2880
ATTTATTTTT	TGAAGGCTAT	GAGCTAAGAA	ACCCTCGTGT	TGATACGGTC	GAATTGGCCC	2940
AGGTCTTTTT	CCCTGAACTG	GAAAAATATA	GCTTGCCGAT	TTTGTGTGCGA	GAATTAGGAA	3000
TTCTCTTAA	ACACGCACAC	ACAGCCCTTT	CAGATGCCCA	AGCTACAGCA	GAATTACTTC	3060
TTTTTTTACG	GAAAAAGATG	ACCCAGCTTC	CTAAAGGTCT	CTTGGAACGC	TTGCTGGAAA	3120
TGGCTGACGC	TCTCCTATAT	GAGTCCTACC	TGGTTATTGA	GGAAACTTAT	CGCAACCAAT	3180
CTATCCTGAG	TTCTCCAGAC	TTGGTCCAAG	TTCAAGGTCT	ATATTTTAAG	AAAACGGAAAG	3240
CTTCTCTGGA	GCCACGAAAA	CTATCTCAAG	ACTTTTCTAA	AAATATTTCT	CTGTTGAACC	3300
TTGAAGTGAG	GGAGGAACAA	GAAAGTTTGT	CTAAAGAGGT	TGGCTTGCTA	TTGAAAGATG	3360
AACCTGTCTC	TCTGATTCAA	GCGCCGACAG	GGATTGGGAA	AACCTATGGC	TATCTCTTAC	3420
CCGCTTTATC	TCAATCCAAA	GAGCGACAAA	TTGTTCTTAG	TGTTCCGACA	AAGATTCTTC	3480
AAAATCAAAT	CATGGAAGAA	GAAGGTAAAC	GCCTCAAGGA	AGTGTCCAT	ACAGATATTC	3540
ATAGCTTAAA	GGGACCACAA	AATTATCTGA	AGTTGGATGC	CTTTTATCAT	TCCTTGCAGG	3600
AAAATGATGA	AAATCGCTTA	TTTAGACGCT	TTAAAATGCA	AGTCTTGGTC	TGGCTTACTG	3660
AGACAGAGAC	AGGAGATTTG	GATGAAATCG	GGCAACTCTA	CCGTTACCAA	CATTTTCTAG	3720
CAGACCTTCG	TCATGATGGG	AATTTATCAT	CCCAGAGCTT	ATTTGTGACG	GAAGATTTTT	3780
GGAAACGTAG	TCAAGAAAGG	GCAGAGACTT	GCAAGCTTTT	AGTGACTAAT	CATGCCTATC	3840
TCGTAACCGA	ACTTGAAGAT	AATCCTGAAT	TTGTCACTGA	CCGTTTACTG	ATTATTGATG	3900
AAGTCCAAAA	GATTTTGTGA	GCTCTAGAAA	ATCTGCTTCA	AGAGACCTAC	GATATACAAT	3960
CTATTATCGA	TTTAATTGAT	AAGGCTTTAG	TAGGAGAAGA	AAACAGGGTT	CAACAACGGA	4020
TACTAGAAAG	TATTCGCTTT	GAGTGTCTCT	ACTTGATAGA	ACAATTTCAG	TCTGGCAAAT	4080
CTAGGAAAAA	TATCTTAGAT	TCTCTGGACA	ATCTCCATCA	GTATTTTTC	GAATTGGAAG	4140
TAGAAGACTT	TGATGAGCTG	GTTTCGTATT	TTACAGCTGA	AGGTGATTAC	TGGCTTGAAG	4200
TAACTGAAAC	GAGTCAAAAG	AAAATTCAGA	TTTCTTCTAC	AAAATCAGGC	CGTACTCTTC	4260

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TGTCCTCTTT	ACTTCCTGAG	AGTTGCCAAG	TCTTGGGAGT	ATCGGCTACT	CTTGAGATTA	4320
GTCAGAGGGT	TTCTTTGGCA	GACCTTTTAG	GCTATCCTGA	AGCTAAATTT	GTCAAGATTG	4380
AATCTCGGGG	AAAACAGGAA	CAAGAAGTGG	TCATGGTCAA	AGATTTCCCT	CTGGTAACAG	4440
AAACCTCCTT	AGAAGTCTAT	GCCAGAGAGG	TAGCTGCTTT	ACTAGTGGAA	ATTCAAGCTT	4500
TCCAGCAACC	GATTTTGGTT	CTCTTTACCG	CTAAAGACAT	GCTTCTAGCA	GTATCGGATT	4560
TACTTACAGT	TAGCCACTTG	GCCCAGTATA	AAAATGGGGA	TGTTTCATCAG	CTAAAGAAAC	4620
GCTTTGAAAA	AGGTGAACAA	CAAATCTTGC	TTGGTGCAGC	AAGTTTCTGG	GAGGGAGTTG	4680
ATTTTCAAG	CCATCCTTCT	GTGATTCAAG	TTGTACCGAG	GCTTCCTTTC	CAAAATCCTC	4740
AAGAACCCTT	GACGAAAAAG	ATTAATCAAG	AACTGAATCA	AGAAGGGAAA	AATGCCTTTT	4800
ATGATTATCA	ATTGCCAATG	GCCATTATTC	GTTTAAAACA	GGCTTTGGGA	AGAAGTATGA	4860
GACGTGAATA	CCAACGTTCC	TTAACTCTTA	TTTTGGATAG	GAGAATCGTC	GGAAAACGAT	4920
ACGGCAAACA	AATAGTAGCA	TCTCTAGCAG	AAGAAGCGAC	TGTTAAAACC	ATCTCTCGAT	4980
CCGAAGTTGA	CGAGGCTATT	GATAGATTTT	TTAATGAGCT	TTGATAAATA	GTATTGTATG	5040
AAAGTATAAG	GTTAGTATAT	ATGAAACGTT	CTCTCGACTC	AAGAGTCGAT	TACAGTTTGC	5100
TCTTGCCAGT	ATTTTTTCTA	CTGGTCATCG	TGTGTGGTGGC	TATCTATATA	GCCGTTAGTC	5160
ATGATTATCC	CAATAATATT	CTGCCCATT	TAGGGCAGCA	GGTCGCCTGG	ATTGCCTTGG	5220
GGCTTGTGAT	TGGTTTGTG	GTCATGCTCT	TTAATACAGA	ATTTCTTTGG	AAGGTGACCC	5280
CCTTTCTATA	TATTTTAGGC	TTGGGACTTA	TGATCTTGCC	GATTGTATTT	TATAATCCAA	5340
GCTTAGTTGC	ATCAACGGGT	GCCAAAACT	GGGTATCAAT	AAATGGAATT	ACCCATATTC	5400
AACCGTCAGA	ATTTATGAAG	ATATCCTATA	TCCTCATGTT	GGCTCGTGTC	ATTGTCCAAT	5460
TTACAAAGAA	ACATAAGGAA	TGGAGACGCA	CGGTCCGCT	GGACTTTTTC	TTAATTTTCT	5520
GGATGATTCT	CTTTACCATT	CCAGTCCTAG	TTCTTTTAGC	ACTTCAAAGT	GACTTGGGGA	5580
CGGCTTGGT	TTTTGTAGCC	ATTTTCTCAG	GAATCGTTTT	ATTATCAGGG	GTTTCTTGGA	5640
AAATTATTAT	CCCAGTATTT	GTGACTGCTG	TAACAGGAGT	TGCTGGTTTC	TTAGCTATCT	5700
TTATTAGCAA	GGACGGACGA	GCTTTTCTTC	ACCAGATTGG	AATGCCGACC	TACCAAATTA	5760
ATCGGATTTT	GGCTTGGCTC	AATCCCTTTG	AGTTTGCCCA	AACAACGACT	TACCAGCAGG	5820
CTCAAGGGCA	GATTGCCATT	GGGAGTGGTG	GCTTATTTGG	TCAGGGATT	AATGCTTCGA	5880
ATCTGCTTAT	CCCAGTTCGA	GAGTCAGATA	TGATTTTAC	GGTTATTGCA	GAAGATTTTG	5940
GCTTTATTGG	CTCTGTCCTG	GTTATTGCCC	TCTATCTCAT	GTTGATTTAC	CGTATGTTGA	6000
AGATTACTCT	TAAATCAAAT	AACCAGTTCT	ACACTTATAT	TTCCACAGGT	TTGATTATGA	6060

1047

TGTTGCTCTT	CCACATCTTT	GAGAATATCG	GTGCTGTGAC	TGGACTACTT	CCTTTGACGG	6120
GGATTCCCTT	GCCTTTCATT	TCGCAAGGGG	GATCAGCTAT	TATCAGTAAT	CTGATTGGTG	6180
TTGGTTTGCT	TTTATCGATG	AGTTACCAGA	CTAATCTAGC	TGAAGAAAAG	AGCGGAAAAG	6240
TCCCATTCAA	ACGGA AAAAG	GTGTATTAA	AACAAATTAA	ATAAGGAGAA	AATCATGGTA	6300
AAAGTAGCAG	TTATATTAGC	TCAGGGCTTT	GAAGAAATTG	AAGCCTTGAC	AGTTGTAGAT	6360
GTCTTGCGTC	GAGCCAATAT	CACATGTGAT	ATGGTTGGTT	TTGAAGAGCA	AGTAACGGGT	6420
TCGCATGCAA	TCCAAGTAAG	AGCAGATCAT	GTCTTTGATG	GAGATTTATC	AGACTATGAT	6480
ATGATTGTTT	TTCTTGAGAG	TATGCCTGGT	TCTGCACATT	TACGTGATAA	TCAGACCTTG	6540
ATTCAAGAAT	TGCAAAGCTT	CGAGCAAGAA	GGGAAGAAAC	TAGCAGCCAT	TTGTGCGGCA	6600
CCAATGCCCC	TCAATCAAGC	AGAGATATTG	AAAAATAAGC	GATACACTTG	TTATGACGGC	6660
GTTCAAGAGC	AAATCCTTGA	TGGTCACTAC	GTCAAGGAAA	CAGTAGTGGT	AGATGGTCAG	6720
TTGACAACCA	GTCGGGTCC	TTCAACAGCC	CTTGCCTTTG	CCTACGAGTT	GGTGGAGCAA	6780
CTAGGAGGGG	ACGCAGAGAG	TTTACGAACA	GGAATGCTCT	ATCGAGATGT	CTTTGGTAAA	6840
AATCAGTAAA	ACGGGAGTTA	TTCTCTCGTT	TTTTATGTGG	AAAAC TCAGG	GAAATCATCG	6900
CTTTTTCAT	AAAAAATGC	TATAATGAAG	GGTATGAAAT	ATCACGATTA	CATCTGGGAT	6960
TTAGGTGGA	CTTTACTGGA	TAATTATGAA	ACTTCAACAG	CTGCATTTGT	TGAAACATTG	7020
GCACTGTATG	GTATCACACA	AGACCATGAC	AGTGTCTATC	AAGCTTTAAA	GGTTTCTACT	7080
CCTTTTGCGA	TTGAGACATT	CGCTCCCAAT	TTAGAGAATT	TTTTAGAAAA	GTACAAGGAA	7140
AATGAAGCCA	GAGAGCTTGA	ACACCCGATT	TTATTTGAAG	GAGTTTCTGA	CCTATTGGAA	7200
GACATTTCAA	ATCAAGGTGG	CCGTCATTTT	TTGGTCTCTC	ATCGAAATGA	TCAGGTTTGT	7260
GAAATTTTAG	AAAAAACCTC	TATAGCAGCT	TATTTTACAG	AAGTGGTGAC	TTCTAGCTCA	7320
GGCTTTAAGA	GAAAGCCAAA	TCCCGAATCC	ATGCTTTTAT	TAAGAGAAAA	GTATCAGATT	7380
AGCTCTGGTC	TTGTCAATTGG	TGATCGGCCG	ATTGATATCG	AAGCAGGTCA	AGCTGCAGGA	7440
CTTGATACCC	ACTTGTTTAC	CAGTATCGTG	AATTTAAGAC	AAGTATTAGA	CATATAAGAA	7500
AAAGGAATAA	GATGACAGAA	GAAATCAAAA	ATCTGCAGGC	ACAGGATTAT	GATGCCAGTC	7560
AAATTCAAGT	TTTAGAGGGC	TTAGAGGCTG	TTCGTATGCG	TCCAGGGATG	TACATTGGAT	7620
CAACCTCAAA	AGAAGGTCTT	CACCATCTAG	TCTGGGAAAT	TGTTGATAAC	TCAATTGACG	7680
AGGCCTTGCC	AGGATTTGCC	AGCCATATTG	AAGTTTATAT	TGAGCCAGAT	GATTCGATTA	7740
CTGTTGTGGA	TGATGGGCGT	GGTATCCAG	TCGATATTCA	GGAAAAACA	GGCCGTCTG	7800

1048

CTGTTGAGAC CGTCTTTACA GTCCTTCACG CTGGAGGAAA GTTCGGCGGT GGTGGATACA	7860
AGGTTTCAGG TGGTCTTCAC GGGGTGGGGT CGTCAGTAGT TAATGCCCTT TCCACTCAAT	7920
TAGACGTTCA TGTTCACAAA AATGGTAAGA TTCATTACCA AGAATACCGT CGTGGTCATG	7980
TTGTGCGAGA TCTTGAAATA GTTGAGATA CGGATAAAAC AGGAACAAC TTTCACTTCA	8040
CACCGGACCC AAAAATCTTC ACTGAAACAA CAATCTTTGA TTTTGATAAA TTAAATAAAC	8100
GGATTCAAGA GTTGGCCTTT CTAAATCGCG GTCTTCAAAT TTCAATTACA GATAAGCGCC	8160
AAGGTTTGGA ACAAACCAAG CATTATCATT ATGAAGGTGG GATTGCTAGT TACGTTGAAT	8220
ATATCAACGA GAACAAGGAT GTAATCTTTG ATACACCAAT CTATACAGAC GGTGAGATGG	8280
ATGATATCAC AGTTGAGGTA GCCATGCAGT ACACAAC TGG TTACCATGAA AATGTCATGA	8340
GTTCGCGCAA TAATATTCAT ACCCATGAAG GTGGAACACA TGAACAAGGT TTCCGTACAG	8400
CCTTGACACG TGTATCAAC GATTATGCTC GTAAAAATAA GTTACTGAAA GACAATGAAG	8460
ATAATTTAAC AGGGGAAGAT GTTCGCGAAG GCTTAAC TGC AGTTATCTCA GTTAAACACC	8520
CAAATCCACA GTTTGAAGGA CAAACCAAGA CCAAATTGGG AAATAGCGAA GTGGTCAAGA	8580
TTACCAATCG CCTCTTCAGT GAAGCTTTCT CCGATTTCCCT CATGGAAAAT CCACAGATTG	8640
CCAAACGTAT CGTAGAAAAA GGAATTTTGG CTGCCAAGGC TCGTGTGGCT GCCAAGCGTG	8700
CGCGTGAAGT CACACGTAAA AAATCTGGTT TGGAAATTTT CAACCTTCCA GGGAACTAG	8760
CAGACTGTTT TTTAATAAC CCTGCTGAAA CAGAACTCTT CATCGTCGAA GGAGACTCAG	8820
CTGGTGGATC AGCCAAATCT GGTGCTAACC GTGAGTTTCA GGCTATCCTT CCAATTGCGG	8880
GTAAGATTTT GAACGTTGAA AAAGCAAGTA TGGATAAGAT TCTAGCCAAC GAAGAAATTC	8940
GTAGTCTTTT CACAGCCATG GGAACAGGAT TTGGCGCAGA ATTTGATGTT TCGAAAGCCC	9000
GTACCAAAA ACTCGTTTGT ATGACCGATG CCGATGTCGA TGGAGCCAC ATTCGTACCC	9060
TTCTTTTAAC CTTGATTAT CGTTATATGA AACCAATCCT AGAAGCTGGT TATGTTTATA	9120
TTGCCCAACC ACCAATCTAT GGTGTCAAGG TTGGAAGCGA GATTAAAGAA TATATCCAGC	9180
CGGGTGCAGA TCAAGAAATC AACTCCAAG AAGCTTTAGC CCGTTATAGT GAAGGTCGTA	9240
CCAAACCGAC TATTCAGCGT TATAAGGGGC TAGGTGAAAT GGACGATCAT CAGCTGTGGG	9300
AAACAACCAT GGATCCCGAA CATCGCTTGA TGGCTAGAGT TTCTGTAGAT GATGTGCAGA	9360
AGCAGATAAA ATCTTTGATA TGTGATGGG GATCGAGTTG TCCTCGTCG	9409

(2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6415 base pairs
 - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

CCTGGGAAAG TCTTGAAAAT TATGATAGAA TGGTGGGAAGG AAAAATTCAG GAGAGTAGTA	60
GTGACTCAAA ATGTTGAAAG TCTTCTCGTA TCCATTGTAA TCAGTGCATA CAATGAAGAA	120
AAATATCTGC CTGGTCTAAT TGAAGACTTA AAAAATCAAA CCTATCCTAA AGAGGATATT	180
GAAATTCTAT TTATAAATGC TATGTCCACA GATGGGACCA CAGCTATCAT TCAGCAATTT	240
ATAAAGGAAG ATACAGAGTT TAACCTCAATT AGATTGTATA ACAATCCTAA GAAAAATCAA	300
GCTAGTGGTT TTAACCTGGG AGTTAAACAT TCTGTAGGGG ACCTTATTTT AAAAAATGAT	360
GCTCATTCAA AAGTTACTGA GACTTTTGTA ATGAACAATG TGGCTATTAT TCAACAAGGT	420
GAATTTGTCT GTGGGGGGCC TAGACCGACG ATTGTCGAAG GAAAAGGAAA ATGGGCAGAG	480
ACCTTGCATC TTGTTGAGGA AAATATGTTT GGCAGTAGCA TTGCCAATTA TCGAAATAGT	540
TCTGAGGATA GATATGTTTC TTCTATTTTT CATGGAATGT ATAAACGAGA GGTTTTCCAG	600
AAGGTTGGTT TAGTAAATGA GCAACTTGGC CGAACTGAAG ATAATGATAT TCATTATAGA	660
ATTCGAGAAT ATGGTTATAA AATCCGCTAT AGCCCAAGTA TTCTATCTTA TCAGTATATT	720
CGACCAACAT TCAAGAAAAT GCTGCATCAA AAGTATTCAA ATGGTTGTG GATTGGCTTG	780
ACAAGTCATG TTCAGTTTAA GTGTTTATCA TTATTTCACT ATGTTCCCTG TTTATTTGTT	840
TTGAGTCTTG TGTTTAGTCT AGCATTGTTA CCGATCACAT TCGTATTCAT AACTTTACTA	900
TTAGGTGCCT ATTTTCTACT TTTGTCATTA CTCACCTTGC TGACTTTATT AAAACATAAA	960
AATGGATTTT TAATTGTGAT GCCCTTTATT TTATTTTCCA TTCACCTTGC TTATGGCCTT	1020
GGGACGATTG TAGGTTTAAT TAGAGGATTT AAATGGAAGA AGGAGTACAA GAGAACAATA	1080
ATTTATTTGG ATAAAATAAG CCAAATAAAT CAAAATATGC TATAATAACA ATATAGTAAA	1140
ACTCTTTTAA GGAGGAGTAG ATTTCTATGA ATAAAAAAT AACAGATTAT GTGATTGATC	1200
TGGTGGAAAT TTAAATAAAA CAACAAAAGC AGGTTTCTG GGGAATATTT GATATTTTCA	1260
GTATGGTGGT TTCCATCATT GTATCTTATA TTTTATTTTA TGGGCTGATT AATCCAGCAC	1320
CTGTTGACTA CATTATCTAT ACGAGTTTGG CCTTCCTGTT CTATCAATTG ATGATTGGTT	1380
TTTGGGGGTT GAACGCGAGC ATTAGTCGTT ACAGCAAGAT TACGGATTTC ATGAAAATCT	1440
TTTTTGGTGT GACTGCTAGC AGTGTCTTGT CATATAGTAT CTGTTATGCC TTCTTGCCAC	1500
TCTTCTCCAT CCGTTTCATC ATTCTCTTTA TCTTGTTGAG TACCTTCTTG ATTTTATGTC	1560

1050					
CACGGATTAC	TTGGCAGTTA	ATCTACTCCA	GACGCAAAAA	AGGTAGTGGT	GATGGAGAAC 1620
ACCGTCGGAC	CTTCTTGATT	GGTGCCGGTG	ATGGTGGGGC	TCTTTTATG	GATAGTTACC 1680
AACATCCAAC	CAGTGAATTA	GAACTGGTCG	GTATTTTGA	TAAGGATTCT	AAGAAAAAGG 1740
GTCAAAACT	TGGTGGTATT	CCTGTTTGG	GCTCTTATGA	CAATCTGCCT	GAATTAGCCA 1800
AACGCCATCA	AATCGAGCGT	GTCATCGTTG	CGATTCCGTC	GCTGGATCCG	TCAGAATATG 1860
AGCGTATCTT	GCAGATGTGT	AATAAGCTGG	GTGTCAAATG	TTACAAGATG	CCTAAGGTTG 1920
AAACTGTTGT	TCAGGGCCTT	CACCAAGCAG	GTAAGGCTT	CCAAAAAATT	GATATTACGG 1980
ACCTTTTGGG	TCGTCAGGAA	ATCCGTCTTG	ACGAATCGCG	TCTGGGTGCA	GAACTGACAG 2040
GTAAGACCAT	CTTAGTCACA	GGAGCTGGAG	GTTCAATCGG	TTCTGAAATC	TGTCGTCAAG 2100
TTAGTCGCTT	CAATCCTGAA	CGCATGTCT	TGCTCGGTCA	TGGGGAAAAC	TCAATCTACC 2160
TTGTTTATCA	TGAATTGATT	CGTAAGTTCC	AAGGGATGA	TTATGTACCT	GTGATTGCGG 2220
ACATTCAAGA	CTATGATCGT	TTGTTGCAAG	TCTTTGAGCA	GTACAAACCT	GCTATTGTTT 2280
ATCATGCGGC	AGCCCACAAG	CATGTCCTA	TGATGGAGCG	CAATCCAAAA	GAAGCCTTCA 2340
AAAACAATAT	CCGTGGAAC	TACAATGTTG	CTAAGGCTGT	TGATGAAGCT	AAAGTGTCTA 2400
AGATGGTTAT	GATTCGACA	GATAAGGCAG	TCAATCCACC	AAATGTTATG	GGAGCAACCA 2460
AGCGCGTGGC	GGAGTTGATT	GTCACTGGCT	TTAACCAACG	TAGCCAATCA	ACCTACTGTG 2520
CAGTTCGTTT	TGGGAATGTT	CTTGGTAGCC	GTGGTAGTGT	CATTCCAGTC	TTTGAACGTC 2580
AGATTGCTGA	AGGTGGGCCT	GTAACGGTGA	CAGACTCCG	TATGACCCGT	TACTTTATGA 2640
CCATTCCAGA	AGCTAGCCGT	CTGGTTATCC	ATGCTGGTGC	TTATGCCAAA	GATGGGGAAG 2700
TCTTTATCCT	TGATATGGGC	AAACCAGTCA	AGATTTATGA	CTTGGCCAAG	AAGATGGTGC 2760
TTCTAAGTGG	CCACACTGAA	AGTGAAATTC	CAATCGTTGA	AGTTGGAATC	CGCCCAGGTG 2820
AAAAACTCTA	CGAAGAACTC	TTGGTATCAA	CCGAAGTCGT	TGATAATCAA	GTTATGGATA 2880
AGATTTTCGT	TGGTAAGGTT	AATGTCATGC	CTTTAGAATC	CATCAATCAA	AAGATTGGAG 2940
AGTTCCGCAC	TCTCAGTGA	GATGAGTTGA	AGCAAGCTAT	TATCGCCTTT	GCTAATCAAA 3000
CAACCCACAT	TGAATAAAAA	AGAAAAACGC	ATAGTATCAA	GTTACACAAC	CTTGGTAATA 3060
TGCGTTTTAT	TATGTAGAGA	CTTATACTCT	TCGAAAATCT	CTTCAAACCA	CGTCAACGTC 3120
GCCTTGCCGT	ATATGGTTAC	TGACTTCGTC	AGTTCTATCC	ACAACCTCAA	AACAGTGTTT 3180
TGAGyTGACT	TCGTCAGTTC	TATCCACAAC	CTCAAAACAG	TGTTTTGAGc	TGACTTCGTC 3240
AGTTCTATCC	ACAACCTCAA	AACAGTGTTT	TGAGCTGAcT	TCGTCAGTTC	CATCCACAAC 3300
CTTAAAACAG	TGTTTTGAGy	TGACnTTCGT	CAGTTCCATC	TACAACCTTA	AAACAGTGTT 3360

1051

TTGAGCTGCC CGCAGCTAGT TTCCTAGTTT GCTCTTTGAT TTTCATTGAG TATTACTTCA	3420
TTTTCTTCTG AAATGGAATT GTTACCCAGT CTATGCTATT GAAAATACGC CAAAAC TTCT	3480
AAGGGTTTGT GAGCGATATA ATCAGGTTGA TAGTTTAGTA GATCTGCTTG CTCTCCAAAT	3540
CCCCAAGTGA TGGCCAATTT CTGAATACCT GTTTCCTCGAG CTCCCAGCAT ATCAAAC TTG	3600
GTATCTCCGA TGATGATGGC TTGTTCTGGT GCTAGTTGAT GTGTCTGCAA GGCTTGGTGA	3660
ATGACATCTG CCTTATGGGG TGCTTCAGGG CTAGAACCAT AAATGCCATC AAAGAAATGA	3720
TGGATTTCCTA AGTTTTTTGC CATGTCTTGA GCAGTAGATG TATCCTTTGT CGTGGTGATG	3780
TAGAGTGATG AACTGCTCGA TAACTCCTCA AGCAAGTCTA TAATCTGAGG AAAGAGTTGA	3840
GCTTCATAGA TGCCTTTTGC CTTATAGTAA GAACGATATA TCTGCACGGC TTCAGAAATT	3900
TGGTCTTTGG ACAGGCAGGT CGCAAACTA CTTTCGAGAG GTGGTCCCAT AAAACCACGA	3960
ATAGTTTTGG CATCAGGGCT AGGCACCCCC AGCTCTTTAA AGGTATAGGT AAAGGCATTG	4020
TGAATCCCGA TAGAACTATC AACGAGGGT CCATCCAAAT CGAAAAAAT CGCTGTGATA	4080
GAGGTCATGG TTTCTCCTAT TTGATAAGCT TATTCTCCGA AAATTTCTTT TTGGAGGCGA	4140
CGACCAGTAG GGGTGGTAGC GAGTCCACCT TCAGCTGTTT CACGAAAGGC AGTTGGCATG	4200
CTTGCTCCTA CTTGGTACAT GGCATCGATC ACTTCATCCA CAGGGATTTT AGATTGATA	4260
CCTGCCAAGG CCATGTCTGC TGCGATGAAA GCAAAGCTAG CTCCCATGGC ATTACGTTTG	4320
ACACAGGGAA CTTGACCAA ACCTGCAACA GGGTCACAGA TGAGGCCTAG CATATTTTAA	4380
ATGACAAAGG CAATAGCTTG ACTGGCCTGA TAAGGTGTTT CACCTGCAGC CAGAGTCAAG	4440
GCGGCAGCAC TCATAGCAGA GGCTGAACCA ACTTCAGCTT GACACCCACC CTCAGCACCT	4500
GAGATGGAGG CATTGTTTGC GATGACTAGT CCAAAGGCAC CAGCAGCAA GAGGAAATCC	4560
AATTGTTGCT CGTGGCTGAG GTCTAATTTT TCAATAGCAG CAGTGAGAAC GGATGGCAGA	4620
CAGCCAGCAC TTCCAGCGGT TGGAGTGGCA CAGACCAAGC CCATTTTGGC ATTGTGTTCA	4680
TTGACTGCGA TGGCATTTTC GGCAGCCGAG AGAATCGTAT AATCTGACAG AGTTTTTCCG	4740
TTTTCGATGT AGTGATCCAA TTTGGCAGCA TCTCCACCTG TCAGGCCACT ACGAGATTTA	4800
TTTTCATTGA GGCCAAGTTG GACAGAGGCT TTCATAACTT CCAGATTGCG TTCCATGAGA	4860
AGGAAGACTT CTTACGTTT GCGACCGGTC AATTCAAAC CTGTTGTAAT CATGAGTTCT	4920
GCGACATTTT CTTGAAAGTC CAGATCTGCT TGCTCGACCA ATTCTTTGAT AGAATAAAAC	4980
ATGCTTCCTC CTATTAAAG AAATTGACAT TGTGGAGATG AGGGATTTTT CGAATTTCTT	5040
CGATAGCCTC ATCACAGTTG CGACTGTCAA CTTGATAAT CATAATGGCT TTTTCACCAG	5100

1052

CTTTTTCACG AGTGACATTC ATCTGGGCGA TATTGATACC ATAGCGGGAA AGCGCCTCTG	5160
TAACAAGGGC AATCATACCT GGAATATCTT GATGAACGAT GATGATAGTC GGTGTATTCA	5220
TATTGAGAGA GACGGCAAAA CCATTGAGTT CGGTTACCTG AATATTTCCCT CCACCGATAG	5280
AAATACCACT CACGCTGATG GTCTTGTGGG CATTTTAAAC AGTAATTTTA GTGGTGTTAG	5340
GGTGAGGGGC ATTGCTGTCT TTCTGAATGG TCCAGACAAT CTGATACCA CGCTTGTGGG	5400
CAATTTCCAG ACTATTTGGA ATTCAGGAT CATCTGTATC CATTCCTAAA ATACCTGCAA	5460
CAAGGGCTAG GTCTGTTCG TGACCACGAT AGGTCTTGGC AAATGAGTTA AAAAGTTGGA	5520
ATTCAACTTC TGTCGGAGTA TCATCAAAAA TGAAGAGAC AATCTTCCCA ATACGAACAG	5580
CACCAGCGGT ATGGCTACTA GATGGGCCAA TCATAACTGG TCCGATGATA TCAAAGACAG	5640
ATTGAAAACG AAGTGATTTC ATCAGTTTCC CCTTATAAAA ATTCTTATCT CTATTATATC	5700
AAAGAATGAG GGGCTTGGCT TTAATTGTGG ATGAAAACCT TTCTAATACC TCAAATAGCA	5760
TAAAAATAGT ATCTTTTATG ACAAAAAACA CCTTATTTAG GGAAATAAAA AATAATTTTG	5820
TAATATTCTT ACATAAAAGT GTCAAGAAAC GGTAATATTT AAAGGGTATG ATAGAACTAT	5880
AGAAAGAAGG AGAATTTTCG AATATGAAAT CAATAACTAA AAAGATTAAA GCAACTCTTG	5940
CAGGAGTAGC TGCCTTGTTT GCAGTATTTG CTCCATCATT TGTATCTGCT CAAGAATCAT	6000
CAACTTACAC TGTTAAAGAA GGTGATACAC TTTCAGAAAT CGCTGAAACT CACAACACAA	6060
CAGTTGAAAA ATTGGCAGAA AACAACCACA TTGATAACAT TCATTTGATT TATGTTGATC	6120
AAGAGTTGGT TATCGATGGC CCTGTAGCGC CTGTTGCAAC ACCAGCGCCA GCTACTTATG	6180
CGGCACCAGC CGCTCAAGAT GAAACTGTTT CAGCTCCAGT AGCAGAAACT CCAGTAGTAA	6240
GTGAAACAGT TGTTTCAACT GTAAGCGGAT CTGAAGCAGA AGCCAAAGAA TGGATCGCTC	6300
AAAAAGAATC AGGTGGTAGT ATACAGCTAC AAATGGACGT TATATCGGAC GTTACCAATT	6360
AACAGATTCA TACCTGAACG GTGACTACTC AGCTGAAAAC CAAGAACGGG TACCG	6415

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

TACCCCTTTC GAATTTTGGC AAAAATTCGG TAAGGCTTTG ATGGTAGTTA TCGCGGTAT	60
GCCGGCTGCT GGTTTGATGA TTTCAATCGG TAAGTCTATC GTGATGATTA ACCCAACCTT	120

1053

TGCACCACTT	GTCATCACAG	GTGGAATTCT	TGAGCAAATC	GGTTGGGGGG	TTATCGGTAA	180
CCTTCACATT	TTGTTTGCCC	TAGCCATTGG	AGGAAGCTGG	GCTAAAGAAC	GTGCTGGTGG	240
TGCTTTCGCC	GCTGGTCTTG	CCTTCATCTT	GATTAACCGT	ATCACTGGTA	CAATCTTTGG	300
TGTATCAGGC	GATATGTTGA	AAAATCCAGA	TGCTATGGTA	ACTACTTTCT	TTGGTGGTTC	360
AATCAAAGTT	GCTGATTACT	TTATCAGTGT	TCTTGAAGCT	CCAGCCTTGA	ACATGGGGGT	420
ATTCGTAGGG	ATTATCTCAG	GTTTTGTAGG	GGCAACTGCT	TACAACAAAT	ACTACAACCT	480
CCGTAAACCT	CCTGATGCAC	TTTCATTCTT	CAACGGGAAA	CGTTTCGTAC	CATTTGTAGT	540
TATTCCTCGT	TCAGCAATCG	CTGCAATTCT	ACTTGCTGCT	TTCTGGCCAG	TAGTTCAAAC	600
AGGTATCAAT	AACTTCGGTA	TCTGGATTGC	CAACTCACAA	GAAACTGCTC	CAATTCTTGC	660
ACCATTCTTG	TATGGTACTT	TGGAACGTTT	GCTCTTGCCA	TTTGGTCTTC	ACCACATGTT	720
GACTATCCCA	ATGAACTACA	CAGCTCTTGG	TGGTACTTAT	GACATTTTAA	CTGGTGCAGC	780
TAAAGGTACT	CAAGTATTCG	GTCAAGACCC	ACTATGGCTT	GCATGGGTAA	CAGACCTTGT	840
AAACCTTAAA	GGTACTGATG	CTAGTCAATA	TCAACACTTG	TTAGATACAG	TACATCCAGC	900
TCGTTTCAAA	GTTGGACAAA	TGATCGGTTT	ATTCGGTATC	TTGATGGGTG	TGATTGTTGC	960
TATCTACCGT	AATGTTGATG	CTGACAAGAA	ACATAAATAC	AAAGGTATGA	TGATTGCAAC	1020
AGCTCTTGCA	ACATTCTTGA	CAGGGGTTAC	TGAACCAATC	GAATACATGT	TCATGTTTCT	1080
CGCAACACCT	ATGTATCTTG	TTTACTCACT	TGTTCAAGGT	GCTGCCTTCG	CTATGGCTGA	1140
CGTCGTAAAC	CTACGTATGC	ACTCATTCGG	TTCAATCGAG	TTCTTGACTC	GTACACCTAT	1200
TGCAATCAGT	GCTGGTATTG	GTATGGATAT	CGTTAACTTC	GTTTGGGTAA	CTGTTCTCTT	1260
TGCTGTAATC	ATGTACTTTA	TCGCAAACTT	CATGATTCAA	AAATTCAACT	ACGCAACTCC	1320
AGGGCGCAAC	GGAAACTACG	AAACTGCTGA	AGGTTTCAGAA	GAAACCAGCA	GCGAAGTGAA	1380
AGTTGCAGCA	GGCTCTCAAG	CTGTAAACAT	TATCAACCTT	CTTGGTGGAC	GTGTAAACAT	1440
CGTTGATGTT	GATGCATGTA	TGACTCGTCT	TCGTGTAACT	GTTAAAGATG	CAGATAAAGT	1500
AGGAAATGCA	GAGCAATGGA	AAGCAGAAGG	AGCTATGGGT	CTTGTCATGA	AAGGACAAGG	1560
GGTTCAAGCT	ATCTACGGTC	CAAAAGCTGA	CATTTTGAAA	TCTGATATCC	AAGATATCCT	1620
TGATTTCAGGT	GAAATCATTC	CTGAAACTCT	TCCAAGCCAA	ATGACTGAAG	CACAACAAAA	1680
CACTGTTCAc	TTCAAAGATC	TTACTGAGGA	AGTTTACTCA	GTAGCAGACG	GTCAAGTTGT	1740
TGCTTTGGAA	CAAGTAAAGG	ATCCAGTATT	TGCTCAAAAA	ATGATGGGTG	ATGGATTGTC	1800
AGTAGAACCT	GCAAATGGAA	ACATTGTATC	TCCAGTTTCA	GGTACTGTGT	CAAGCATCTT	1860

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CCCAACAAAA	CATGCTTTTG	GTATTGTGAC	GGAAGCAGGT	CTTGAAGTAT	TGGTTCACAT	1920
TGGTTTGGAC	ACAGTAAGTC	TTGAAGGTAA	ACCATTTACA	GTTTCATGTTG	CTGAAGGACA	1980
AAAAGTTGCA	GCAGGAGATC	TCCTTGTAC	AGCTGACTTG	GATGCTATCC	GTGCAGCAGG	2040
ACGTGAAACT	TCAACAGTAG	TTGTCTTCAC	AAATGGTGAT	GCAATTAAAT	CAGTTAAGTT	2100
AGAAAAACA	GGTTCTCTTG	CAGCTAAAC	AGCAGTTGCT	AAAGTAGAAT	TGTAATATAC	2160
TTGAGGTTGG	AAGCTGTATT	CCAACCTCTT	ATTTTGGGAG	AAAAGAATGA	AATTTTAAAC	2220
ACTCAATACT	CACAGTTGGA	TGGAGAAAAG	AGCAGAGGAA	AAATTCCAGA	TTTGTGCTGA	2280
AGATATTCTT	GAAAAGGACT	ATGATTTGAT	TTGTTTTCAT	GAAATCAATC	AGGAGATGAC	2340
CTCGTCAGAG	GTGGAGGTTA	ATGACCTTTA	TCAAGCTTTG	CCAGCAGCTG	AGCCTATTCA	2400
CCAAGACCAT	TATGTTAGAC	TCTTGGTTGA	AAAGTTGTCT	GAGCAAGGGA	AAAATTACTA	2460
CTGGACCTGG	GCCTATAACC	ATATCGGCTA	TAACCGCTAC	CACGAAGGTG	TGGCTATCTT	2520
GTCTAAAACA	CCTATTGAAG	CCAGAGAAAT	TTTGGTTTCA	GATGTGGATG	ATCCAACAGA	2580
CTATCATACT	CGCCGTGTTG	CCCTAGCTGA	AACTGTAGTC	GATGGCAAGG	AGCTAGCAGT	2640
TGCCAGTGTT	CATCTCTCTT	GGTGGGATAA	AGGTTTCCAA	GAAGAATGGG	CACGATTTGA	2700
GGCTGTCTTG	AAAAAATTGA	ACAAGCCACT	TTTACTAGCT	GGAGATTTCAT	ACAATCCGGC	2760
TGGACAGGAA	GGTTACCAAG	CTATTTTAGC	TAGTCCATTA	GGCTTACAAG	ACGCATTTGA	2820
AGTTGCTCAA	GAGAAAAGTG	GTAGCTATAC	TGTTCCGCCT	GAAATTGATG	GCTGGAAAGG	2880
GAACACTGAA	CCCCTTCGAA	TGGATTATGT	CTTTACTACC	AAAGAGTTAG	CGGTGGAAAA	2940
TTTACATGTC	GTATTTGATG	GTAACAAGAG	TCCACAAGTG	AGTGATCACT	ATGGCTTGAA	3000
TGCTATATTA	AACTGGAAAT	AATAACTGAA	AAGAGGTTGG	AACTATAAAA	TTCCAGCCTT	3060
TTCTTACTAG	AGAAGCTACT	GGAAATAGCC	TAAATAAGTG	AGACTACTGT	AATGGAATAA	3120
AATATGGTAT	AATTGATAAG	GTAGATAGAA	TCGAGGATGT	TATGTCATTT	ACGAAATTTC	3180
AATTTAAAAA	CTATATTAGA	GAAGCCTTGA	AGGAGTTAAA	ATTTACAACCT	CCAACAGAGG	3240
TGCAAGACAA	GTTGATTCCCT	ATTGTTTGGG	CAGGTCGTGA	CCTAGTAGGA	GAATCAAAAA	3300
CAGGTTCAGG	TAAGACTCAT	ACTTTCTTGT	TACCGATTTT	CCAGCAATTA	GATGAAGCTA	3360
GCGATAGTGT	ACAAGCAGTG	ATTACTGCAC	CGAGTCGTGA	GTTGGCTACT	CAAATTTACC	3420
AAGTAGCGCG	TCAGATTTCAT	GCTCACTCAG	ATGTCGAAGT	TCGTGTGGTT	AATTATGTGG	3480
GTGGTACGGA	TAAGGCTCGC	CAGATTGAGA	AATTGGCAAG	CAATCAGCCT	CATATTGTTA	3540
TTGGAACACC	AGGCCGTATC	TACGACTTGG	TTAAATCTGG	TGATTTAGCT	ATTCATAAAG	3600
CCAAGACATT	TGTTGTTGAT	GAAGCAGATA	TGACCTTGGA	TATGGGATTC	TTGGAAACTG	3660

1055

TTGATAAGAT TGCTGGCAGT CTTCCAAAAG ACTTGCAATT CATGGTCTTC TCAGCGACTA	3720
TCCCACAAAA ACTGCAACCA TTCTTGAAAA AATACTTATC AAATCCTGTT ATGGAGAAAA	3780
TTAAGACCAA AACGGTTATT TCTGACACCA TTGATAATTG GTTGATTTCG ACCAAGGGAC	3840
ATGATAAGAA TGCTCAAATT TACCAGTTGA CTCAGTTGAT GCAGCCGTAT TTGGCAATGA	3900
TTTTTGTTAA CACTAAAACG CGTGCTGATG AATTGCATTC ATATCTGACT GCTCAAGGCT	3960
TGAAGGTTGC AAAAATCCAT GCGGATATTG CCCCTCGTGA ACGCAAGCGA ATCATGAATC	4020
AGGTGCAAAA TCTGGATTTT GAGTATATTG TCGCAACAGA TTTGGCAGCG CGTGGGATTG	4080
ACATTGAAGG TGTGAGCCAT GTCATCAATG ATGCCATTCC GCAAGACTTA TCTTTTTTTG	4140
TTCATCGTGT TGGTCGTACT GGACGAAATG GCCTACCAGG TACAGCTATT ACCCTTTATC	4200
AGCCAAGTGA TGA CTGGAT ATCCGTGAGT TGGAGAAATT GGAATCAAG TTTAGTCCTA	4260
AGATGGTCAA AGACGGGGAA TTTCAAGATA CCTATGACCG TGATCGTCGT GCCAACCGTG	4320
AGAAAAACA AGATAAACTT GATATCGAAA TGATTGGTTT GGTAAAAAG AAAAGAAAA	4380
AAGTCAAACC GGGTTATAAG AAGAAAATTC AATGGGCGGT TGATGAAAAG CGCCGTAAAA	4440
CCAAGCGTGC TGA AAAATCGC GCTCGCGGTC GTGCAGAGCG TAAAGCTAAA CGCCAAACAT	4500
TTTAATAGAA ATTGTTGGAG TATTGAGCTC CAACTTTTTT ATTTATGAGA ACGAACTATC	4560
TAAACCGAAA CACTACATTA AAGACTGCAA ATTGCGATTA AAAATGGTAT AATGATAAAG	4620
TTATATAGTC CCGATAAGAT GGTAGGTATT TATTACGAAG AGTTTTCCCTA TCAGTACTTT	4680
GTAACCTCTAT AACAAATTTT TTTAAGGGGG GACATTTTTA TGTGAGAGCG TAAATTATTC	4740
ACGTCTGAAT CTGTATCTGA GGGGCATCCG GATAAGATTG CAGACCAAAT TTCAGATGCG	4800
ATTTTGGATG CTATTTTAGC AAAGGATCCA GAGGCGCACG TTGCTGCTGA AACAGCTGTA	4860
TATACTGGTT CTGTCCACGT TTTTGGTGAA ATTTCTACAA ATGCCTATGT GGATATTAAC	4920
CGTGTGGTTC GTGATACCAT TGCAGAGATT GGTATACCA ATACAGAATA TGGATTTTCT	4980
GCTGAGACGG TGGGAGTACA CCCATCTTTG GTGGAACAAT CTCCTGACAT CGCTCAAGGT	5040
GTAAACGAAG CCTTGGAGGT TCGTGGAAAT GCTGATCAAG ATCCACTGGA CTTGATTGGA	5100
GCAGGTGACC AAGGGCTCAT GTTTGGATTT GCAGTAGATG AAACAGAAGA GCTTATGCCA	5160
TTGCCAATTG CACTCAGTCA TAAATTGGTT CGTCGTCTGG CAGAACTTCG TAAGTCTGGA	5220
GAAATTAGCT ATCTCCGTCC AGATGCAAAA TCACAAGTTA CAGTTGAGTA CGATGAAAAAT	5280
GACCGTCCGG TACGTGTAGA TACAGTCGTT ATTTCTACTC AGCATGATCC AGAGGCCACT	5340
AATGAACAAA TCCATCAAGA TGTGATTGAC AAGGTCATCA AAGAAGTTAT TCCATCTTCT	5400

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TATCTTGATG	ATAAGACAAA	ATTCTTTATC	AATCCGACAG	GTCGTTTGT	AATCGGTGGT	5460
CCTCAAGGGG	ACTCAGGTTT	GACTGGTCGT	AAGATTATTG	TAGATACTTA	TGGTGGCTAC	5520
TCTCGTCATG	GTGGTGGTGC	CTTCTCTGGT	AAAGATGCGA	CTAAGGTGGA	TCGTTCAGCC	5580
TCTTATGCGG	CTCGCTATAT	TGCCAAGAAT	ATCGTTGCAG	CAGACCTTGC	TAAGAAGGCA	5640
GAAGTGCAGT	TGGCCTATGC	TATCGGTGTT	GCGCAACCTG	TTTCTGTTCG	TATCGATACT	5700
TTCGGTACAG	GAACAGTAGC	TGAAAGTCAA	CTTGAAAAAG	CGGCTCGTCA	AATCTTTGAC	5760
CTTCGCCCTG	CAGGGATTAT	CCAAATGCTG	GACCTCAAGC	GTCCAATTTA	CCGTCAAACA	5820
TCGGCTTACG	GTCACATGGG	ACGTACAGAT	ATTGATCTTC	CATGGGAACG	TTTGGATAAG	5880
GTAGATGCTT	TGAAAGAAGC	AGTAAAATAA	GATTTTAAAG	GGGGAACGTC	CTCTCTTTTT	5940
TATAGTTTTT	AACTATACTG	GGATACTGTT	CTGAAAATCC	ATTTTGCGAA	AGTAGAGATT	6000
TACATGTATA	GTAGATTGAA	ACTAGAATAG	TACACCTCAA	CTTCTAAAC	ATTGTTAGCA	6060
ATCAATTGTA	CTGTCCTGAT	CGATTTCTCC	TGTTCTTGTT	TCATTTTACT	ATATTTCTTT	6120
AAAAATGATA	AAGGTTAAGA	TTTCTCCTCG	TAATAGATAA	TCTTGGGGAT	ATTTCAATCC	6180
AAAGTTTAT	TCGTTATCAC	TTGACTATTG	CAAGGTTTTC	TAGAGCAACA	GAGTCATGGA	6240
ATGGACTCAT	GGTTGAGATT	TCTCCTTGTT	GCTTGGACTT	CATTCAAAG	TCTGTTACCC	6300
AAGCCTTGTT	CAAACTTCTA	ATACACTAGC	TGTTTCCATA	GCATGACTTC	TGTACTAGAC	6360
TTTCTTTTCC	GAATAAATAG	ATAGAACCAC	AGAATCTAGT	AAACCTAGAA	TTAAAATTAT	6420
GGTATAATAT	TAGCAATAAA	AGAAATCTGG	AGGATTAGAA	TCATGGTATC	AACGAAAACA	6480
CAAAATGCTG	GTTTTGAGTT	TGACAATTGC	TTGATGAATG	CAGCAGGTGT	GGCTTGATG	6540
ACGATAGAGG	AGTTAGAAGA	GGTCAAAAAC	TCAGCGGCAG	GAACCTTTGT	TACTAAGACA	6600
GCGACCTTGG	ACTTCCGTCA	GGGGAATCCT	GAGCCACGCT	ACCAAGATGT	TCCACTTGGT	6660
TCCATCAACT	CTATGGGCTT	GCCAAATAAT	GGCTTAGACT	ATTATTTGGA	TTATCTTTTA	6720
GATTTGCAGG	AAAAAGAGTC	GAACCGAACT	TTCTTCTTAT	CTCTGGTCGG	CATGTCTCCA	6780
GAGGAAACCC	ATACTATTTT	GAAAAAGTC	CAAGAGAGTG	ATTTTCGTGG	TCTGACTGAG	6840
CTAAATCTTT	CCTGTCCAAA	TGTTCCAGGT	AAACCTCAGA	TTGCCTATGA	TTTTGAGACA	6900
ACAGACCGGA	TTTTGGCAGA	AGTGTGTGCT	TACTTCACCA	AACCTCTTGG	AATTAAATTG	6960
CCACCTTATT	TTGATATTGT	TCACTTTGAC	CAAGCGGCAG	CTATTTTCAA	CAAATATCCG	7020
CTCAAGTTTG	TCAACTGCGT	TAACCTCTATC	GGAAACGGCC	TCTATATAGA	AGACGAATCT	7080
GTCGTTATTC	GGCCTAAGAA	TGGTTTTGGT	GGAATTGGTG	GAGAATACAT	CAAACCGACT	7140
GCTTTAGCCA	ATGTTACGCG	CTTTTATCAA	CGTTTAAATC	CTCAAATCCA	AATTATCGGA	7200

1057

ACAGGTGGCG TTCTGACTGG TCGAGATGCC TTTGAACACA TCCTCTGTGG AGCAAGTATG 7260
 GTGCAGGTGG GAACGACCCT TCACAAAGAA GGCGTCAGTG CTTTGTGACCG CATTACCAAT 7320
 GAACTGAAAG CAATCATGGT GGAAAAAGGC TACGAGAGCT TAGAAGATT T CCGTGGGAAA 7380
 TTGCGCTATA TTGACTAAAT TAAATCGAAA AATCTGAAGA AAGGAGAGAC GATGCTAGCC 7440
 ATTGAAGAAA GTCAGAAGTT GACTTTATCA AATTTACCGA GCCTGAGCCT ATTTACAGGG 7500
 ACAGATCAGG GTCAGTTTGA AGTGATGAAG AGTCAAATGT TGAAACAGAT TGGGTATGAT 7560
 TCTGCTGACC TCAACTTTGC CTACTTTGAT ATGAAAGAAG TAGTTTACAA GGATGTGGAA 7620
 CTGGAGTTGG TCAGCCTTCC TTTCTTTGCG GATGAGAAAA TCGTGATATT AGATTATTTT 7680
 ATGGATATCA CGACTGCTAA GAAACGCTTT TTGACAGATG ATGAGCTTAA GTCATTTGAG 7740
 GAATACCTTG ACAATCCTTC TCCAACAACC AAGTTGATAA TCTTTGCAGA AGGAAAGCTG 7800
 GATAGCAAAA GACGGTTAGT CAAATTACTT AAGCGTGATG CCAAGGCCTT CGATGCAGTA 7860
 GAAGTAAAAG AACAAGAATT GCGCCAGTAC TTCCAAAAGT GGAGTCAGAA ACAAGGTCTG 7920
 CAGTTTACCA ATCATTCTTT TGAAAATCTC CTCATCAAGT CGGGGTTTCA ATTTAGCGAA 7980
 ATCCAGAAAA ATCTTCTCTT TTTACAGTCC TATAAGGCGA ATTCTGTTAT TGAGGAAGAG 8040
 GATATTGTTA ACGCAATTCC CAAGACTTGC AGGACAATAT TTTTGATTTA ACTCAGTTTA 8100
 TTCTGACTAA AAAGATGGAT CAGGCGCGCG ATTTGGTGAG AGACTTGACC TTGCAAGGGG 8160
 AAGATGAAAT CAAACTGATT GCAGTCATGC TGGGACAATT TCGGACTTTT ACTCAGGTGA 8220
 AGATTTTGGC GGAGTCTGGC CAAACAGAAT CGCAGATTGC AAGTAGTTTA GGTAGTTATC 8280
 TGGGACGTAA CCCAAATCCT TATCAAATCA AGTTTGCATT AAGAGATTCG AGAGGACTTT 8340
 CTTTGAGCTT TTTGAAGCAA GCTATTTTCCT ATTTGATTGA GACAGACTAT CAGATTAAGA 8400
 CAGGTCTTTA TGAAAAAGGT TTCCTTTTGT AAAAGGCACT CTTACAGATT GCTAGTCAGG 8460
 TCAATTGACA TTTGTTGAAA CTACTAACCC GCGG 8494

(2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9707 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

CCGGTCAGTT CGTTCAGTAC AAGGAATCAT AATGAACGAT CAATCAGAAA AAAAGACTAG 60

1058

AAAGAAGACT GTATGGATAA TCGACCAATT GGTTTTTTTGG ATTCGGGTGT CGGGGGCTTG	120
ACCGTTGTGC GCGAGCTCAT GCGCCAGCTT CCCCATGAAG AAATCGTCTA TATTGGAGAT	180
TCGGCGCGGG CGCCCTATGG CCCCCGTCCT GCTGAGCAAA TTCGTGAATA TACTTGGCAG	240
CTGGTCAACT TTCTCTTGAC CAAGGATGTC AAAATGATTG TCATTGCTTG TAACACTGCG	300
ACTGCGGTCTG TCTGGGAAGA AATCAAGGCT CAACTAGATA TTCCTGTCTT GGGTGTAATT	360
TTGCCAGGAG CTTCGGCAGC CATCAAGTCC AGTCAAGGTG GGAAAATCGG AGTGATTGGA	420
ACGCCCATGA CGGTACAATC AGACATATAC CGTCAGAAAA TCCATGATCT GGATCCCGAC	480
TTACAGGTGG AGAGCTTGGC CTGTCCCAAG TTTGCTCCCT TGGTTGAGTC AGGTGCCCTG	540
TCAACCAAGT TTACCAAGAA GGTGGTCTAT GAAACCTGTC GTCCCTTGGT TGGAAAGGTG	600
GATAGCCTGA TTTTGGGCTG TACTCATTAT CCACTCCTTC GCCCTATTAT CAAAATGTG	660
ATGGGGCCAA AGGTTTCACT CATCGATAGT GGGGCAGAGT GCGTACGGGA TATCTCAGTC	720
TTACTCAATT ATTTTGAAAT CAATCGTGGT CGCGATGCTG GACCACTCCA TCACCGTTTT	780
TACACAACAG CCAGTAGCCA AAGTTTTGCA CAAATTGGTG AAGAATGGCT GGAAAAAGAG	840
ATTCTGTGG AGCATGTAGA ATTATGACAA ATAAAATTTA TGAATATAAG GATGACCAGG	900
ACTGGTATGT TGGGTCTTAT AGTATTTTGT GTGGCGTTAA CAGTTTGAGC GACTATAAGA	960
CAGATTTTCC TCTGTTTGAA TTCTCCAAAA TATTTGGAGA TGAAGAGTAT GGTTCCTCCG	1020
TTTCAGTTAC TGTTTTACGC TATGGTTCTA TCTACCGTTT GTTCTCCTTT GTGGTAGACA	1080
TGCTTAATCA AGAAATGGGA CGAAACTTGG AAGTTATTCA ACGTCATGGG GCCCTGCTCT	1140
TGGTTGAAAA TGGGCAACTC TTGTATGTAG AATTGCCTAA AGAAGGGGTC AATGTTTCATG	1200
ATTTCTTTGA GACAAGCAAG GTCAGAGAAA CCTTGTGTGAT TGCGACTCGT AACGAAGGTA	1260
AAACCAAGGA ATTCCGAGCT ATCTTTGATA AGTTAGGCTA CGATGTGGAA AATCTTAATG	1320
ACTACCTTGA CCTGCCTGAA GTAGCAGAAA CAGGTATGAC CTTTGAAGAA AATGCCCGCC	1380
TTAAGGCAGA AACCATTCTT CAATTAACGG GCAAGATGGT TTTGGCAGAT GATTCTGGTC	1440
TCAAAGTCGA TGTCCTTGGT GGCTTACCAG GCGTCTGGTC AGCTCGTTTC GCAGGTGTGG	1500
GAGCAACTGA CCGTGAAAAT AATGCCAAAC TCTTGACGA ATTGGCCATG GTCTTTGAAC	1560
TCAAGGACCG CTCGGCTCAG TTCCACACAA CCCTAGTCGT AGCCAGCCCA AATAAGGAAA	1620
GTTTAGTTGT TGAAGCAGAC TGGTCAGGTT ATATTAACTT TGAACCTAAG GGTGAAAATG	1680
GCTTTGGCTA TGATCCCTC TTCCTTGTAG GAGAAACAGG TGAGTCATCA GCTGAATTAA	1740
CCCTGGAAGA AAAAAATAGT CAATCTCACC GTGCCTTAGC CGTTAAGAAA CTTTGGAGG	1800
TATTTCCATC ATGGCAAAGC AAACCATCAT TGTAATGAGC GATTTCCATG GCGATAGCTT	1860

1059

GATTGTGGAA GAAGTCCGTG ATCGCTATGT GGGCAAAGTC GATGCTGTTT TTCATAACGG	1920
CGATTCTGAA CTACGTCCGG ATTCTCCACT TTGGGAGGGC ATCCGCGTTG TTAAAGGGAA	1980
CATGGAATTTC TACGCCGGCT ACCCAGAACG TCTGGTGACT GAGCTTGATT CGACCAAGAT	2040
TATCCAAACT CATGGTCACT TGTTTGACAT CAATTTCAAC TTTCAAAAGT TGGACTACTG	2100
GGCTCAGGAG GAAGAGGCCG CTATCTGCCT CTATGGTCAC TTGCATGTGC CAAGTGCTTG	2160
GTTGGAAGGC AAGATCCTCT TTCTAAATCC AGGTTCTATC AGTCAACCAC GAGGTACCAT	2220
CAGAGAAATG TCTATGCTC GTGTGGAGAT TGATGATAGT TACTTCAAAG TGGACTTTTT	2280
GACACGAGAT CACGAGGTGT ATCCAGGTTT GTCCAAGGAG TTTAGCCGAT GATTGCCAAG	2340
GAGTTTGAGA CTTTCTTGTT GGGGCAGGAG GAAACTTTTT TGACCCCTGC TAAAAATCTA	2400
GCTGTGTTGA TTGATACCCA CAATGCGGAT CATGCGACCC TCTTGCTCAG TCAGATGACC	2460
TATACCCGTG TTCCCGTTGT GACAGATGAA AAACAGTTTG TTGGGACGAT TGGACTCAGA	2520
GATATTATGG CTTATCAGAT GGAGCATGAC TTGAGCCAAG AAATCATGGC GGATACGGAT	2580
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GTCTTGACACA AGCTAGTAGA TGAGTCCTTC TTACCGGTTG TGGATGCAGA GGGTATTTTC	2700
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AGTAAGGAAT ATGAGATTCG ATGCCAATGA GAGACAGGAT TTCAGCCTTT TTAGAGGAAA	2820
AGCAGGGCTT GTCTGTCAAT TCCAAGCAGT CCTATAAGTA TGATTTGGAG CAATTTTAG	2880
ACATGGTAGG TGAGCGGATT TCTGAGACCA GTCTCAAGAT TTACCAAGCC CAGCTAGCCA	2940
ATCTAAAAAT CAGCGCCAG AAGCGAAAGA TTTCGGCCTG TAACCAATTT CTATACTTTC	3000
TCTATCAAAA AGGAGAGGTG GACAGCTTTT ACCGCTTGGA ATTAGCCAAA CAAGCTGAAA	3060
AGAAGACGGA AAAGCCAGAG ATTCTATACC TAGACTCTTT TTGGCAGGAA AGCGACCATC	3120
CAGAGGGCCG CTTGCTAGCG CTCTTAATCC TAGAAATGGG GCTCTTGCCC AGTGAGATTT	3180
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CCCAACAGAG GATTGTCACC ATTCCCACGG CCTTGCTTTC AGAATTGGAA CCCTTGATGG	3300
GGCAGACCTA TCTTTTGAA AGAGGAGAGA AACCCTATTC TCGTCAGTGG GCCTTTCGTC	3360
AGTTAGAATC TTTTGTCAAG GAGAAAGGTT TTCCATCCTT ATCAGCTCAA GTCTTACGTG	3420
AACAGTTTAT TCTAAGACAA ATAGAAAACA AGGTCGATTT GTACGAAATT GCAAAAAAAT	3480
TAGGATTAAA AACAGTCCTG ACCTTAGAAA AATATAGATA ATGGATATTA AATTAAAAGA	3540
TTTTGAAGGA CCCCTGGACT TGCTCTTGCA TCTGGTTTCT AAGTACCAGA TGGATATCTA	3600

1060

CGATGTGCCC ATTACGGAAG TCATCGAACA GTATCTAGCC TATGTCTCAA CCCTGCAGGC	3660
CATGCGTCTG GAAGTGACGG GTGAGTACAT GGTCAATGGCT AGTCAGCTCA TGCTGATTAA	3720
GAGTCGTAAA CTCCTTCCGA AGGTAGCAGA AGTGACAGAC TTGGGGGATG ACCTGGAGCA	3780
GGACCTCCTC TCTCAAATCG AAGAATATCG CAAGTTCAAG CTCTTGGGTG AGCACTTGGA	3840
AGCCAAGCAC CAAGAACGGG CCCAGTATTA TTCCAAAGCG CCGACAGAGT TGATTTACGA	3900
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CCTAGCCAAG AAAAAAGAGG AGTTTGACACA AAATCACACG ACGATCTTGC GGGATGAGTA	4020
TAAGATTGAG GACATGATGA TTATCGTGAA AGAGTCCTTG ATTGGACGAG ATCAATTGCG	4080
CTTGACGAGT TTGTTCAAGG AAGCCCAGAA TGTCCTAAGAG GTCATCACCC TCTTTTGGC	4140
AACCCTAGAG TTAATCAAAA CCCAGGAGTT GATCCTCGTG CAAGAGGAGA GTTTTGAGGA	4200
TATCTATCTC ATGGAAAAGA AGGAAGAAAG TCAAGTGCCT CAAAGCTAGA CTTGATAGAG	4260
AGGAAAGATG AGTACTTTAG CAAAAATAGA AGCGCTCTTG TTTGTAGCGG GTGAAGATGG	4320
GATTCGGGTC CGCCAGTTAG CTGAACCTCT CTCTCTGCCA CCGACAGGCA TCCAGCAAAG	4380
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CTCTAAGGCG CCTATCAACC AGAGCTTGTG TCGGGCTGCC CTTGAGACCT TGTCCATTAT	4560
TGCCTACAAA CAGCCGATTA CGCGGATAGA AATTGATGCC ATCCGTGGAG TTAACCTGAG	4620
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ATTGGGGCGC CCCAACCTCT ATGTGACTAC GGATTATTTC CTAGATTACA TGGGGATAAA	4740
CCATTTAGAA GAATTACCAG TGATTGATGA GCTTGAGATT CAAGCCCAAG AAAGCCAATT	4800
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CTATCTACAA CGAAGAAAAG GTCTACTATC TGCTTAACAA ACCACGCGGT GTGATTTCCA	5040
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GTATTTACCC TGTGGGTCGT TTGGACTGGG ATACATCAGG TGTCTTGATT TTGACCAATG	5160
ATGGGGACTT TACAGACGAG ATGATTCAAC CTCGTAATGA GATTGACAAG GTTTATGTCG	5220
CGCGTGTTAA AGGTGTGGCC AATAAGGACA ATCTCCGCC CTGACCCGT GGTCTTGAGA	5280
TTGATGGTAA GAAAACCAAG CCAGCTGTTT ATGAAATTCT CAAAGTGGAC CCAGTCAAAA	5340
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TTGAAGCTGT TGGTCTCCAA GTAGATAAGT TGTCTCGGAC TCGTTTCGGA CACCTAGACT	5460
TGACAGGACT CCGTCCAGGA GAATCCCGTC GTCTTAATAA AAAAGAAATC AGCCAACTAC	5520
ACACCATGGC TGTAACTAAG AAATAATGAA ACGAATTTTA ATAGCGCCTG TCGCCTTTTA	5580
CCAACGTTTT ATCTCACCAG TCTTCCACC CTCTTGTCGC TTTGAGCTGA CTTGTTCCAA	5640
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CGCATCCTAT CAGGTTTGAG TGAACCTGAT AGGATGCGTT TTAGAATGTC AAAATTTTAT	5880
ACTCTTCGAA AATCTCTTCA AACC GCGTCA GCTTTCATCT GCAACCTCAA AACAGTGTTF	5940
TGAGCAACCT GCGGCTAGTT TCCTAGTTTG CTCTTTGATT TTCATTGAGT ATTAAATTGA	6000
GTTTGAAGTG GCTTATTTCA AAGCTTTTGT TATGTCCTCA ATCATGAGTT TTGTTGATTC	6060
AAGTCCGCCT CCGCTTAGAT ACCAGAGGTC TGGTGTTAGT TGGATAATCT TACCATTTTT	6120
AGCAGCAGGT GTTTCAGCGA TAAGGGCATT TTCTAGGACA CCGTCGTTGC TAGAGTTGTC	6180
CCCACCGATG GCAAGGGTAC GGTTGATGAC AAAGAGGATG TCAGGGTTGA TTTCTTTGAC	6240
ACTTTCAAAG CTGACTTCTT GTCCGTGGCG TGAGTCTTCA AATTTTGTAT CAGTTGGTTT	6300
GAATTTCAAG GTTTGGTACA AGAAAGAGAA ACGAGATTTG GCACCAAAGG CTGCCATTTT	6360
TCCTTCATTA AGGAGGATCG CAAGGGCTTT TTTGTCAGAG CTTTCATTTT TAGTAGCGAC	6420
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GTTTGTACTA CATGCACCAA GTAGGAGCAA GAAGCTGGCC ACTAGGGCAG TGAAATAAAG	6960
TTTAAGGGAT GTTTTCATAA TTTCTCCTTT TTAAAATGTG ATAACGATTT AGGGAGTCTC	7020
TTAATCTTAT TGACTAAGAG ACTGAAGGTT CTCTAACTTG AGCTTTTATG TTACTAGCTA	7080
TAGATACAGA TCTTTTGTG ATTGATATCA GCTAGCGTGA TGGGAATCTC ATAAAGTTGA	7140

1062						
CTGAGCAGGT	CAGCCTGCAT	GATTTGATCG	GTTCCTCCCT	TGCTAAAGAC	CTGGCCGTCC	7200
TTGAAGGCGA	CAATTTTCATC	TGCATACTGA	CTGGCCATGT	TGATATCGTG	GAGGACGATG	7260
ATAATGGTCT	TGCCGAGTTC	CTCCACCAGT	CGTCGAAGAA	TCTGCATCAT	GCTGACGCTT	7320
TGCTTGATAT	CGAGATTGTT	GAGTGGTTCG	TCCAGCAAGA	TAAAGTCCGT	ATCCTGGGCC	7380
AGTACCATAG	CGATAAAGAC	GCGCTGGAGT	TGCCCCCTG	ACAGGCTATT	GATGTAGCGG	7440
TCTTTTAAGT	TGGTCAGTTC	TAAATAGTTC	AGAGTTTCTC	GGATTTTTTC	CCAGTCTTCT	7500
GATCTAAGTC	GACCTCGGCT	GTAGGGAAAA	CGTCCAAAAC	TGACCAGTTC	TTCAACAGTC	7560
AATTTGGCTT	GGTAATTGAT	TTTCTGTTTT	AGGATGGTTA	GTTCTTGGGC	CAGTTC TTGC	7620
GAATTCCAGC	TCTCGATTTC	ACGTCCTTTG	ATACTGAGAA	CTCCCTGATC	TTTCTTG GTT	7680
AGCCTGCTCA	TGATGGAGAG	GAGAGTCGAT	TTTCCAGCAC	CATTTGGACC	AATAAAGGCT	7740
GTCAGTTTTT	GAGGACTGAC	TTCAAGCGAA	ATGCCTTGCA	AAATATCCTG	TTTTTGAATG	7800
GATTTGTCAA	TGTTTTCCAG	TTTCACTGAC	GAGACCTCCT	ATATAGTAAG	ATAAAGAATA	7860
AGAAGCCACC	CACACTCTCA	ATGATCATAC	TGATACGAAT	TTCCAGTGCA	AAGACTCGTT	7920
CAATCAAGGC	TTGCCCCAAG	GTTAAGCTAA	TAAATCCAAC	CAGAATGGCC	ACTATAAAGA	7980
GTAAC TTGTG	CTGATAGTCT	TTGACAATCA	GGTAGGTGAG	GTTGGCCAGT	ATAAAGCCGA	8040
AGAAGGCCAT	AGGTCCTACC	AAGGCAGTGG	CCGTTGAGGT	CAAAAGCACG	ATTCCCCAGA	8100
GGAGCTCTTT	CTGTTCTTTT	TCAACATCGA	GTCCCAATAT	CTGAGCCGTT	TCTCTTTGCA	8160
GGTGCAAGAC	ATCTAGAACG	ACTGCTTTTC	GAAAGAAAAA	GATTGTCAAA	GCGAGGATGA	8220
TCAGAGAACC	GATGGCTAGG	ATGGAAGTGT	TGAGATGTTG	AAAGGAGGCA	AAAAGACTAT	8280
TTTGACAGTTT	ATCGTATTCG	TTTGGATCCA	TTAGGACTTG	AAGGAAGGTG	CTGATATTTT	8340
GAAAGAGACT	TCTGAGCGCT	AGACAGATCA	GCAGGACGAA	GACCAGGTCT	TGCTTCATCA	8400
GTGTCTTCAA	GTAACCTTGT	AAGGCGAGAA	AGAAGAGGGA	CTGGACAAGA	AGTAAGACTA	8460
GGAAT TCTAA	GATAGGGGAT	TTGCCAAGTT	GAAGAAACTT	GCTTTCAAAA	ACCAGTAGTA	8520
GGGTTTGTAG	TAGGACGTAG	AAGGATTCAA	TTCCCAAAAT	ACTAGGCGTC	AGGAAGCGAT	3580
TTTCCGTCAG	GGTTTGAAAA	CTAATGGTCG	AAATCCCAGT	CGCGATGGCT	ACCAAGAGAT	8640
AAACGATGAT	CTTTTGGGAA	CGCAACTTCC	AAGCAAAGGC	TGACAAGTGA	GTGATGGGCC	8700
AAAAGTAGAG	AAGACAAGCT	CCGATGGCAA	GAATAATGAG	AATCCAGAAG	AGCTTGGTAT	8760
GTTTGCTTTT	AGTCTGCATC	TTTTCGTCCC	CCTCTCCAGA	GAAGTAGGAT	AAAGACGAGA	8820
CTACCGATGA	TTCTTAGCAA	GAGACTGACA	GACAACTCAT	AGGGCCTAAT	CAGAACTCGG	8880
GATAGGATAT	CGCAAGCCAG	AACTAGATTG	GCACCAACCA	GTGCGACCAT	GAGTTTGGTT	8940

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TGACTTAGAT TATCTCCATA GCGCTTGCGA ACAAGATTGG GAACGATAAC TCCGAGAAAT	9000
GGTAGGCCAC CCACGGTAAT CATGGTGACG CTTGTCGTTA GCGCCACCAG AAAGAGGGCC	9060
AGTTTTTCAA GTAGGGAGTA GGAAATCCCC AAACCTCTCGC TGGTTTCTTT CCCTAGATTC	9120
ATGATGGTGA AGGTTTGGGA TAATTTCCAA ACGGTTATCA GGATGATGAG GCCTAAGAAG	9180
AGCCACTCAT ACTGATGGGT CTGAATCATG GAGAAGGAGC CCTGGGTCCA GGCAGTCATA	9240
CTCTGAACCA GATTGAAACG ATAGGCGATA ACTTCTGTGA CTGAGCCGAT AATCCCGCTA	9300
TAGATGATCC CAATCAGAGG CAACATCCAC CTTTCCTTTA CAGTAAAAAT GGTCATAAAG	9360
GCTAGGAAGA AGAGGGTGAA TACGATGGAT GAAACAAAAG CGAAGAGCAT CTTGTGGGTC	9420
AGACTAGCCG ATGGAAAGAC AAAAAGGCTC AGCACCATT CAGTTTGGC GGCTTCAGTC	9480
GTTCCAACTG TACTCGGTGC AGCAAATGA TTTTGGGTAA TAGTCTGCAT GAGAAGGCCT	9540
GCCATACTCA TACTAGAGGC AGTCAGGAGA ATACTGATAG TTCTTGGGAG ACGGGACTCT	9600
TGAAAGAGGA GCCAGGTCTG CTGGTCGAAA TCAAATAGCT TTCCCCATGA AAAATCACTG	9660
GTCCCAATGC TAATAGAGAG AAAGACTAGG AGTAGAAGTA AGCCAGG	9707

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5910 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CCGCAATTAT GCTTGAAAAG GAGTATACTT ATAAGTAACG CAAACGTTTG CGTCTGAAAA	60
ATACGCAACG TTCCATTATT TTAACACACG AGGTGCTATT ATGAAAAAAC GTCAAAGTGG	120
TGTGTTGATG CACATCTCTT CTCTTCCAGG AGCTTACGGA ATCGGATCAT TTGGTCAAAG	180
TGCTTACGAC TTCGTTGATT TCTTGGTCCG TACAAAACAA CGTTACTGGC AAATCCTTCC	240
ATTAGGAGCA ACTAGTTACG GGGATTCTCC TTACCAATCT TTCTCAGCCT TCGCAGGAAA	300
CACTCATTTT ATCGATTTAG ATATCTTGGT GGAGCAAGGT TTGTTGGAAG CAAGTGACCT	360
TGAAGGAGTT GACTTTGGTA GCGATGCGTC TGAAGTTGAC TATGCTAAAA TCTACTATGC	420
ACGTCGTCCT CTTTGTAGAA AAGCGGTGAA ACGTTTCTTT GAAGTCGGAG ATGTTAAAGA	480
TTTTGAGAAA TTTGCTCAAG ACAACCAATC ATGGCTTGAG CTCTTTGCTG AGTATATGGC	540
TATCAAAGAG TATTTTGACA ATCTTGCTTG GACTGAATGG CCAGATGCAG ATGCTCGTGC	600

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TCGTAAAGCT TCAGCACTTG AAAGCTATCG TGAGCAATTG GCAGACAAGT TGGTTTACCA	660
CCGTGTGACT CAATACTTCT TCTTCCAACA ATGGTTGAAA TTGAAAGCTT ACGCTAACGA	720
CAACCACATC GAAATCGTTG GGGACATGCC AATCTACGTA GCGGAAGATT CAAGTGATAT	780
GTGGGCAAAT CCACATCTCT TCAAAACAGA TGTCAATGGT AAGGCTACTT GTATCGCAGG	840
ATGCCCACCA GATGAGTTTT CTGTAACTGG TCAGCTTTGG GGTAATCCAA TCTATGACTG	900
GGAAGCAATG GACAAAGACG GCTACAAATG GTGGATTGAA CGCTTGCGTG AAAGCTTCAA	960
AATCTACGAT ATCGTTCGTA TCGACCACTT CCGTGGCTTC GAATCTTACT GGGAAATCCC	1020
TGCTGGTTCC GATACAGCAG CACCTGGTGA GTGGGTGAAA GGTCCAGGTT ACAAGCTTTT	1080
TGCAGCCGTT AAGGAAGAAC TTGGTGAGCT AAACATCATC GCAGAAGACC TTGGCTTCAT	1140
GACAGATGAA GTGATCGAAT TCGTGAACG TACTGGCTTC CCAGGAATGA AGATTCTTCA	1200
ATTTGCCTTC AAGGAGAAAG ACGAAAGCAT TGATAGCCCA CACTTGGCAC CTGCTAACTC	1260
AGTTATGTAC ACAGGAACAC ACGATAACAA TACGGTTCTT GGTGGTACC GTAATGAGAT	1320
TGATGATGCG ACTCGTGAGT ACATGGCTCG TTACACGAAC CGTAAAGAAT ACGAAACAGT	1380
GGTACACGCT ATGCTTCGTA CAGTATTTTC ATCAGTTAGC TTTATGGCAA TTGCAACTAT	1440
GCAAGATTTA CTAGAATTGG ATGAGGCAGC TCGTATGAAC TTCCCATCTA CCCTTGGTGG	1500
AAACTGGTCT TGGCGTATGA CTGAAGATCA ATTGACACCA GCTGTCGAGG AAGGTTTGCT	1560
TGACTTGACA ACAATTTATC GCCGAATTAA TGAAAATTTG GTAGATTTAA AGAAATAAGA	1620
CAATAATCAG GAGACAACCT AACATGTTAT CACTACAAGA ATTTGTACAA AATCGTTACA	1680
ATAAAACCAT TGCAGAATGT AGCAATGAAG AGCTTTACCT TGCTCTTCTT AACTACAGCA	1740
AGCTTGCAAG CAGCCAAAAA CCAGTCAACA CTGGTAAGAA AAAAGTTTAC TACATCTCAG	1800
CTGAGTTCTT GATTGGTAAA CTCTTGTCAA ACAACTTGAT TAACCTTGGT CTTTACGACG	1860
ATGTTAAAAA AGAACTTGCA GCTGCAGGTA AAGACTTGAT CGAAGTTGAA GAAGTTGAAT	1920
TGGAACCATC TCTTGGTAAT GGTGGTTTGG GACGTTTGGC TGCCTGCTTT ATCGACTCAA	1980
TTGCTACTCT TGGTTTGAAT GGTGACGGTG TTGGTCTTAA CTACCACTTT GGTCTTTTCC	2040
AACAAGTTCT TAAAAACAAC CAACAAGAAA CAATTCCAAA TGCATGGTTG ACAGAGCAAA	2100
ACTGGTTGGT TCGCTCAAGC CGTAGCTACC AAGTACCATT TGCAGACTTT ACTTTGACAT	2160
CAACTCTTTA CGATATTGAT GTTACTGGTT ATGAAACAGC GACTAAAAAC CGCTTGCGTT	2220
TGTTTGACTT GGATTGAGTT GATTCTTCTA TTATTAAAGA TGGTATCAAC TTTGACAAGA	2280
CAGATATCGC TCGCAACTTA ACTCTCTTCC TTTACCCAGA TGATAGTGAC CGTCAAGGTG	2340
AATTGCTCCG TATCTTCCAA CAATACTTCA TGGTTTCAAA CGGTGCGCAA TTGATCATCG	2400

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ACGAAGCAAT	CGAAAAAGGA	AGCAACTTGC	ATGACCTTGC	TGACTACGCA	GTTGTCCAAA	2460
TCAACGATAC	TCACCCATCA	ATGGTGATTC	CTGAATTGAT	TCGTCTTTTG	ACTGCACGTG	2520
GTATCGATCT	TGACGAAGCA	ATCTCAATTG	TTCGTAGCAT	GACTGCCTAC	ACTAACCACA	2580
CAATCCTTGC	TGAAGCGCTT	GAAAAATGGC	CTCTTGAATT	CTTGCAAGAA	GTGGTTCCTC	2640
ACTTGGTACC	AATCATCGAA	GAATTGGACC	GTCGTGTGAA	GGCAGAGTAC	AAAGATCCAG	2700
CTGTTCAAAT	CATCGATGAG	AGCGGACGTG	TTCACATGGC	TCACATGGAT	ATCCACTACG	2760
GATACAGTGT	TAACGGGGTT	GCAGCACTCC	ATACTGAAAT	CTTGAAAAAT	TCTGAGTTGA	2820
AAGCCTTCTA	CGACCTTTAC	CCAGAAAAGT	TCAACAACAA	AACAAACGGT	ATCACTTTCC	2880
GTCGTGGCT	TATGCATGCT	AACCCAAGAT	TGTCTCACTA	CTTGGATGAG	ATTCTTGGAG	2940
ATGGTTGGCA	CCATGAAGCA	GATGAGCTTG	AAAACTTTT	GTCTTATGAA	GACAAAGCAG	3000
TTGTCAAAGA	AAAATTGGAA	AGCATCAAGG	CTCACAACAA	ACGTAAATTG	GCTCGTCACT	3060
TGAAAGAACA	CCAAGGTGTG	GAAATCAATC	CAAATTCTAT	CTTTGATATC	CAAATCAAAC	3120
GTCTTCACGA	GTACAAACGC	CAACAAATGA	ACGCTTTGTA	CGTGATCCAC	AAATACCTTG	3180
ACATCAAAGC	TGGTAACATC	CCTGCTCGTC	CAATCACAAT	CTTCTTTGGT	GGTAAAGCAG	3240
CTCCAGCCTA	CACAATCGCT	CAAGACATTA	TCCATTTAAT	CCTTTGCATG	TCAGAAGTTA	3300
TTGCTAACGA	TCCAGCAGTA	GCTCCACACT	TGCAAGTAGT	TATGGTTGAA	AACTACAACG	3360
TTACTGCAGC	AAGTTTCCTT	ATCCCAGCAT	GTGATATCTC	AGAACAAATC	TCACTTGCTT	3420
CTAAAGAAGC	TTCAGGTACT	GGTAACATGA	AATTCAATGT	GAACGGAGCT	TTGACACTTG	3480
GTACTATGGA	CGGTGCTAAC	GTGGAATCG	CTGAGTTGGT	TGGAGAAGAA	AACATCTACA	3540
TCTTCGGTGA	AGATTCAGAA	ACTGTTATCG	ACCTTTACGC	AAAAGCAGCT	TACAAATCAA	3600
GCGAATTCTA	CGCTCGTGAA	GCTATCAAAC	CATTGGTTGA	CTTCATCGTT	AGTGATGCAG	3660
TTCTTGACGC	TGGAAACAAA	GAGCGCTTGG	AACGTTTTTA	CAATGAATTG	ATCAACAAAG	3720
ACTGGTTCAT	GACTCTTCTT	GATTTGGAAG	ACTACATCAA	AGTCAAAGAG	CAAATGCTTG	3780
CTGACTACGA	AGACCGTGAC	GCATGGTTGG	ATAAAGTCAT	CGTTAACATT	TCTAAAGCAG	3840
GATTCTTCTC	ATCTGACCGT	ACAATCGCTC	AGTATAACGA	AGACATCTGG	CACTTGAAC	3900
AATACTCTTC	GAAAATCTCT	TCAAACCACG	TCAGCTTTAT	CTGCAACCTC	AAAGCAGTGC	3960
TTTGAGCAAC	TGCGGCTAGC	TTCTAGTTT	GCTCTTTGAT	TTTCATTGAG	TATAAGATAC	4020
AAATTTATAC	TAATACATTT	TGTAAAAAAG	CGAGTTTCGA	TTGAAATTCG	CTTTTTTAAT	4080
GATGTAGATT	TGGGTCAATC	TTGTCTAAAA	ATAGGGAAAT	CCTAGATACA	GTGAAGGCTT	4140

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TAAATGCTGG	TTTTTACTGT	CCTCAGCCTT	ATATTTTTTTC	GTAGTTGGTT	ACCTCATATC	4200
TATTATATTC	GCTTACATAA	AGTATTATAA	TATAATTGTA	GGAAAGAAGG	TGTTTTTATG	4260
ATATACACAC	TTAAATTGGT	GTTGTTTATT	ACCTTTCTTG	TAATAAGCTT	GTTACCTGAT	4320
AAGATTTTTG	GAAAAATAA	AAAAATTGG	AAAATAGTTT	TTGCAATATT	GACGGCAGTG	4380
GCAGCATTGT	CATTTATGTA	CTAAGTTATT	TTAAGAATGT	AGGGAAATAA	ACCCTACATT	4440
CTTTTTAGTT	TTTCTGTTT	TCTAAATCT	ATTTATCCAA	GCGATTCAAC	ATTCTTGCT	4500
TCTTCGCTTC	AAGTCTGCA	CGCTTTCTT	CGATTTCCGC	ATGTTTTTTC	TCGAGTTCAG	4560
AACAAC TTGC	ACCATTGCTA	AATTCTTTTC	GCCATCAGGA	GATAGGGTGA	GTCGACATGT	4620
CTATTACTCA	CCCAAAGCAG	TCCTACAAAG	CAGGAATTTT	CTGTTACTTT	TTTGGAATA	4680
GTAACGTTTA	TACAGCTTTG	ACACTTCGTA	TCAAAGCGCC	AAACACACTC	CGAGGGGTTT	4740
ACAGAAAGCA	GAAAAGGAAT	GATCTGGTAT	AAGATCATTC	CTTTTCyCTC	TTTTTCTTTA	4800
AGTAATTATA	TACAATGTAC	GACGAAGTCG	TCATTGCAAT	GCTGATCCAC	CACCTAAAGG	4860
GAAC TTAAA	CAACATTGAT	AAGATAAAGA	ATATAACAA	CGAAAATACG	TTATACCCAA	4920
TTAATTTTAT	TGTATATCTC	ATGATTAAAA	GTTAATCCTT	CCGTGT TAG	GAATGGCATC	4980
ATTTTTATCC	CATAATTGTG	CTAAATAAGT	CCCCGGTGAT	AATAAATTCA	TAGCGAATTC	5040
TAAAGCAACA	TCATTTACAA	ACCAACTACC	TAGATATCTA	GAAATTGCTG	AACGAATAGC	5100
ACTTTTTGCT	GCATGTTTTC	CTTTTACTTT	AATTAGATTT	GCAAGGCCTG	CAGTAGTTCC	5160
TCCTAATGCT	AAAGCTATTG	CAGTATCTAA	TAGAGCACCC	ATTTGATTAA	CTGTAATACC	5220
TTGCCAAACT	GCTCTAAATG	GAGAGTATGT	AGGTGGGATT	GTATAATCGC	CTTGTAATTG	5280
TCGGTTAATT	ACTTCTTTGA	TCCATTGTTG	TGAGACGTCT	GGATGAAAAG	ATTGGATTTC	5340
GTTTGCAAGT	GTATTGATTT	GTCTTCTGT	TAGAGAAGTG	ACAGGTTGAA	GTTCCATATT	5400
TGTTTCAATT	TGTGATACTT	GTTCAGAAGC	GTATACAGCT	GAAACACTTG	GAATCGCTGA	5460
TACAATTAAC	ACAATTGACG	TCAAAAAAAC	CGAAATAAAT	TTCATTAATT	TGTTCATGAG	5520
CTTTTCTCCT	TTTTATTTGC	ATCTGCTTAC	ATTTTATCAT	ATACTGTTAT	TATAGTCAAA	5580
AAAATATGCT	ATTATGTTAA	AAAAATATTT	TTCAAAATAT	AAATGGACGG	ATTTATTTTG	5640
GATTTTATTT	GTTATTTTGA	CCTGCCTCTA	TATTGGTAAC	CATGATTTGT	TTACTCTCAA	5700
TCATCAAGAA	TTCTCTTTTC	GTGGTAGCGT	TTGGGGTCTG	GTA CTGGCCT	TATATCACTT	5760
ACTATTCATT	GATAAGTTTG	TTATATCGAA	TCGAAAATAA	AGATTAGAGC	TATGCTTGAC	5820
TGTGTACTTT	TAGGATTTAT	TTTGGAGGAA	GATTTTGTCT	CTATTATTTA	TTATTTTAAA	5880
TTTATTTATT	TTGTATAAGA	TCTATTCCTT				5910

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(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5406 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

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GGCATAGCGA CTCATTTTTT CAACTGTCCA GGCTGGATAC CAGACTAATT TAACCTCAGT      60
ATCCGTTACT TCTGGAACCT CTATCATAGC ATCATAAATC TGGTCTGTCA AAAGGTCTGC      120
TAAGGGACAA CCCATAGTTG TCAAAGTCAT GTCAATCTCT GTTTGCCCTG TGTCACCGTC      180
AAAACGAATC TCATAGATCA AACCAAGATT GACAATATCG ATTCCCAACT CAGGGTCGAT      240
GACTTCTTCC AAGGCTGTTA AAATCCGTGT TTTGATGTTT TCAATTGCT CTTCTGTATA      300
AGCCATATTT TCCTCACTCT TAGTCTTCAA TAAATCACG AAGCGGTTTG CTACGACTTG      360
GTTGGCGTAG TTTTCTCAA GCCTTTGCTT CAATCTGACG GATACGCTCA CGAGTTACGT      420
TAAAGACTTT CCCCACATCT TCAAGTGTGC GCATTTTTC ATCATCTAGT CCAAACGTA      480
GACGCAGAAC ATTTTCTTCA CGGTCTGTAA GAGTATCTAA GATTTCATCC AATTGCTCAC      540
GCAAGACGAT ACGAGTCGTA TAATCCACTG GATTTTCAAT CACTTCATCT TCGATAAAGT      600
CTCCAAGGTG GCTATCGTCC TCTTCACCGA TAGGAGTTTC AAGAGATACT GGTTCCTGGG      660
CAATCTTCAA GATTTCACGA ACCTTATCAG GTGTCATATC CATTCGTTCA GCAATCTGTT      720
CTGGTGTCGG ATCTTGCCCC AATTCTTGAA GGAGATTCG CTGTTACGA ACCAATTTAT      780
TGATAGTTTC AACCATGTGA ACTGGGATAC GGATGGTACG AGCTTGCTCC GCAATAGCAC      840
GAGTGATAGC CTGACGAATC CACCAAGTTG CATAAGTTGA AAAGTTGAAC CCTTTAGAAT      900
AGTCAAACCT GTCAACCGCC TTCATCAAGC CCATATTTCC TTCTTGAATC AAGTCAAGGA      960
ACTGCATACC ACGACCGACA TAGCGTTTGG CAATGGAAAC AACCAAACGA AGATTGGCTT     1020
CCGCAAGACG TTGTTTGGCT TCGATATCAC CAGCTTCAAC AGCCAGTGCC AACTCTTCTT     1080
CCTCTTCATT GGTCAAGAGA GGAACGACCC CTATTTCTTT CAAGTACATA CGGACAGGGT     1140
CATTGACCTT AGCAGAAGTT GACCCAATCA AGTCCTCATC GCTGAGTTCT GGTTCCTTCT     1200
CATTGCTGAG AACACGCGCA CTTGGATTTC CTTCGTTATC TGTGATAGAA ATGCCTGCAT     1260
CCTGAATCCG TTGCAAGAGA TCTTCAATCC CATCAGCGTC CAAGGTAAAA GGAATAACCA     1320
GACTTGCATT GATTTCATCA TCTGTTGCTG TCCCTTTTGG CTTATGATTA CGGATAAATT     1380

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CTGCTACCTG	TACGTCAAAT	GTGTGTTACTT	CTTTTTGTGTTT	TGTTGCCATT	ATTACTCCAT	1440
TCTTCTCTTT	TGGGAAATTA	AACGTTCCAA	TTCTTCTAGG	GCTGTATCTG	TATCTCCTAC	1500
ATGGCTAGCT	TCCTGCACCT	TCTTTTTGAT	TCTCATATTG	TCCTGATTCA	AGAGAGCCTT	1560
GTTTCGAGTC	ATCTCTACTT	CACTAAGTTC	CTGCGGCGAT	ATCTCAGCAG	GCAAATCCTG	1620
AGCTAAAACT	TGGTACCAAG	CTCTTTCAAC	TTCTCTGTGC	TGCTCTGCTA	AAACTTCTGG	1680
AGGAAGATTT	CCATACTGGC	CAAGCAAGTC	ATATAAGACC	TGAAATTCAG	GTGTAGCAAA	1740
TGCAAAGTCT	TCTCGCAAAC	GGTAATCGTT	CAAAACAAGA	GGGGATTCCA	TCATCCGATA	1800
GAGTAGATGG	GCTTCTGCCC	TCATAATAGC	CGATAACTGC	TTGGTGACAG	GCATGGTGAT	1860
TGGCGTCGGT	CTGGAAATTC	CTTCCATGCG	ATTCTGCCTT	TGCACCTGAC	GACTCTCATT	1920
AACAATCTGC	TCAATCTGGG	TATAATCAAA	GGACGCCAGA	CTGTCAGCTA	AAATATGAAT	1980
ATAGCTGTTT	TGAGCAGCGA	TGGACTTTTC	TTGAACAATC	AAGGGAGCTA	TTTTTTCAAG	2040
AAACTCAATC	TGAGCCTGCA	GATTTTCACT	GTTTTCAGGT	TTGTACTGAT	GAATGTAGAA	2100
CTCAATCGGA	CTAATACGAG	TTTTTCGTTAA	TAGATAGGCC	AAGTCTTCTG	GACCATTTTTT	2160
TTGTAGATAC	TCATCAGGAT	CCAAGTTATC	AGGCATGCTG	ACGATTTGCA	CAGGCATATC	2220
ACCAATTTC A	TCCAATGCTT	TCAATGTCGC	GGCTTGCCCA	GCCTTATCTC	CATCGTAAAC	2280
AAGAACCAAT	TTCTTGGTTA	ACCTTTTCAG	ATGCTCAACA	TGCTCTCGAC	TCAAGGCTGT	2340
TCCCATCGAC	GCCACAGCAT	TTTCGATTCC	AGCCCGATAG	GCTGCAATAA	CATCCATGAA	2400
TCCTTCCATC	AGGTAAATCT	CACTAGCTTT	TCCAGAAGAT	CTTTTTTGCCC	TATCCATATG	2460
ATATAAATCG	TAACTTTTGT	TAAAAATTGC	AGTCGATCGG	CTGTTTTTAT	ACTTAGAAGT	2520
TTGTGAATCC	GTTTTTTGCC	AGATACGACC	TGAGAAGGCA	ATGACCTTTC	CTTGGTCATT	2580
TGTCAGGGGA	AACATAATGC	GATTGTGAAA	GGTGTCTACA	AATTGATTGG	CATCCGAGAG	2640
ATAAACAGG	CCTGAATCCA	GTAAATCCTC	TTACAGATAC	TGATCAGACA	AACGTTGATA	2700
GAGATAGTTT	CGTTCTGGAG	GTGCTAAACC	AATCCAAAAA	TGTTTAAGCA	CTTCATCTGT	2760
CAACCCCCGC	TGATAAAGGT	AATTTCTGGC	CTCTTCGCCC	ATAGTCGTTG	TCATGAGAAT	2820
AGCATGGTAA	AATTTGGCTG	CATCTTCGTG	CATATCATAA	AGAGCTTGGT	GAGGTGAGGC	2880
TGACTTCTGC	TCACTATAAA	GCGGTTTTTC	AACCTCAATT	CCAACACGCT	GACCTAAGAT	2940
TTGGACTGCT	TCTATAAAGG	GAACCCCTTG	GTA CTCTCG	ATGAACTTAA	AGACATCACC	3000
TGAGCGACCA	CAACCGAAAC	AGTGATAAAA	CTGCTTGTC	TCTACAACAT	TGAAAGATGG	3060
TGTTTTTTCA	CCATGAAAAG	GACAGAGCCC	TAGATAGTTC	CGTCCTGCCT	TTTGTAAGA	3120
AATCACATCT	CCTATGACTT	CCACAATGTT	GGCATTGTTT	TTGATTCTT	CAATGACTTG	3180

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TTTGTCAACC	ATACACAATA	CCTCCATGTT	ATCATAGTTT	ACTTTATATA	GTATACTTTA	3240
TTTCAGAAAA	AAAGTAAACC	ATTTCACTCA	TTTCCCCTAC	TTTATTCAAA	GAGTTGATAA	3300
TAATCAGAGA	TTTTCATTTT	TGCTTTTTCT	TCTTGGTTTA	AATCTTGGAT	AATTCGTCCT	3360
TCTTTCATGA	CAATCAAGCG	ATTGCCGTAT	TTGAGAGCAT	CTTCCATATG	ATGAGTAATC	3420
ATAAGGGCTG	TTAGCTGATC	TTTCTTAACA	AATTCATCTG	TCAATTCCAT	CAAAGCAACA	3480
CTAGTCTTTG	GATCCAGGGC	AGCAGTATGC	TCATCTAACA	GGAGTAATTC	AGGTCGCTTC	3540
AAGGTTGCCA	TCAAGAGACT	CAAAGCCTGT	CTTTGTCCAC	CTGATAAGAA	CTCAATCGGT	3600
GTATTCAAGT	GTTTCTCAAG	ACCATTTTCCT	ACTTTTTCAA	TGGTTGCCTG	AAATTCATCC	3660
TTATAGCTAG	TCAAGCGTCG	TGGTAACAAT	CCACGCTTTT	CACCACGAAA	CTTGGCGATT	3720
AAAAGATTTT	CAGCGACCGT	CATACGGGGA	GCTGTCCCCA	TCTTTGGATC	TTGGAAGACA	3780
CGAGACAGGT	ACTTGGCACG	CTTCTCGGGT	GAAAACTTAG	TGAGATCTTC	ACCTAAAAATA	3840
CGGATAGTTC	CACTAGTTAG	TGATAAGGTC	CCTGCTATAG	TGTTAAAGAG	AGTTGATTTT	3900
CCAGCACCAT	TTCCGCCCAA	AATCGTGATA	AAGTCCCGTT	CAAAAATTTT	TAAGGAAACA	3960
TCATTTAAAA	TAATCTTTTC	TTCATCAAAG	CCATTTTAA	CGATTTTGGT	TGCATTTTTT	4020
AATTCTACAA	TTGCTGTCAT	TTGCTTAACT	TGGCTCCTTT	CAAGATTGTT	TGCTTAAATG	4080
TTGGAATCAT	GAGGCAGACT	GCTAAAATCA	AGGCACTGTA	TAAACGAAGG	TAACTTGTAT	4140
TAAAGCCAAG	TGCGATAACT	GCCCACACTA	AAAATTGATA	AGCGATAGAA	CCTACAACGA	4200
TAGTAACCAA	ACGCTCTGCC	AAGCTCAAAC	TCTTGAAAAT	AACTTCTCCA	ATAATCAAAC	4260
TTGCAAGCCC	CACAACGATA	ACCCCGATCC	CTCGAGACAC	ATCGGCATAA	CCTTCTTGCT	4320
GAGCAATGAG	GGCACCTGCA	AGGGCAATCA	CACCATTTGA	TAAGACCAAG	CCCATGAGCT	4380
CCATGCGTCC	AGTATGAATC	CCGAAACTTC	TAGCCATATC	AGGATTATCC	CCTGTAGCAA	4440
TATAGGCTTG	TCCGAGTTTA	GTGTCCAAGA	AAAAGAGCAT	GAGAGCAATA	ACAATACTCA	4500
CAAAGATGAG	ACCTGTCAAG	AGTTGATTCA	AA'TCCGAATC	AAAAGGCAAA	ACATCCTGAA	4560
TTTGCTTGGT	TCCAAGCAGG	CCTAAATTTC	CACGTCCCAT	AATCAAGAGC	ATGATTGAGT	4620
GACAAGAAGT	CATCACCAAA	ATCCCTGAGA	GCAAGGTTGG	GATCTTCCCT	TTTGTATAAA	4680
GAAGGCCTGC	TGCCATTCCA	GCCAAACAAC	CTGCTCCTAC	AGCAACAAGT	GTCGCTAAAA	4740
ATGGGTTTAC	GCCTTTGGTT	ATCAAAGTGA	CAGCAACAGC	TCCCCCAAGA	GGGAAGGAAC	4800
CTTCTGTCGT	CATATCTGGA	AAGTTTAAAA	TCCTAAATGT	CATAAAGATT	CCCAGACCTA	4860
GAATAGCCCA	GACAAATCCT	TGAGAAATAA	TGGAAACAAT	CATATTTTAT	TTAATCCTTT	4920

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CTATATTCAT CTTTTTAAAA AATGGGAAGA GTCTCCTCCT CCCTACCTTA TTTATTCGAT	4980
GACTTGTCCT GCTTCTTTGA GAACAGACTC AGGAATAGTA ATACCTAGTT CTTGTGCTAT	5040
TTTTTTATTG ATGACTGACT TACCAGTTGA AAAGACATTG ACTGGGGTAT CGGCTGGTTT	5100
TGCACCTTTC AAGACTTGCA CAATCATTTT ACCTGTTGCC ACACCAAGGT CATGTTGGTC	5160
AATTACAAC TATGCCAAAC CACCTACTTC TACCATAGCT GTCGCACTGG GATAAATTGG	5220
TTTCTTAGAA CTTTGATTGC TAGAGACAAC CGTTGGAAAT CCTGATGCAA TGGTGTATC	5280
AATTGGAACC CAAATAGCAT CTACCTTGCT AGTCATAACA GTGACAGTTG AGGCAATTTC	5340
ATTTGTTGAA GGAAGTCAA ATGTTTCCAC TGTCAGACCT GCCTTTTCAG CATAAGCCTT	5400
AAATTC	5406

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAGCTTGCTC TTA CTATTAT AGCAGATGTT ATAGCTGGAA TTATCTTGTA TTTCGTCTGC	60
AAATGGCTAG ATGGTAAGAA GTAGACCGAA TGACTAGCCT ATAAACACCC GTTAAATCGC	120
TAAGATACGT CAAAAAAGCC CTTAACTATG GCACTAGTTA GGGGCTTTGG TGTTCTAATG	180
AACCTTATAC ACTAACTACA TTCTAGCATA TAAGCCCAGA TATTTCAAGA GTTTTATTTA	240
TTGTTTAAAG TTCTGAAAGG TCTATAATGA AGTTAGCCAT CTAGTATCAA AAAACCGACT	300
AGCTCTTATG AACTAGTCGA TTTCTCATCA ATGCGCCAAC ATTTCTTGGG CGATTTCTTG	360
GCCAGATAGG TTATCTGGGT AGTAGGTTGG CCAGTTGTCC ATTTCTTCAA AGAGGGCTTC	420
TTGGCTTG TG CCTCCAAAGA AGATATGGAA ATGTTCTGCC TTAAGTGGGG CAACATTGAG	480
GTCACTAAAC TGAACATACT TGAATTGTCC AGCGTCAGCA TCTGTGGCTT CAAAGAGGAA	540
ACGCACGCCA CGATTGCCTT TCTTGTAAGT CAAAATTTTC TTACCGACAT ACTTGTAAGT	600
GTATTTCTTG CTTTGTCAC CTTGAACAAA TTCCATAGTA TTATCAGTAA TGTTAATCTT	660
AGTCACATCT GTATGATAGC CTTTGTGATA GTAAGCCTTG TACTCAGCCT GGGTCATCTT	720
ACCAGTCAAC TTAGCCTTGT AGTCAAAGAC TTGGTCAAAC GTGCCGTCTT CAAGGAAAGG	780
ATAAACTGAT TGCCAGTTAC CTGCATAGTC ACTCAAGGTG CGGTCCTTGA CAGCTGCATC	840
CTCGAAGTAA CCATTTTGGA CTGTCTTGGT ATCCTCTGCC TTTTCAGGTT CAATTGCTGG	900

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GCCTTCTTGG TCTGTTGTTT GTTTCAAAGC CTTGAGGTTT TTCTCCATCA CGGAAATGTA	960
GTTTTCTCCA GCCTTGGTGT CCTCTTCTGT CAGACTTTCT AAAGGATTGA GGACATCAGT	1020
TTTGACACCT GCTTCTTTTG AAAGTGTGTT AGCAAGGGCT TGTGAGGCAT TTCTTCAAAA	1080
TAGATATAGG CGATTTTATT TTTCTTGACA TACTCTGTCA ATTCTGCCAA GCGAGCAGCT	1140
GATGGCTCTG CATCTGGAGA AAGTCCTGAG ATTGCGACTT GTTTGAGTCC ATAGTCCAAG	1200
GCAAGATAGT TAAAGGCTGC GTGTGAGTC ACAAAGCTCT TTTGTTTTGC TTGAGACAAA	1260
CCTTCTGCGT AAGCCTTATC CAAGGCTTGC AATTTTTCGA TATAGGCAGC TGCATTCTTC	1320
TCAAAGGTCT CTTTTTATC AGGATAATCT GCTGACAAGC TGTCGCGGAT GTGCTCTACT	1380
AGTTTAATGG CACGAAGTGG TGATAACCAA ACATGGGGGT CAAACTCATG GTGATGACCT	1440
TCTTCTCCAT GGTGATGGTC TCCCTCTTCT TCCTCGCCAC CTGGCAAGAG CAACATATCG	1500
CCTGTCGCCT TGATGGTTT CACTTTTTTC TTATCCAAGG TATCTAGCAA TTTAGGTACC	1560
CATGTTTCCA TGTTTTCAT TTCATAAAGC AAGGTATCTG CATCTTGGAT TTTGGCAACT	1620
GCCTTGGCAG ATGGTTCGTA TTCATGAGGT TCTGTCCCAG CACCGATTAG GAGTTCTACA	1680
TTAGCCGTAT CTCCTGCGAC TTGCTTGGTA AATTCATAGA CAGGGTAAAA GGTGTGCACG	1740
ATATTGAGTT TACCATCTGC CTGTTTTTGA TTGGAACAAG CCACTAAAA CAAGGCACAT	1800
AGACTGGCTA GTAATAAGCT AATTTTTTTC ACGTTCGTCT CCTATTTGAT AAAACGTCCT	1860
ACTAAACTGA TTAGTATAAA GACAGTTACA AAAATAATGG TAATACTTGC ACTTGCAGGT	1920
GTTTCTGCAT AGTAGGAAAT GTAAAGTCCT GCTACCATT CCAAAAAGCC AATCGCACTG	1980
GCAAGCAGCA TAACCGATTT AAAGTTTTTC CCCAGACGCA GGGCAATACT AGCTGGCAAG	2040
ACCATAATGG TCGATAACCAG AAGAGCTCCT GCTGCAGGAA TCATAAGGGC AATAGCCACC	2100
CCTGTCACCA TGTAAAAAG AATGGACATG GTACGAACG GCAAGCCATC CACAAAGGCC	2160
GTATCTTCGT CAAAAGTTAA GATATACATA GGACGAAGAA AGAGAAAGGT CAAAATCAAA	2220
ACAACCGCCG CAATGACAAA GAGGGAATG ACCTGTTCTT CACTGATAGT CACGATCGAA	2280
CCAAAGAGAT ATTGGTCCAA ACTCATTGAA CTCGAGCTTT TACCCTTGCT CATGACAATC	2340
AGAGAAACAG CCAGACCTGT TGACATGAGG ATAGCTGTCC CGATTTCCAT AAAGCTCTTG	2400
TAAACCGTAC GGAGATACTC CAGAAAGACC GCCGAATCA AGACAATGGC AATAGTAGAA	2460
ACAGTTGGAG AAATCCCCAA AACCAGACCA AAGGCTACAC CTGAAAGTGA GACGTGGCTA	2520
AGGGTATCAC TCATCAAACCT CTGACGACGC AAGATGAGGA AGGTTCCCAA TACCGGTGAG	2580
AAAAGACTCA TAGCAATAAC CGCCAAAAAG GCGCGTTGTA TAAAGTCGTA AGATAATAAA	2640

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CTAAGCATGG	CCCACCTCCT	GGCCATTCTC	ATGAACATTG	AAACAACGCC	ATGGCGAGTC 2700
TTGGTTACGG	ACTAGATGAA	TATTGCGATC	CGCATAATCC	TTAACTTCTT	CAGGGTCATG 2760
GGTAATCATC	AAAACAGCCT	TGCCATGATG	ATGGGCGCTG	TGGTGCATGA	GTTCGTAAAA 2820
TTCATTTTTA	CTTCCTGCAT	CCATCCCCGT	TGTCGGCTCG	TCTAGGATAA	ACACATCAGG 2880
GTCAGAAGCA	AACATACGCG	CAATTACCGC	TCGCTGCTTT	TGTCCCCCAG	ATAGAGACCC 2940
CAAGCGTTTG	TCTCGATGTT	CCCACATGCC	AACTGAGTCC	AGACTAGCCT	TGATATGCTC 3000
CTCATCATGA	GCATTCAAAC	GACGGAACCA	GCCTTTTCTC	GGATAGCGAC	CCGACTTGAC 3060
AAATTTCATAG	ACCGTACTTG	GAAAACCAGC	ATTAAAACTG	GCAATTTGTT	GAGGAAGATA 3120
GGCTATTCTC	AATTTCTTAC	CTTGCGTATT	TGTCTTTGAA	ATAGCCACCT	TTCCAATGCG 3180
TGGTTGCAGA	ATTCCAAGAC	TAGCCTTGAT	GAGCGTCGTC	TTAGCCGCTC	CATTTTCCCC 3240
AGTCAAGGTA	ACAAATPCCC	CACTATCAAC	ACAATAATTG	ATATGTTCAA	GAACAGGCTC 3300
CTTATCATAA	TAGAAGGACA	AATCCTCTAC	CGTAATATAT	CTCATTTATTT	GATTTCTCCT 3360
ACTAAAGCAG	TCAAAAACCG	CTGAATCACT	TTTTGTTCAT	TTGGAGTAAA	CTGAGTCGCC 3420
ACTTGTTCAT	AGGTTAAAG	TGTATGCTCA	TGGTGATGGT	GGTGCTCCTC	AGCGATTGGA 3480
CGAGCCAAGT	CAGTCAACTG	ATAAAAAATC	ACACGCGCAT	CTTTAGAATC	TTTAGATGTT 3540
TCCAACATCC	CTTCCTTGAC	CAAAGACTTA	ATGGCCTTGG	TAAGTCCCGC	CTGACTGACA 3600
TTGAGACGAC	GGGCCAATTC	TGAATTTGTT	AAAGATTCCT	CTGACAAGAG	CATAAGGATA 3660
TGCTCCTGAG	TATTGGTCAG	GGCCACCTCG	CTAGTGCAAT	GACCTATTAG	GATTTTCATGC 3720
TGATTTTCCG	CCTGCAAAAT	CACCTCATTC	AAAAAAGCAT	TGATATCCTT	TGCTAGCTGT 3780
CTCATATCTG	ACTCCTTTCC	TTTTAGACTT	CTCTTTTTTA	AGAGAAAAAT	ACTATTCTTT 3840
GACATTTTGT	TTACCAGTTA	ATTATATCAC	AAGCAAAAAA	AGAGTCAAGA	AAAAACGTGA 3900
AAACTAGTTT	CATTCTTGAA	CTCTTCTATA	TTATATTATC	TATTGAAATT	CTTTGACATC 3960
TCCATCATAA	GTCGCCCAAT	CTTTGCTGAA	AAAGCGCTCA	TTCAGATGGT	AAGTCGGAGC 4020
TGGTGTGGGA	TTGGATAGGA	AAGGATCAAC	TGCCTTGTC	AAAGCCAACC	AACCCAACCA 4080
ACCAAGGTGA	ATGGTGTCCCT	TCATAAAGAA	AGGCTCCCCG	CCGTCCTTAG	AAAAATCTGC 4140
TATATTGGTA	AAACCTTGAC	TTTCTAACTG	GTAGCGAATC	TTCTGCACCG	TTTGTGGTA 4200
CATATCCTCT	CGTAGACCAG	CATAGTTCAT	CCATTTTTTA	TTAACAGGTG	GAATGATAAA 4260
AATCGGGTTT	ACCTTAGATT	TAGAAAACCTG	TGTTAAAAACC	AACTGCAAGT	CATTATACTC 4320
TGGCGACTTG	AGATAGGTAA	AGCTTTTCTG	AGAATCCTTT	AATTTCTTCA	AATCCTTCTT 4380
GATCTGCTCA	TTATAGAAAT	AATTTTCCAT	TCCCATCTCA	TTATTGGAAG	TATTTTCTTC 4440

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AGCATCTGCT	TTGACAACAT	CTTCTATTGC	CTGATAAGAA	AACTGGTCTG	GCAAGATTTT	4500
TAAATACCTA	GCTACATGCT	TATCGTAGTT	AACATAGCCT	CTAACCGAAA	ACTGACCAAA	4560
AAAGGAAGCT	TGGCGTTCAT	TAAAACGAGC	CAATAATTCA	ATCATTTTCAT	TGTCTGCTGT	4620
CGACAATTCT	TCTTTACTTG	CCAACTTCTG	AACCAGGTCC	TTCATAGCTA	CGTTTGGGAA	4680
CTGTTGCAGT	AAGCGAGTCG	CTGCATATTG	ACTAGCCTGA	TCCCCAGATT	GATGTTTCAG	4740
AAAACCTAGT	AACTGGTCTC	CATTAAAATA	CTGCTGGAAG	GCTGCTGGAT	CATAGCCATT	4800
TTTACTGAAC	CACCTGAGGTG	AGATAACATA	CACAACTTGT	TTATTCTCCA	GCTGTGGTAA	4860
CATCTGTTGC	ATTCCAAAAT	ATTGGTTAAG	CGATGCAGCT	CCCCCCTGTC	CTAAAAGATA	4920
AGGACGGTAG	GAACGATTGT	ATTTCTCAGC	TAATACCGCA	GGATGAGCAC	CGTCAAAACG	4980
AAGCCATTCA	CTAGAGCCAA	AGAAGGGAAC	AAAACGCACA	TTTGGAATCAG	ATAGTGCTCT	5040
GACTTTTTGA	CTTCGCTCCT	TAAAACATATC	GATAGTAGTA	GCCACTGCTG	AACGCTTTTC	5100
AGCTCCTAGA	TTATGATGCA	TCTCAGTAGG	ATAAAAGAAA	ATGAGCAGAA	AAACCAACAA	5160
ACCAGCGATC	AAGACCGGTC	CGAAGATCAT	CCATAAGCGT	TTAAGCATTT	TGTAGCTCCA	5220
CAATACCAGC	TATGATTTTA	TTAGCTGTAT	TCCAGTCGTC	ACGACCAAAC	TCTGTTACAG	5280
GGACACGAAT	GTCAAAACGG	TTCTCAATCT	CCACAATCAA	CTCAACCGTT	CCCATACTAT	5340
CCAAGACACC	TGCATCAAAA	AGATCTTCAT	CCATCATGTC	AGAAACATCT	TCCATAAACA	5400
ACTCATCAAT	AATTTCAATA	ACTTCTGATT	TGATATCCAT	ATTTTATTTC	CTTTTATTTT	5460
TTAAACCATA	GATTATTCAA	GAATCCAGAA	AAGATTAAGA	ATGACAACAT	GACAACATGG	5520
AAAGTGACAA	CCATGCCAAG	CAACTGAATC	CAGCGATTCT	CAGGTAGGGC	AGCCTTCCCT	5580
GCTTTTTC	GTTCCTTAT	GAGCGTTTTT	TTCTTGCGAA	CCCAGGCATC	ATTGATGACC	5640
AAGCCTAGTC	CATGAAAGAG	TCCATAGGCG	ATATAGTACC	AGGTCACACC	ATGCCAAAAT	5700
CCCATAATCA	GCATATTTAC	AATGTAGGCC	ATGCTTGAGG	TTACATTACG	ATTTTAAAG	5760
ACTTTCCTTC	TGGTTAACAC	CATCACCATT	CGCATAAAGA	CAAAGTCACG	GAACCAGAAG	5820
GACAGACTCA	TATGCCAGCG	ATTCCAAAAC	TCCTTTAAAT	CCCTTGATAA	AAAGGGCTTG	5880
TTAAAGTTGA	TAGGGCTACG	GATTCCCATC	AAGTTTGAGA	TGGCCAAAGC	AAACATAGAA	5940
TAACCTGCAA	AGTCAAAGAA	GAGTTCCAGA	CCAAAAGTAT	ACATAACTGC	CAAGGCATAG	6000
AGATTAAAGA	AGCCACCTGA	CTGCAAGGCT	AAATTCCTCA	GAGGAGGTAG	TAAGGTCTCT	6060
CCTAAAACAT	GAGCTAGGAT	AAACTTATAC	AAAAAGCCCC	ACATGATATA	GCGGACAGAT	6120
TCATCCAGCA	TATCCATCAA	CTCATCTCGC	TCAGGAATAG	CCTGATAATT	TTTATTAAAT	6180

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CGCTTAAAGC	GATCGATTGG	ACCACTCGAG	AAAGTTGGCA	TGAAGAGAAG	GAAACGGAGG	6240
AATTTCCAGA	GGGTAAAATC	CTTAATCACT	CCATCTCTCA	GCTCGATGAC	AATTTCAACC	6300
GAACGAAAGG	TCAGGTAAGA	AATTTCCCAAG	AACCCAAGCA	AAGACTGCGT	TCCATTGATA	6360
GCTGGTTGCA	CCTTGACAAA	GATAATCGGA	AGTAGGGACA	GAAAACCTAAC	TAAGTAGAAG	6420
ACCCACTTGC	CATCCTTGCT	TTTTTCGATAA	TGCTTGTAGA	AAAGCAGGAG	CAATATTTCC	6480
CAGCAAAGGT	AAATACCCAA	GGCAGCTAGT	TGATTGGTCT	TTCCACCCAC	CAACATGGTG	6540
ACAATAAAGA	AGAGACTTAC	CAACACTTCA	TACCAGGCAA	AGCGTTTCTT	GAAAAAGAGA	6600
CCTATAAAGA	TGGGCAAGGT	TGCAGCAATC	ACATAAACAA	AATACTGAGG	ATTGCCATAT	6660
GGCTCTAAAT	GAGGAAGCTG	TTGAAAAAAC	TCCATCATCT	CTTATTCACC	TCGTTAATCA	6720
ATCCTTTGAT	GTCAATCTTT	CCATTTGGAG	TTAGTGGCAA	ACTGTCTCGG	TAAAGGAATT	6780
TAGATGGCAT	CATATAGGAC	ATCATGATGT	CTGTCAGGTC	TTCCCTTGATG	GCCTTGGTAA	6840
TATCGATATC	TCGCTCAAAC	TGCTCACGAA	CACCGTCTTT	TAAGATGACA	TAAGCCAATA	6900
GATTTTGATC	CTTGTGGTCC	TTGTTATAGC	GCGGTACTGC	GACAGCAGAT	TCGATAAAGC	6960
GAGACTTGTT	GAGGTTTTGA	GAGACATCTT	CTAACTCAAT	GCGGTAACCG	TTAAACTTAA	7020
TCTGGAAGTC	CATGCGTCCG	CCGTAGAGAA	GCAAGCCCTC	ATCTGTCATG	GTTCCACAT	7080
CGCCTGTGTG	ATAGGCTGGC	AGATCTTCAA	ACTCAAAGAA	GGCTTCTGCT	GTTTTTTCAG	7140
GATTGTTTCA	ATAACCTTTT	GAAACAGCTG	GCCCAGAAAC	AATGATTTCT	CCCTGCTCAC	7200
CATTTGGCAG	TTTATTTCCCT	TCCTCGTCAA	TGATAAAGGT	TGGAGAATCA	GCCTTGGTAT	7260
AGCCGATTGG	TAGGCGTTTG	AGAGTCGCTA	ACATCTCGTC	TGTCACGGCA	ACTGCTGACA	7320
GAGCTACTGT	CGCTTCTGTT	GGGCCGTAAG	CATTGATGAT	ACGGGCATTT	GGGAAACGCT	7380
CGCGCAGTTT	TTGAGCTGTT	TTGACCGTCA	ATTCTTCACC	ATCAAAGTAG	AAATGCGTGA	7440
TTCCAGGCAT	TTTCTCACTG	TTGAAGTATT	CAGACAACAT	GGCCATATCT	GCAAAGGATG	7500
GTGTTGATGT	CCAGATAGCG	ATTGGCAATG	AAAAGATAGC	CGCAAAGAGT	TGCTTAAACT	7560
CCTGAGTGAT	GACTGAAGGA	AGAGTGAAAA	GCGTACCACC	AAGTGCCAAG	GTCGGTGCCC	7620
AATACATGAC	AGACAAGTCA	AAAGAATAAG	GTGGCTGTGC	CAGCATTTGC	GGACGACTCG	7680
GTGTCGCAAA	TTCTTATCC	GTAATCATCC	AGTTTGTAAG	GCTGAGGAGA	TTATCATGTG	7740
AAATCTGCAC	TCCCTTAGGC	TTACCAGTCG	TACCAGAAGT	AAAGATAATG	TAGTAATTAT	7800
CATCTCCCTT	GACTGGATGC	GTGATTTTCA	AGTTATTCCC	TTGGGCAAAG	GCTTCTTGAA	7860
CCTGAGCTAG	ATTTATCATT	GGTGTAGAAA	CCTGCTCCAA	GGGAAAGGCT	GAAATGGCAA	7920
TAATCAAGCT	TGGCTCTGCT	ACTTCTAAAA	TAGCTGAAAC	TCGCTCCAAG	GCCGAATGGC	7980

1075

TATCAATTGG AATGTAGGCA TGACCTGACT TAGTCAGCGC TACAAAGGTT GCCAACATTT	8040
CATATTCTTG GCCACCAAAA ACAACCACAG GAGACTTCTC AGGCAAGCCT AGTTGGTCAA	8100
TGACTGCAGC CAAACTATCC GAATCAGCCT TTAATCGCC ATAAGTGTGT TCCTGCCCCA	8160
AAACATTATA GACAGGATAG CTAGGCTGTG TCTGAGCAA ATGCTCAATG GTTTCATCA	8220
TATCTGCTAT TGGTTTATTT GACACAATAG GGATTCTCCT TCAAGTTAAA ATTCATTATA	8280
GATAAAGCTT CCTTGACCCT GACCAAGATA GCTAAAGAAG TAAAGCAGCC CTAGAAAGAT	8340
AAGAAAATAC AAGGCTGTCC GACCAAGAAA GAGGTACAAT TCTTTTCTCT GTTTCATCAA	8400
GAAAAACCAT TCATTTCTGT AATTTTTCGC TAAATAAGA GTGATTCTTA CTAGCTTATT	8460
TTTCTACCAT TGTACCACTT TATATAGTAT CTTTTCATT GTTTACCGTA TGTTTCCAAT	8520
AGATTTCAGC TTATTTTAAG GATTATACAG TTTTCTATG TATATTTCA AATAGAGTGA	8580
TCCTGCTTCA AAACCTCATT TCAGGAGACA ATGAAGTAAA TCTTCCATA ATAAAACACA	8640
CAATATCAAG TTTTTTCAAC ACCTGATACT ATGCGCTTTT CTGATTTTAA AAGACTTTTT	8700
AACCACTCTC TCATTTAAAA TAATCTCGTC TGATATAAAT TAAAATAGCT TCTATCATCA	8760
GACAAATGGC TGATAGCCAA AAACGTATGC TAATACCAA ACTCTCAGTA ATATAGCTCA	8820
TTAGCAAAAC AAATACTGAA AATGCTAATG TAGAAATCAC TTCAAGAACG GAATAGACAT	8880
TAACATAAATG ATTTTCTCTC ACTGTTTCTT GAAGAAATAC ACTTTCAGGA ACTTCTTTTA	8940
GTTGCGATAA CATACCAACT AAAGCTGAAA ATAATAAAAA CATCTGTGCG TTTGGAAAAT	9000
ATAGAATAGT CAGTGTCAT ATTTCCATAG CTACAAGAGG AAAAAGAATA CTTTCCCCC	9060
AAATCATTCA TACCTCTCTC AACTAGATGT AACTTACAAA ACCCCTGACC TCATGAGCCA	9120
CTTCTCTCCT CCTCATGAGG TCAGTTTAC TTTCTGCTGT TCCAGTATCG TTTTCTCTCG	9180
CTAGATTTCC TCAAAAGGGC AGACTCCTCC CTTGGTGCCT CACACGATTT TTTCATCTCG	9240
ACTGTCTTTT AATGCATCAT TAACGACGCT TTTCTTCTAG GTGGTTCATA AGGAACAGGA	9300
AGATTTCAGT TGACTTTTCT AATCCTAGAA TAAAGTGCTG AAAACAATTC GGAATAGGCA	9360
TAGAGACTAG ACAATTTGAG GAGCTGCTTG CGTCCTGTTT GAACACATTT TCCCACCACG	9420
TGAAGAAAAA GATGGCGGAA GCGTTTGATT GTTAAAGTTT GGAAGTCACC TCCAGCTAGA	9480
TGTTTGAGAA AAAGATAGAG ATTGTAGGCG ATACAGCTCA TCATCATACG AACTTCGTTT	9540
TTGATTAAGG TTGAACTATC CGTTTATCG CCAAAAAATC CCTCCTTCAT CTCCTTGATG	9600
AAATTCCTCG CTTGACCACG TCCACGATAA AGCTGAAACT GGTCTTGGcT gTTCCACTCG	9660
TCATATTTGT AACGAGAGAA ATAACATCGT AGAACAAGTA TCCTTCTTTT C	9711

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(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3025 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

CCCCTTTGTC AAAACTGTAA AATTAACGAC TCAACAATTC ATCTTTACAC CAATCTCAAT	60
GGAAAACAAA AACAAATTGA CCTCTGTCAA AACTGCTATA AGATTATCAA AACAGATCCT	120
AACAATAGCC TCTTCAAAGG TATGACGGAT CTGAACAATC GTGACTTCGA TCCCTTTGGT	180
GATTTCTTCA ATGATCTAAA CAATTTGAGA CCTTCTAGCA ATACTCCTCC TATTCCCCCA	240
ACCCAATCAG GTGGAGGTTA CGGTGGAAAC GCGCGTTATG GTTCCCCAAA TCGTGGATCT	300
GCTCAAATC CGCCACCTAG CCAAGAAAAA GGCCTGCTGG AAGAATTTGG TATTAATGTA	360
ACTGAAATG CCCGTCGTGG AGACATTGAC CCCGTTATG GCGCGACGA TGAGATTATC	420
CGTGTTCATCG AGATTCTCAA TCGTAGAACC AAGAATAATC CTGTCCCTTAT CGGTGAACCT	480
GGTGTGCGAA AACGCGCCGT TGTGGAAGGT CTAGCTCAGA AAATTGTCGA TGGCGATGTG	540
CCACATAAAC TCCAAGGTAA ACAAGTCATC CGTCTGGATG TGGTTAGCTT AGTTCAAGGA	600
ACGGGGATTC GAGGACAATT TGAAGAACGC ATGCAAAAAC TCATGGAAGA AATTCGCAA	660
CGTGAAGACA TCATCCTCTT TATCGATGAA ATCCATGAAA TTGTTGGTGC TGGTTCTGCG	720
AGTGATGGTA ATATGGACGC AGGAAATATC CTCAAGCCAG CCCTTGCTCG TGGAGAACTG	780
CAACTAGTCG GTGCTACTAC CCTCAATGAA TACCGTATCA TTGAAAAGGA TGCTGCCCTC	840
GAGCGTCGTA TGCAGCCTGT TAAAGTCGAT GAACCAACGG TGGACGAAAC AATCACTATT	900
CTCAAAGGGA TTCAAAAGAA ATACGAAGAT TACCACCACG TTCAATATAC AGATGCTGCG	960
ATTGAAGCAG CTGCAACTCT TTCCAATCGC TACATCCAAG ATCGCTTCTT GCCTGACAAG	1020
GCCATTGACC TCCTAGATGA AGCTGGTTCT AAGATGAACT TGACCTTGAA TTTTGTGGAT	1080
CCTAAAGTAA TTGATCAGCG CTTGATTGAG GCTGAAAATC TCAAGTCTCA AGCTACACGA	1140
GAAGAAGATT TTGAGAAGGC GCCTACTTTC CGCGACCAGA TTGCCAAGTA TAAGGAAATG	1200
CAAAAGAAAA AGATCACAGA CCAGGATACT CCTAGCATCA GCAGAAAAAC TATTGAGCAC	1260
ATTATCGAGC AGAAAACCAA TATCCCTGTT GGTGATTTGA AAGAGAAAGA ACAATCTCAA	1320
CTCATCCATC TAGCCGAAGA TCTCAAGTCT CATGTTATTG GTCAAGATGA TGCAGTCGAT	1380
AAGATTGCCA AGGCTATTCT CCGTAATCGT GTCGGACTTG GTACCCCTAA CCGCCCAATC	1440

1077

GGAAGCTTCC TCTTCGTTGG GCCAACTGGT GTCGGTAAGA CAGAACTTTC CAAACAAC TG	1500
GCTATCGAAC TTTTGTGGTTC TGCTGATAGT ATGATTCGCT TTGATATGAG TGAATACATG	1560
GAAAAACATA GTGTGGCTAA GTTGGTCGGC GCTCCTCCAG GTTATGTTGG CTATGATGAG	1620
GCTGGTCAAT TAACTGAAAA AGTTCGCCAC AATCCATATT CTCTCATCCT TCTCGATGAA	1680
GTGGA AAAAG CTCACCCAGA TGTATGCAC ATGTTTCTTC AAGTCTTGGA CGATGGTCGT	1740
TTGACAGACG GGCAAGGACG CACCGTTAGC TTCAAGGATG CCATCATTAT CATGACCTCA	1800
AATGCAGGTA CAGGAAAGAC CGAAGCTAGC GTTGGATT TG GTCTGCTAG AGAAGGACGT	1860
ACCAATTCTG TCCTCGGTGA ACTCGGTAACT TTCTTTAGCC CAGAGTTTAT GAACCGTTTT	1920
GATGGCATT TCGAATT TAA GGCTCTCAGC AAGGATAACC TCCTTCAGAT TGTCGAGCTC	1980
ATGCTAGCAG ATGTTAACA GCGCCTCTCT AGCAACAACA TTCGTTTGGA TGTAAGTATG	2040
AAGGTCAAGG AAAAGTTGGT TGACCTAGGT TATGATCCAA AAATGGGAGC ACGCCCACTT	2100
CGTCGGACTA TTCAAGACTA TATTGAGGAC ACAATCACTG ACTACTACCT TGAAAATCCA	2160
AGCGAAAAAG ATCTCAAAGC AGTTATGACT AGCAAGGGAA ACATTTCAGAT TAAATCTGCC	2220
AAAAAAGCTG AAGTTAAAAG TTCTGAAAA GAAAAATAAA TCCTATAAAA AAGGAGTAGA	2280
AAATGAAATT TTTCTGCTTC TTTTCTTACT AAAATAACTG TAATTTCTTG ACAGCTTGCC	2340
CTTTGTCCAT TATGATATAT AGTAGACTGA ATCTGAAATA GTACGAAACA ATTGCTAAAA	2400
CATTTATAGA AATTAATTTT ACTTTCCCAA TCGATTGTGTT CTCATCTTAT TTCAATCTGC	2460
TATAGTCAAT TGAACAAGA ACAAGACAAA AGAGCCTCAT AAAAGGTATT GCAACTTGGT	2520
AATACCTTTT TGAGGTGCTT TTTGATATGA GCCCATGTTT TCTCAATAGG ATTGTACTCA	2580
GGTGAGTAGG GAGGAAGAGG TAAAAGTTTA TACCCAAACT CTTCACACAA GAGTCTAAC	2640
TTACCCATTC TATGGAATCT TGCATTATCC ATAATAATAA CCGATGGTGT GGTTAATGTT	2700
GGTAAGAGAA ACTTCTGAAA CCAAGCTTCA AAAAAGTCGC TCGTCATCGT CTCTTCGTAA	2760
GTCATTGGAG CGATTAATCT ACCATTCAAT TGTTAGACCT GCAACCAAAG AAATCTCTCTG	2820
ATATCTTCTT CCAGATACTT TGCCTCTTCT TAACTGACCT TTTAATGAGC GACCATATTC	2880
TCGATAAAAA TAAGTATCGA ATCCTGTTC GTCAATCTAA ACAGGTGCTA GGTGCTTTAA	2940
ACTATTAAAA TTCTTAAGAA ATAAGGCTAC TTTTCTGGG TCTTGTTTCAT AGTAGGTGTA	3000
GTTCTTTTTT TTTTCGAGTG TAGCC	3025

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4104 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

TTTAAGGTTT TAAAAAAGT TTTCGAAAGG TTTCTTCTTT ATTTTTTAAG GGAGAGATAA	60
CGTTGATATC TAAATCGTGG TCAAAGCCGG CAATTTTCC TTTAGATGTG TATTGGTGAA	120
TATCATAATC TAAATCAGTT TTAGGACTGC TCTCCAAAA TCCTGAGTCT GAGCCGTAGA	180
CGGAATCCAA ACAGAGGTAA ACTTGCCTGT ATCAATACTG TGTTCCTCCA TGAAGTAGAC	240
ACCAACGTAG ATGCCGATGT TTTTAGCACC CAGTGATGCT AGTTTGTGCTC GAAAGTTTTC	300
GACACCTTCG TTCATATTAG ACATGGTTTT GTCTTCCACG TCAAGCCAAT AGTAACTAGG	360
GCTGTAAGGA GAGGCAGCAT TGTAAGAAAC TTCGGCAGCC TTTTCCATTT CTTGGACACT	420
TTTTCCAGCT ACATAAGCGT AGACAGCAAC TGGGACATTC CGCTTTTGAA GTTCAGTGAT	480
ATGACTCTTA TAGGCCTTGT CTATTCCATT GATAAATGAA GCATCATTTT CTTTGTGCGT	540
TTGAGCACCA CTGTGAACAC GAACAATAGC ACCTGAAATA TTTTGTGAGA GGCATCGTA	600
GTTGATTTCC TCAGGACGCT GCCAGCCAGA GAGGTCAATA ATCGGTTTGT CTAAGTGTTT	660
CAAAGCCTGT GCTTCAATCT GTGCTATATT GGATTTTGTT TTAAACGATT GGCTGTCATT	720
AAGTGGGCGA TTGATGATTA AAATGAACAT CATAATCCCA AAAAACTAA ATAAAATAAG	780
TGGATGAATT TGTTTTCTCA TATCTTATAA TTCTACCTA AAAATCAAAA AAAATCAAAA	840
AAATGGGTAA AGGAAGAGAC TTTAGAGCAT TTTTTCATTC AAGAGTGCGG AATGATTTGA	900
AATATGGTAT AATAAAGGG AATTTCTACA GAAAAGAGAA GATTATGTCA AATTTGCCA	960
TTATTTTAGC AGCGGGTAAA GGGACTCGCA TGAAATCTGA TTTGCCAAAA GTTTTGCACA	1020
AGGTTGCGGG TATTTCTATG TTGGAACATG TTTTCCGTAG TGTGGGAGCT ATCCAACCTG	1080
AAAAGACAGT AACAGTTGTA GGACACAAGG CAGAATTGGT TGAGGAGGTC TTGGCTGGAC	1140
AGACAGAATT TGTGACTCAA TCTGAACAGT TGGGAACCTG TCATGCAGTT ATGATGACAG	1200
AGCCTATCTT AGAAGGTTTG TCAGGACACA CCTTGGTCAT TGCAGGAGAT ACTCCTTTAA	1260
TCACTGGTGA AAGCTTGAAA AACTTGATTG ATTTCCATAT CAATCATAAA AATGTGGCCA	1320
CTATCTTGAC TGCTGAAACG GATAATCCTT TTGGTTATGG ACGAATTGTT CGTAATGACA	1380
ATGCTGAGGT TCTTCGTATT GTTGAGCAGA AGGATGCTAC AGATTTTGAA AAGCAAATCA	1440
AGGAAATCAA CACTGGAACA TACGTCTTTG ACAACGAGCG TTTGTTTGAG GCTTTGAAAA	1500
ATATCAATAC CAATAACGCT CAAGGCGAAT ACTATATTAC AGACGTCATT GGTATTTTCC	1560

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GTGAACTGG	TGAAAAAGTT	GGCGCTTATA	CTTTGAAAGA	TTTTGATGAA	AGTCTTGGGG	1620
TAAATGACCG	TGTGGCGCTT	GCGACAGCTG	AGTCAGTTAT	GCGTCGTCGC	ATCAATCATA	1680
AACACATGGT	CAACGGTGTT	AGCTTTGTCA	ATCCAGAAGC	AACTTATATC	GATATTGATG	1740
TTGAGATTGC	TTCGGAAGTT	CAAATCGAAG	CCAATGTTAC	CTTGAAAGGG	CAAACGAAAA	1800
TTGGTGCTGA	GACTGTTTTG	ACAAACGGTA	CTTATGTAGT	GGACAGCACT	ATCGGAGCAG	1860
GAGCGGTCAT	TACCAATTCT	ATGATTGAGG	AAAGTAGTGT	TGCAGACGGT	GTGATAGTCG	1920
GTCCTTATGC	TCACATTCGT	CCAAATTCAA	GTCCTGGTGC	CCAAGTTCAT	ATTGGTAACT	1980
TTGTTGAGGT	GAAAGGATCT	TCAATCGGTG	AGAATACCAA	GGCTGGTCAT	TTGACTTATA	2040
TCGGAACTG	TGAAGTGGGA	AGCAACGTTA	ATTTCCGGTG	TGGAACATAT	ACAGTCAACT	2100
ATGACGGCAA	AAACAAATAC	AAGACAGTCA	TTGGAAACAA	TGTCCTTTGT	GGTTCAAATT	2160
CAACCATTAT	TGCACCAGTA	GAACCTGGTG	ACAATTCCTT	CGTTGGTGCT	GGTTCAACTA	2220
TTACTAAAGA	CGTGCCAGCA	GATGCTATTG	CTATTGGTCG	CGGTCGTCAG	ATCAATAAAG	2280
ACGAATATGC	AACACGTCTT	CCTCATCATC	CTAAGAACCA	GTAGGAGCCT	ATCATGGAGT	2340
TTGAAGAAAA	AACGCTTAGC	CGAAAAGAAA	TCTATCAAGG	ACCAATATTT	AAACTGGTCC	2400
AAGATCAGGT	TGAATTACCA	GAAGGCAAGG	GAAC TGCCCA	ACGGGATTTG	ATTTTCCACA	2460
ATGGGGTCTG	CTGTGTTTTA	GCAGTAACGG	ATGAACAAAA	ACTTATCTTG	GTCAAGCAGT	2520
ACCGCAAAGC	TATCGAGGCT	GTCTCTTACG	AAATTCCAGC	CGGAAAATTG	GAAGTAGGAG	2580
AAAACACAGC	CCCTGTGGCA	GCTGCCCTTC	GTGAATTAGA	GGAAGAAACA	GCCTATACAG	2640
GGAAATTAGA	ACTCTTGTA	GATTTTTATT	CAGCTATTGG	CTTTTGTAAT	GAGAAGTTAA	2700
AACTATATTT	AGCAAGCGAT	TTGACAAAAG	TGGAAAATCC	GCGTCCGCAG	GATGAGGATG	2760
AAACCTTGGA	AGTCCTTGAA	GTGAGCTTAG	AAGAAGCGAA	AGAATTAATC	CAATCAGGTC	2820
ATATCTGTGA	TGCCAAGACA	ATTATGGCTG	TTCAGTATTG	GGAGTTGCAG	AAAAAATAGA	2880
GGAGGTCAGT	ATGGGTAAAT	CTTTATTAAC	GGATGAAATG	ATTGAAAGAG	CTAATAGAGG	2940
CGAAAAAATT	TCAGGTCCTC	CTTTGCTAGA	TGATAATGAG	GAAACTAAGA	TTTTACCAAC	3000
CTCTTCTTCC	CGTTTTGGTT	ATGCCAATCC	TAAGGATCAT	GGTTTTAGCC	AGGAAACCTT	3060
GAAGATTCAG	GTCGAACCAT	CTATTCATAA	AAGCCGTCGT	ATTGAAAATA	CCAAGAGAAA	3120
TGTCTTCAAT	TCTAAGTTGA	ATAAAATCTT	ATTTGCGGTC	ATCTTTCTCT	TGATTTTGCT	3180
TGTTTTAGCA	ATGAAACTTT	TGTAATAGAA	AAGGAATTGA	AATGAAAATA	GGAATTATTG	3240
CTGCTATGCC	AGAAGAACTG	GCTTATCTGG	TCCAGCATTT	AGATAATGCC	CAGGAGCAAG	3300

1080

TTGTTTTTGG GAATACCTAT CATACAGGAA CCATTGCTTC TCATGAAGTC GTTCTGTAG	3360
AAAGTGAAT TGGTAAGGTC ATGTCTGCTA TGAGTGCGC GATTTTGGCT GATCATTTCC	3420
AGGTGGATGC CCTTATTAAT ACGGGTTCAG CTGGGGCAGT AGCAGAAGGT ATCGCTGTTG	3480
GGGATGTCGT GATTGCTGAC AAATTAGCCT ATCATGACGT GGATGTCACA GCTTTTGGCT	3540
ATGCTTATGG ACAAATGGCG CAACAACCGC TTTATTTCGA ATCAGACAAA ACCTTTGTTG	3600
CTCAAATCCA AAAGAGTTTA TCTCAATTGG ACCAAAACCTG GCATCTTGGT TTGATTGCTA	3660
CAGGAGATAG TTTTGTGCA GGAAATGACA AGATAGAAGC GATTAAAGTCC CATTTCACAG	3720
AAGTTTTAGC CGTGGAGATG GAGGGGGCAG CTATTGCTCA AGCAGCGCAT GCCCTCAATC	3780
TCCCAGTCTT AGTCATCCGA GCTATGAGTG ACAATGCCAA CCATGAAGCA AACATCTTTT	3840
TTGATGAGTT TATTATCGAA GCTGGACGTC GCTCTGCCCA AGTCTTGTTG ACCTTTTGA	3900
AGGCTTTAGA TTAAGCGGAA ATTTGACAGT TTTTCTAGCT TATGATAAGA TTTAAGTAAA	3960
GAAAAGCTAG AAAACGTTTC AGAGGATATT ATGAGTATTG AAATGACCGT CAGTGAGATT	4020
GCAGAGGTCT TAGGATTATC TCGCCAAGCA ATCAATAACC GTGTCAAAGA ATTACCAGAA	4080
GAAGACACAG ATAAAAATGA CAAG	4104

(2) INFORMATION FOR SEQ ID NO: 170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8876 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CACGGATAGG CTCGGCTTTC ATCAGTCCTC AGGCTGATTT ACTAATAGCA ACTTTCCTCG	60
ACAAAGTCCA CAGCGATACG TnTGGGTATC AATCCTACGC TTACGCTGAT ACCTTTGCTG	120
GCAGGATTGG CAACGATAGA GCTTGATTGG CTTGGAGTTA CTATTGGGCA AGGATGGTAC	180
AAACCGTAAT CCATCCACTG CTTTCAACAG TTCCTTAAAA TCCCGATCCT TGTGTTGATA	240
GCCTTTCCCT TGAAAATAGA GGTGATAATG ACAGAGTTCA TGTCGGACAA TTTTCCTAAA	300
AACGTCCAAC CCCAGTTCCT GATAAACCTT GGGATTAAAA TCCAAATGCC CATCTTTGGG	360
GAAAAATCGC CCACCTGTCG AACGTAGACG CCTATTCCAC TGGACATGAT GGATAAAAGG	420
TCTGCCGAAG TCTTCTAGTG AAACCTGCTT GACGTAATCA GTCAGTTTCA TTTGGAGCTA	480
GGAGAGACAG ATTAACTTTT TCACGTTTCA TATCAATTTT CTTAACCCAA ACGCTCACCA	540
AATCTCCAAC TGCCACCACT TGACTAGGGT GTTTGATAAA CTTGCGACTC ATATGGGAAA	600

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TATGGATGAG	ACCGTCCTCA	TGAATTCGGA	TATCAACAAA	AGCACCGAAA	TCAACAACGT	660
TACGCACCAC	TCCTTCTAGC	TTTTGTCCAA	CCACTAAGTC	CTTGATATCT	AGGACATCTT	720
GGCGAaCACA	GGTGCGTCAA	AGGAATCACG	GAAATCTCGA	CCTGGTTTGA	GAAGATCTGC	780
AATGATATCT	TTAAGAGTTT	CTGGACCAAG	GTCTAACTCT	TGCGCCATT	CCTTGACTGA	840
AAGCGACTTG	AGTTTGCTTT	GGCCTCTTC	GTTTAGGTCT	TTAATATCTA	AACGTTTGAA	900
GAGTTCCTTA	ACTGCAGTGT	AATTCCTGG	GTGAACCTCT	GTATTATCAA	GGATATTGCT	960
ACTTTCAGGG	ATACGAAGGA	AACCAGCAGC	CTGCTCAAAG	GCCTTGCTC	CCAGACGAGG	1020
AAC TTCTTG	ATTTGGGCGC	GTGAAGTGAT	TTTTCTTCT	TCCTCGCGGT	ATTTGACAAT	1080
ATTTTCAGAG	ATAGTTTGT	TGAGTCCAGC	TACGTGTGAA	AGAAGAGCTG	GGCTAGCTGT	1140
ATTGACATTG	ACACCAACTT	GGTTAACCAC	TGTATCGACA	ACAAAGTCCA	GA CTCTCAGA	1200
TAGTTTCTTC	TGACTGACAT	CGTGTGGTA	TTGACCGACA	CCAATTGACT	TAGGATCGAT	1260
TTTGACCAAT	TCCGCAAGAG	GATCTTGCAA	ACGACGGGCG	ATAGAAATGG	CAGAGCGTTT	1320
TTCAACGGTC	AAGTCTGGAA	ACTCTGACG	AGCAAGTTCG	CTGGCAGAA	AGACAGAAGC	1380
ACCACTTTCA	TTAACGATAA	CATAGCTGAC	TTCAGGGAAA	TCTTTCAGAA	CTTCCGCTAC	1440
AAAAGCTTCA	CTTTCACGAC	TGGCCGTTCC	ATTTCCAATG	GCAATAATCT	CTACACCGTA	1500
TTGACCAATT	AAATCTGCTA	AATCTTCTT	GGCTTCTTCG	ATTTGACGAG	CTGATGCTGG	1560
TTTAACAGGA	TAAATAACCT	GAGTTGTCAG	CATTTTTCCT	GTTGCATCCA	CGACAGCTAG	1620
CTTGGCACCT	GTACGAAAGG	CTGGGTCAA	TCCAAGAACC	ACGCGCCCTT	TCAGTGAGC	1680
AACCAAGAGG	AGATTGCGCA	GATTGTCAGA	AAAAAGTTGG	ATAGCTCCTT	CTTCAGCTTT	1740
CTCAGTTAAT	TCTGTCCGAA	TACGACGCTC	GATAGCAGGC	AAGACCTTTT	TCTTAACGGA	1800
TTGCTGAACA	ACTTCATCAA	TATAAGCATT	TTTCACCTTG	AAACGAGTAG	CAAAGAAGGC	1860
AAGAATACGG	TCCGTCGCAT	GTTCAAAACC	GATCTTCAAG	ACACCAAGTT	TCTCCCCACG	1920
ATTGAGAGCC	AAGGTACGAT	AGCCTTG CAT	AGTTCCAAC	GTCTCTGAAA	AATCATAATA	1980
AATCTGAAAA	ACCTGCTTTT	CATCAAGACT	TTCATCCTTG	GCTTGAGAAG	TAAGTTTAGA	2040
GTGTCTCAGC	ACTTCCTGAT	AAGTCATAGA	ACGCAAGGTC	ACATCTTCCG	ATAAGGCTTC	2100
GACCAAAATA	TCAACTGCAC	CGGTCAAGGC	TTCTTGCCA	GTGCAAATC	CTTCACAGAC	2160
GAAC TTTTCA	GCTTCTTCT	CTAAGTCAAC	TATATTCTGC	AAAATCAAGC	GAGCAAGAGG	2220
AAAGAGTCCA	GCTTCACGGG	CAATGGTTGC	CTTGGTACGA	CGCTTTTCCT	TATAAGGAAG	2280
ATAGAGTTCT	TCAACGTCTG	CTAATTTTTC	GGCAACTAAG	ATAGCTTCTT	CCAATTCCTT	2340

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GGTCAACTTA CCTTGTTCTT GAATCTTAGC TAAGACAGCT TCCTTACGGT CATTGAGATT	2400
TGTCAGACTT TTATCCAAAT CAATAATAGC CTTAATCGCC ACCTCATCCA GACTACCAGT	2460
CATGTCCTTG CGATAACGCG CGATAAAGGG AATAGTCGCC CCTTCAGCTG TCAAACCTTAG	2520
AACGGTATCA ATTTGCTTTA ACGTCACTCC CAAATCCTGA GAGATTTTTT CATATTTTTT	2580
ATCCATAAAT CTATTATACC ACAAGCTAAA CGTTTCAAAT TAACTCGTAG AACATTTAAA	2640
AAATATGTAG GAAATAGATT TATATGCTAC AGCGCAATAA CTTGCACCTA AAGAGCATTG	2700
CCACCTTTTT TTAACCAAGC CATGATATCA AAAGTATTTA ATGGATCAGA CATAATAGCC	2760
AGTTCTGGAA GATGTTCCCTG ACCTGGAATA ACACATTGAC TTTTCAAATT TTTATATGGA	2820
CGATTGACTA AAATTAATTT ATTAGAATAA GGAAGATTAT CCATCTTATT TAAAATTTCT	2880
TCACTAGCTG AATCTTTATT ATCAAATTTA AAATAAAGAT TATPCCAATT TATGCGTTTT	2940
TTTCTTTTTT CCCACTTAGT TCGTGCTTCT TCAATACTAG AATAATGTAG AAAATGAATA	3000
TCTATATCTC CTAAGTGCCC CAAAGGATAA ACTTCATGAG TCCAGCTCGG TGAAATAAGT	3060
TCCTCTTCGA AAACAAGTTC TTGTTCATA TAATAACGAA AATGCTTTGT AAGTTTATAA	3120
TAATCATCAG GAAGAATAAA TAAACCAACA AAAGGTGTTC TATATTGAAA ACCAAGCTGT	3180
TTATAAATTA ATCCTCCAAC ACAATTATTA CTTATAATCG TAAAATCTAA TCTATCAAGC	3240
TCAAGAAAAG GGAAAATTC TTTCTCTGCA GCTATTAACT TATGATAAAC AATATCAGAA	3300
TCTAAATATT CACCGTCATT TTTTAACCAA GCACTAAAAT TTGCCAATTC TTGAATATAT	3360
TGTTTTTTCG CTCTTTCTAT ATCATAGTTT TCTAAGACGG CGCAATCTTT GATTCTATTT	3420
TCATAATTTT CTAATATGAT TTTGTAGGAG TCTTTTAGAG GTTTAGCATC TATAACAGGT	3480
TTATAGATAT ATGTCGGGAA ATTAATATAG GTTGCAGTTT TAGAGTGAAT ATAAAGTCTC	3540
CAAATAAGGT TGTTTATATC AAATTGATTT ATTTTTCGTA AAAGCTTACT ATTGAATAAT	3600
TTTCCAAATA ATGAGCGATA TTGTTTTCTA ATTCGATGAT CTGTATCATC CATCTTTTGT	3660
AAAACCTGAA CATTCGTAA ATTTTCTGTC AACCAATTAT CCCCCAAAA AGGATAAAAG	3720
TAAAATACTC CATCAACCAA ATCAGCAAAA TGACCAAGAA CAACATCAGA ATCGGATAAT	3780
TTTATCGCAT GATACATCTT TTCAAATGTC CAATCAAATA ATGAATCATT TGAAGATAGA	3840
AACGTAATAT AATCTCCTGT AATCATATCA GACAACTCAG CAAAAGAATT CTCATCTATA	3900
ATCTTAATAT TAAATGATAG ATTCATCTGT TGGCTAATGG AAGCTATCTC CTCTGTAGAT	3960
TGATTTACAA TAATAACTTC TATATCTTTT AATGTTTGTC TCTCCACTAT TGACAAAGAC	4020
TCTAATAAAC TATTTTTATC TCCTTGATGT AACAAAACAA CACTAATTGA GTAAGTCAGT	4080
TTGACTACCT CCCATAATTT TCTGATAATG ATTTTCTTTT TATTTAATTA TAGCACAATT	4140

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ATGATATATA TCAGGTAATA TCAAGCTATA TTATCTCTTA GCTACTCAAT TTGAAATTTT	4200
AACCTTTTCCC TTTTCCGCAA AATAATAGTA TAATAGAGGT AGAATCTAGA ATCGAGGTAC	4260
ACCTATGGCT GTCAAATTTA CAAAACGAGA CGACTTGGAC AAGATGTTTG AAGAGTTTGC	4320
TAAACTCCCT GATTTGAAAC AAGTTACTTT CCCTGATGAC AAAGAGAAAA AAGTCAAAGC	4380
AGAAAAGAAA AACTAGATGA CTGCTTTTCA ACAACTCCCA TCTAGTGTAC TTCAAACTGG	4440
AGCCATTTTT CTCTCCATTA TCATTGAAGC CCTTCCCTTC GTTCTGATAG GAAGCATTGT	4500
CTCAGGGCTG ATTGAAGTTT ATATCACACC TGACAAGGTT TATCATTTTC TCCCTCGAAA	4560
TCGTTGGGGG AGAATCTTTT TTGGGACCTT TGTCGGTATA CTTTTCCCTT CTGTGTGAATG	4620
TGGAATCGTC CCCATCATCA ATCGTTTTCT GGAAAAAAG GTTCCAAGTT ACACGGCCGT	4680
TCCTTTTCTT GTGACAGCAC CTGTTATCAA TCCCATGTGT CTTTTTGCGA CCTATTCTGC	4740
CTTTGGCAAC TCCTTCCATG TCGCCCTATT ACGAGCTCTG GGTTCCATTC TTGTGGCTGT	4800
AATAC TAGGA ATTTTCTAG GATTTTCTG GCAAGAACCG ATTCAGAAAG AAAATCGTCT	4860
GGCTTGTCAT GAGCATGATT TTTCTTACTT GAGTTCGTCA AAAAAAGTTT TTCAAGTCTT	4920
TGTGCAGGCC ATTGATGAAT TTTTGTATAC GGGGCGTTAT TTGGTATTTG GCTGCCTCTT	4980
TGCTTCTATA ATACAGGTCT ACGTTCCGAC TCGGATTCTG ACCTCTATCA GTGCGACCCC	5040
TCTTTTGTCC ATCCTGCTCT TGATGATTTT AGCCTTTCTT CTTTCGCTCT GTAGTGAGGC	5100
GGATGCCTTT ATAGGTGCTT CTCTTCTCTC GAGTTTCGGT TTGGCACCAG TTCTGGCCTT	5160
TCTCGTCATT GGTCCAATGC TGGATATCAA AAATATTCTC ATGATGAAAA ATTACTTGAA	5220
AGCACGATTT ATCAGTCACT TCATAACAAT TGTAACCTCT GTCGTCTTAG TCTATTCTCT	5280
CTTGATTGGA GTTATCCTAT GATTCGATTT TTAGTTT TAG CTGGCTATTT TGAAGTACT	5340
ATTTACCTCC ATCTGTCGGG CAAACTAAAC CAGTACATCA ACATGCACTA TTCTATCTG	5400
GCCTATATCT CCATGGTGCT TTCTTTTATC TTGGCTATCG TTCAATTGTA TATCTGGATG	5460
AAGCAAGTCA AAACCCACAG TCATCTGAAC AGCCGATTAG CCAAGATAAC GAGTATTTCT	5520
CTTCTGGCTA TTCCAATTGT CATCGGCTTA ACTTTCCCAA CTGTTAGCTT GGATTCTCAG	5580
ACTGTTTCTG CTAAAGGTTA TCATTTCCCC CTATCGGAAG GAACGGATCT AGCCATTCAG	5640
ACAAGCGAAG GGACGACAAG CCAATATTTG AAACCAGATA CCAGTTCCTTA TTTTTCAAAA	5700
TCAGCCTATG AAAAGGAAAT GCGAACGGCG GCGGATAAAT ACTTATCCCA AGATAGTATT	5760
CAGATCACTA ATGAAAATA TATGGAAGTC ATGGAGGCTA TCTACGACTA TCCAGATGAG	5820
TTTGAGGGCA AGACAATCCA GTTTACAGGC TTTGTCTATA ACGACCCAG TCATGCCAAT	5880

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AGTCAATTTC	TGTTCCGATT	CGGCATTATC	CACTGTATCG	CAGATTCTGG	TGTCTATGGA	5940
TTGCTGACCA	AGGGCAATAC	CCGGCAGTAT	GAAAACAACA	CTTGGATAAC	AGCCAAAGGA	6000
AAACTGGTCA	ATCACTACCA	TAAAGAACTC	AAACAAAACC	TTCCAACCTT	GGAAATCGAC	6060
AGCTTTACCA	AAGTCGATAA	ACCAGAAAAT	CCCTATGTAT	ATAGAGCTTT	TTAAGAAAAT	6120
CAAGATAAAA	ACGAACAAGT	TCTCTTCTGA	ATAACAGAAA	AAGAGCCTGT	TCGTTTTTTG	6180
TTATATGAAA	ATTAGTGACT	TGTAGATTTT	CATCTTATAC	CATTCCCAGC	AATACAAGTA	6240
GCTCATAGAA	AATAAGCGAG	CCACTCATTC	ATTAGACTAG	CGATTTCTTT	AGGTGCTTGA	6300
GTATAAAGCT	CATGGCCAAA	GTTTTCTAAA	AAAATAGTAT	CAAAATAGTC	TGGCAATTCT	6360
TTTAGGGCTT	CCTCTCTCCA	TGTAGCTTCA	TTAGGATAGC	GAGGACTAAT	AAACAAGGTA	6420
TCTCCCCTT	CTCTCTTAAA	AGCTTGTATT	TTTCTCCGTA	GcGGAGTATC	GCTTCTATAT	6480
TTTCATAATT	TATAGCCAAC	TCATATCTAT	TATACTCAAC	ATTCCAGTGA	TAAGACTGTC	6540
TTACAGCTTT	CTCCATATTT	TCTGACCAAT	GCTTTGCTTC	AGATTTTCT	TTAGAAGTAA	6600
GAACATCTAA	GTCCGAAACA	ATTTGAGATT	TGATATAATT	TTTAGTTTCC	TCTAACTCTG	6660
TATCCAAAGG	TAAATCTTA	TCTAAATCTA	GATAGCCACC	ATCCAAAAGA	ATCAGTTTCT	6720
TTACTTCTTC	AAATTCCGAT	GCGAAATAAC	GAGCTAAATC	TCCTCCAAGA	GAATGGCCTA	6780
TCAGACAGAT	AGATTCTTCC	TCTACAATTT	CATTTTTTAA	CCATGATTTT	AATTCTGTTT	6840
CATCTCGAAG	ATGCTTTTCA	TATGGATTTA	GAAAATAGAC	CTGCGAATCT	AGTTCTTGAA	6900
GAAAATCCTT	GCTATGATAG	GCATTGCTTC	CCAAACCGCC	AATAAAATAT	TTTTTCATTC	6960
TCTACTTAAT	ACTATGCTTA	TTCATCTTTT	GTTCAAAGAT	AGTTGTGATA	ATCTGACGCA	7020
ATTCTTCGCG	TTTTTTTTCT	GGAATCTCAC	CACTTGTTTG	AGCTACAGCG	TAGAGTTCAG	7080
GGTATTCAAT	TGAAATGCGT	TTAATCGTAC	GTGTTGTAGC	ATGTTTTCTG	ACAAAAACG	7140
GGATTGCTT	AATCAAGTCT	TGTGGGACTA	GCGCCAGAAT	CTTCTCAGTA	GTTTCTTTGT	7200
CACTAATATT	AGACATTGTA	AGCCTTTTCT	TAATCATTTT	CTGTTCTTTT	TCTGTAAAAT	7260
CTTTTAATTC	CATTGATTA	GTCCTCCTAT	TTTCTCTAAG	TTAAATTATG	TACTAATACA	7320
GATGAAACTA	CAAAGAATAA	ACTTTAAGAA	ATCTTCTCAC	TGATAAGATT	TTAGCATTAG	7380
ACTTCCTGCG	AAACAAAATA	TGGTATAGTA	GTTCTATGAA	TTATGAAGCA	AGTAAACAAC	7440
TAAGTGATGC	ACGATTTAAA	CGTCTTGTTG	GTGTTGAGCG	CACGACTTTT	GAAGAGATAT	7500
TAGCTGTATT	AAAAACAGCT	TATCAACTTA	AACACGCAAA	AGGTGGACGA	AAACCTAAAT	7560
TAAGCCTAGA	AGACCTTCTT	ATGGCCACTC	TTCAATATGT	GCGAGAATAC	CGCACTTATG	7620
AAGAAATTGC	GGCTGATTTT	GGTATTCACG	AAAGCAACTT	AATCCGTCGG	AGCCAATGGG	7680

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TTTAAGTAAC TCTTGTTC	AGTGGTGTTA CGATTTCAAG	AACTCCTCTC AGTTCTGAGG	7740
ACACGGTAAT GATTGATAGC	CATTCCCATC AATATCGTAT	CTTTGGACAT AGCCAATAAA	7800
TGTTTCATTT TTGCGTGGTT	TCTGGCTATT AACGATTGAA	ATAACCCACC AACTTATCAA	7860
AAATAGAAAT AAAAATCCTA	AGATTACTGT CATATCATAA	CACTATTAAA GTTTAACCCA	7920
CTTATCATTA TCCATGATAA	AAGGCTTAGC CAGTCCCTCG	CCTGTATAAT CCGCATACTT	7980
GGTGCCCAA TACTTGTAGC	AATCTTCCTT ACTAGCAAAT	TTAATCGCTT GGTAGGGCTC	8040
TTCGAAAGTC AATTTCTCTA	CAAATAAGAA ACCGTCATCA	GCAGGTACTA AGACCCCAAC	8100
GTGGCCTACA AACAGATACT	CGCCATCCAA ATTGTCGTGC	AAGACTACAG ACAGCATTCG	8160
AGCTTTTTC	TTGAATTGAA ATTGTGAGAA	GAATGCTTCC ATCTTTTCAG	CGTGAACCTT 8220
GACATCTGTA GTTGACTCAG	TTGGAAGTCT CGAAAATAGA	ATATCAAACCT CTTCTTATC	8280
TTGTGAATCA AAGACCTTTC	CTTTATCAAT CGCATCATTA	TCTAGGAAAA GCAACTGGTC	8340
ATTCTTTTCA AGCTTTGGAA	TGGTGACTGA ATTTTTCAAA	AGACAATAAC TATTGATACG	8400
GCAGTTGGTC CCAACAAAAT	CGCCCTTCTT TTGATTCCAG	AGATGACTGA TTTTCTCAAC	8460
ATCGTATTCG GTGTGAGTAA	AGGAAGTGAA ATCTCCTGAT	AAGCCAGTTG AGCCGACAAT	8520
GGTATTATAG TCATTAACGA	GATTAATAAA TGCATCAACA	CTATTGGGAT CCAAGTGAGC	8580
TGATAAGAGA GATTTGACCT	CTTCTGTACT TACCTGGTTG	TTTAGGTTGG TGTATGAAGC	8640
TTTCCATGGA ACTTTCGCTG	AACTGCTTTG CCTTTGATTC	GTCCCCTCAG AAGTAGCATG	8700
TTGTGTGTTA CAAGCAGCCA	AGCCTAAAAA CAAGGCTGAA	CAGATTCCTA ATGTGGCTAA	8760
TTTTCTTGAT TTCTTCATTT	CTTTCTCCTA AATGTCTTGG	ATTAAAGTTT CTTTAACTAT	8820
TGCTTTACAG ATATTGATTA	CTTTCTCATT TAATGTGTTT	ATCGTCTTTC CTCCGG	8876

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14736 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

CGCAAACCTTT CGCGGTCGGA	AGGTAGTTTT ATGACACGAT	TTGAGATACG AGATGATTTT	60
TATCTCGATG GAAAATCATT	TAAGATTTTA TCTGGTGCCA	TTCATTATTT TAGGGTTCCT	120
CCAGAGGATT GGTATCATTC	GCTCTATAAC TTGAAGGCTC	TTGGTTTAA TACGGTAGAG	180

1086						
ACTTATGTTG	CTTGGAATTT	ACACGAGCCT	TGTGAAGGTG	AGTTTCATTT	TGAAGGTGAT	240
CTGGATTTAG	AGAAATTTCT	CCAAATAGCG	CAGGATTTGG	GTCTCTACGC	AATTGTGCGT	300
CCGTCTCCAT	TTATCTGTGC	GGAATGGGAA	TTCGGTGGCT	TACCAGCTTG	GCTCTTGACC	360
AAGAACATGC	GAATTCGCTC	ATCCGACCCA	GCATATATCG	AGGCAGTTGG	TCGCTACTAT	420
GATCAGTTAT	TGCCAAGACT	GGTGCCTCGT	TTGTTGGACA	ATGGTGGCAA	TATTCTCATG	480
ATGCAGGTTG	AAAATGAGTA	TGGTTC TTAC	GGAGAAGATA	AGGCTTACCT	GAGAGCGATT	540
CGACAGCTAA	TGGAAGAGTG	TGGCGTAACC	TGTCCCTCT	TTACATCAGA	TGGTCCATGG	600
CGAGCTACTC	TGAAAGCTGG	AACCTTAATT	GAAGAGGACC	TCTTTGTAAC	AGGAACTTT	660
GGTTCTAAGG	CACCTTACAA	CTTTTCGCAG	ATGCAGGAAT	TCTTTGATGA	ACATGGTAAG	720
AAATGGCCAC	TCATGTGTAT	GGAGTTCTGG	GATGGTTGGT	TCAATCGCTG	GAAAGAACCG	780
ATTATCACAC	GGGATCCTAA	GGAATTGGCA	GATGCAGTTC	GAGAGGTTTT	GGAACAAGGC	840
TCTATCAATC	TTTACATGTT	CCACGGTGGT	ACAACTTTG	GTTTCATGAA	TGGTTGCTCA	900
GCTCGAGGAA	CTTTGGACCT	GCCACAAGTT	ACGTCTTATG	ATTACGATGC	CCTTCTGGAT	960
GAAGAAGGAA	ATCCAACTGC	TAAATATCTT	GCAGTCAAGA	AGATGATGGC	AACACATTTT	1020
TCAGAGTATC	CGCAGTTGGA	ACCACTCTAC	AAAGAGAGTA	TGGAGTTGGA	TGCTATTCCA	1080
CTAGTTGAAA	AAGTTTCTTT	GTTTGAAACC	TTAGATAGCT	TGTCAAGTCC	TGTAGAAAGT	1140
CTCTATCCTC	AAAAGATGGA	GGAGCTGGGA	CAAAGTTATG	GCTACCTACT	TTATCGAACA	1200
GAAACAACT	GGGATGCAGA	AGAAGAAAGA	CTTCGTATCA	TTGATGGTCG	AGATAGGGCC	1260
CAGCTGTATG	TCGATGGTCA	GTGGGTTAAA	ACTCAATATC	AGACAGAGAT	TGGGGAAGAT	1320
ATTTTTTATC	AAGGTAAAAA	GAAAGGGCTA	TCTAGGTTAG	ATATCTTGAT	AGAAAATATG	1380
GGGCGTGTCA	ACTATGGGCA	TAAGTTCTTA	GCGGATACGC	AACGTAAGGG	AATTCGGACA	1440
GGGGTCTGTA	AGGATCTGCA	TTTCTTACTA	AACTGGAAAC	ACTATCCACT	CCCACTAGAC	1500
AATCCTGAGA	AAATTGATTT	TTCAAAAGGA	TGGACTCAAG	GACAACCAGC	CTTTTACGCT	1560
TATGACTTTA	CAGTCGAAGA	GCCAAAAGAT	ACTTACCTAG	ACTTGTCTGA	GTTTGGTAAG	1620
GGGGTTGCCT	TTGTCAATGG	GCAGAATCTA	GGACGTTTTT	GGAACGTTGG	CCCAACTCTC	1680
TCACTTTATA	TCCCTCATAG	CTATCTCAAG	GAAGGTGCCA	ACCGCATCAT	TATCTTTGAA	1740
ACAGAAGGTC	AATATAAAGA	AGAGATTCAT	TTAACTCGTA	AACCTACACT	AAAACATATA	1800
AAGGGGGAAA	ACTTATGACA	ATTGTAGGAT	GCCGTATTGA	TGGACGTTTG	ATCCACGGAC	1860
AAGTAGCCAA	TCTTTGGGCT	GGAAAACATA	ATGTTTCACG	CATTATGGTT	GTAGACGACG	1920
AAGTTGTCAA	CAACGATATT	GAAAAGAGTG	GTTTGAAACT	TGCGACACCA	CCAGGTGTGA	1980

1087

AATTGAGTAT TTTGCCAGTT GAGAAAGCTG CAGCCAATAT TCTTGGTGGC AAATACGATA	2040
GCCAACGTCT CTTTATCGTG GCTCGTAAAC CAGACCGCTT CCTTGGTTTG GTAGAAGCAG	2100
GTGTACCACT TGAAACCCTT AATGTTGGGA ATATGTCTCA AACACCAGAA ACTCGTTCTA	2160
TTACACGTTC TATCAACGTA GTAGACAAGG ATGTGGAAGA CTTCCACAAA CTGGCAGAAA	2220
AAGGTGTTAA ACTTACTGCT CAGATGGTTC CAAATGATCC AATTTTCAGAC TTTTGTAGCT	2280
TATTAATAATA GGAAAAAAT TTTTAGGAGG TCATTGTTAT GATACAATGG TGGCAAATTT	2340
TACTTCTCAC TTTGTACTCA GCTTATCAA TCTGTGATGA GTTGACGATC GTTTCATCTG	2400
CAGGTTCCTCC TGTATTTGCT GGTTCATTA CTGGTTTAAT CATGGGAGAT GTGACTACTG	2460
GTTTACTTAT CGGTGGTAAC TTGCAACTGT TCGTTCCTTG GGTGGTACC TTCGGTGGTG	2520
CTTCTCGTAT CGACGCAACT TCTGGTGC GG TCTTGCAC ACCTTCTCTG TTTCACAAGG	2580
AATTGATGCA CCGCTTGCCA TTACTACAAT CGCTGTACCA GTAGCAGCTC TCTTGACTTA	2640
CTTCGACGTT CTTGGTCGTA TGACTACTAC CTTCTTCGCT CACCGTGTGG ATGCTGCAAT	2700
CGAACGCTTT GACTATAAAG GTATTGAACG CAACTACTTG CTTGGTGC GA TTCCGTGGGC	2760
TCTATCTCGT GCCCTTCCAG TCTTCTTTGC CCTTGCTTTT GGTGGTGCCT TTGTACAATC	2820
AGTAGTAGAC TTCGTTGAAG CCTACAAATG GGTGTCAGAT GGCTTGACAC TTGCAGGACG	2880
TATGCTTCCA GGTCTTGGAT TTGCAATCTT GCTTCGTAC CTTCCAGTTA AACGTAACCT	2940
TCACTACCTT GCTATGGGAT TTGGTTTGAC AGCTATGTTG ACTGTTCTTT ACTCATATGT	3000
AACAGGTCTT GGTGGCGCTG TTGCTGGTAT CGTAGGTACT CTTCTTGCTG AAGTTGCTGA	3060
AAAAATTGGT TTCGTGAACA ACTTCAAAGG TTGTCTATG ATTGGTATTT CTATCGTAGG	3120
TATTTTCCTT GCAGTGCTTC ACTTCAAAAA TAGCCAAAAA GTAGCTGTAG CAGCACCTTC	3180
TACACCATCA GAAAGTGGGG AAATCGAAGA TGACGAATTC TAATTACAAA CTTACAAAAG	3240
AAGATTTTAA TCAAATCAAC AAACGTAGCT TGTTTACTTT CCAATTAGGT TGGAACACG	3300
AACGTATGCA AGCTTCTGGT TACCTTTACA TGATCTTGCC TCAGTTGCGT AAAATGTATG	3360
GTGATGGAAC TCCTGAATTG AAAGAAATGA TGAAAGTTCA TACTCAATTC TTCAATACTT	3420
CACCATTCTT CCATACCATT ATCGCTGGTT TTGACCTTGC CATGGAAGAA AAAGATGGTG	3480
TAGGTTCAAA AGACGCCGTT AACGGTATCA AGACAGGTTT GATGGGACCA TTCGCTCCTC	3540
TTGGGGATAC AATCTTTGGT TCACTTGTAC CTGCTATCAT GGGGTCAGTC GCAGCAACTA	3600
TGGCTATCGC TGGCCAACCT TGGGGGATCT TCCTTTGGAT TGCAGTTGCA GTAGCGTATG	3660
ACATCTTCCG TTGGAAACAG TTGGAATTTG CTTACAAAGA AGGGGTTAAC CTTATCAACA	3720

1088

ACATGCAAAG	TACCTTGACA	GCTTTGATTG	ACGCTGCATC	TGTACTTGGT	GTCTTCATGA	3780
TGGGTGCTCT	TGTAGCAACA	GTGATTAAC	TTGAAATTC	TTACAAGTTG	CCAATCGGTG	3840
AAAAGATGAT	TGATTTCCAA	GACATCTTGA	ACCAAATCTT	CCCACGTTTG	CTTCCAGCAA	3900
TCTTTACTGC	CTTTATCTTC	TGGTTGCTTG	GTAAGAAAGG	TATGAACTCT	ACTAAAGCTA	3960
TCGGTATTAT	TATCGTACTT	GCTTTGGCTC	TTTCTGCCCT	TGGTCACTTT	GCACTTGGA	4020
TGTAATTCCT	TATGACTAAA	TCATTAATTT	TGGTGAGCCA	TGGTCGCTTC	TGTGAGGAGC	4080
TTAGAGGTAG	CACAGAAATG	ATTATGGGCC	CACAAGACAA	CATTTACACA	GTAGCTCTTC	4140
TTCCAGAAGA	TGGCCCAGAA	GAATTTACTG	CTAAATTTGA	AGCTGTTATT	GAAGGATTGG	4200
ATGATTTCCCT	AGTCTTTGCG	GATCTTCTCG	GTGGGACACC	TTGTAATGTG	GTGAGTCGCT	4260
TGATCATGGA	AGGTCGTGAT	ATTGACCTTT	ACGCAGGGAT	GAATCTTCCA	ATGGTGATTG	4320
AATTTATCAA	TGCGAGCCTT	ACAGGCGCAG	ATGCGGACTA	CAAGAGCCGT	GCTGCAGAAA	4380
GCATTGTGAA	AGTTAATGAC	CTGTTAGCGG	GCTTCGATGA	TGACGAAGAT	GAATAATACT	4440
CTTCGAAAAT	CTCTTCAAAC	TACGTCAACG	TCGCCCTTGCC	GTAGgTATAT	GTTACTGACT	4500
TCGTCAGTCT	TATCCGGCAA	CCTCAAAACG	GTGTTTGTAG	CTGACTTCGT	CAGTCTTATC	4560
CGGCAACCTC	AAAGCAGTGC	TTTGAGCAGC	CTGCGGCTAG	TTTCCTACAG	ATTTTAGTTG	4620
GAACTCGATT	CAATTCATGT	GACAACGTGA	AAATCGTTAG	AGCATTTTAT	ATAGAATATA	4680
CATGGGAATG	TAGCTTACTC	CCATTCCCAT	ATTTAATAGA	AAAAGAGGAA	CTCAATGCTA	4740
CATTATACAA	AAGAAGACTT	GCTCGAATTG	GGTGCAGAAA	TCCTACGCG	TGAAATCTAC	4800
CAACAGCCTG	ATGTATGGAG	AGAAGCTTTT	GAATTTTATC	AAGCAAAACG	TGAAGAAATT	4860
GCAGCCTTCC	TACAAGAAAT	CGCTGATAAA	CATGACTATA	TTAAGGTTAT	CTTGACAGGT	4920
GCTGGGACTT	CTGCTTATGT	GGGAGATACC	TTGCTACCTT	ATTTTAAGGA	AGTCTATGAC	4980
GAACGCAAAT	GGAATTTCAA	TGCTATTGCG	ACAACAGATA	TCGTTGCCAA	TCCAGCAACC	5040
TATTTGAAAA	AAGATGTGGC	AACTGTCCCT	GTGTCTTTTG	CTCGTAGTGG	GAATTCGCCCT	5100
GAAAGTTTGG	CGACTGTGTA	TTTGGCCAAA	TCCTTGGTGG	ATGAGCTTTA	TCAAGTGACG	5160
ATTACTTGTG	CAGCAGATGG	TAAATTGGCT	CTTCAAGCTC	ACGGTGATGA	TCGTAATCTC	5220
TTGCTCTTGC	AACCAGCTGT	CTCTAATGAT	GCTGGATTTG	CCATGACTTC	TAGCTTTACG	5280
TCTATGATGT	TGACAACTCT	CTTGGTCTTT	GATCCTACAG	AATTTGCTGT	TAAGTCTGAA	5340
CGTTTGAAG	TTGTATCTAG	TCTTGCCCGT	AAAGTTTTAG	ACAAGGCAGA	AGATGTCAAA	5400
GAGCTCGTTG	ATTTAGACTT	TAACCGTGTG	ATCTATCTAG	GCGCTGGTCC	TTTCTTTGGA	5460
CTTGCTCATG	AAGCTCAGCT	CAAGATTTTG	GAATTAAC	CTGGTCAAGT	TGCGACCATG	5520

1089

TATGAAAGCC CAGTTGGCTT CCGTCACGGT CCAAAATCTC TTATCAACGA CAATACAGTT	5580
GTTTTGGTCT TTGGTACAAC GACAGACTAC ACTCGTAAGT ACGACTTGGA CTTGGTTCGT	5640
GAAGTTGCTG GTGACCAGAT TGCTCGTCGT GTTGTGCTTT TGAGTGATCA AGCTTTTGGT	5700
CTTGAAAATG TCAAAGAAGT GGCCCTTGGT TGTGGCGGTG TCTTGAATGA TATTTACCGT	5760
GTCTTCCCTT ACATCGTTTA TGCCCAACTC TTTGCTTTAT TGACTTCACT CAAGGTAGAA	5820
AATAAACCAG ATACACCGTC TCCTACAGGT ACAGTAAACC GTGTAGTACA AGGTGTCATA	5880
ATTCACGAAT ATCAAAAGTA AGACAGTGTT TATGAATTCT TGACAAGAGG ATTTGTAAAT	5940
TATCAGATAA ACCATAGATT GTCAGTACGC TTTCTATGGT TTGTTTGCTT GAGAGAAATA	6000
GTAAAAGGAG AACAGAATGA AAGCATACAC AGAGCGTGTA TTTGGAAATG TTGAGGGTGA	6060
GGATGTCTTG GCCTATCGAT TTGAGACAGA CGGTGGCTAC CAACTTGAGG TTATGACTTA	6120
TGGTGCGACT ATCTTGCGCT ATGTCGCACC TGACAAGGCT GGAAATTTTG CCAATGTTAT	6180
CTTGGGATTT GATGACTTTG ATAGTTATGT AGGCAATAGT CCCAAGCATG GAGCAAGTGT	6240
AGGTCCTGTA GCGGGTCGTA TTGCAGGTGC GACCTTTGAG CTCAATGGTA AGACCTATGA	6300
CCTTGAGGTT AATAATGCTA GCAACTGTAA TCACAGTGGT TCAACTGGTT GGGATTCCAG	6360
CTTGTTTGAA GTTGAAGAAG TAAGCGATCA TGGCTTGACT CTCTACACAG AGCGTACAGA	6420
TGGGACAGGA GGGTTCCCTG GAAATCTCAA GATTGGATC AGTTATCACT TGAAGAAAC	6480
TGGTGCCTAT GAAATCAGCT ACAAGGTAAC GACCGATCAG GATACGCTGG TCAATCCAAC	6540
CAACCACAGC TATTTCAACT TGTCTGGTGA TTTCACGCAG ACGATTGACC GTCATGTCTT	6600
CCAATAAAC ACAGAGGGCA TTTACTCAAT CGCTCCTGAC GGTGTTCCCTG CCAAACTCC	6660
AGAAGCCAAC CGTGATGTGG TCAAACACGT CTACAATGGT ACCTTGTTGA AGGATATCTT	6720
TGCAGAAGAA GATGAGCAAA TCCAGCTGGC ATCAGGTTTG GATCATCCAT TTGCCCTTCC	6780
TGCAGGCCAT GACAATGCTG GATTCCTTTA TGACCAAAAT TCAGGTCGCT TCCTGCTTTT	6840
CAAGACAGAA GCTCCTTGCT TTGTGGTCTA CACAGCAAAC TTTGTGGATG AAAGTGCAT	6900
CATAGGAGGT CAGCCAATGC TACAGCACAA TGGGATTGCT CTTGAAGCGC AAGCTTTACC	6960
AGATGCCATT CACAGTGACC TTAAAGGCCA AGTCATTCTT AAAGCTGGTC AAACCTTCAC	7020
CAGTAAGACA CGTTATGAAC TTGTTGTGAA GTAAAAGAGT CATTGCGCCT ACTTTTGGGA	7080
GCTAGGAATA GGTACGCAGA GACAAATAGT AGGAAAATAT GATATAACTA AGCGTTGAAA	7140
GCTATCTGTT AATATAATAT TCAAACCTACA ATAAGGAGTA AGAAAGAAAC GAAGAAAATT	7200
GTATTTGCTA GTGCCTTGGC TTTGACCTTG GCTGGAGCAG TTTTGACAAA TGATGTTTTT	7260

1090

GCGAACGACA GACTTGTGGC AACACAAACT ACTGATGGTA AAAATGAAAA TGTATTGACC	7320
TCAGAGGTGC TAAAACCTTC TAGTGGCAAT GTTTTGGTTG GAATCAAAGG AGAATTTGTG	7380
GCTCCTCATC AACAACTAT TTTGGATGCC ATCAATGCTA TCTGTAAAGA AGCGGCTGAC	7440
GAAGGTTTGG TAGATAAGTA TGTCCCTATC AAATGATCAA CTGACCTAGA AAAGGCAGCT	7500
TTTGCCAGAG CTACAGAAGC ATCTATAACC ATGGATCATA CCCGTCTTTC TAGCAAAGAT	7560
CTTTGGAGTG CCTTTCCAAC TTCTAATAGT ATAATGGGAG AAAATTTGGC ATGGAATCAT	7620
GACGGTTTTC TAAAAGCTAT TGAACAATGG CGTGCTGAAA AAGCAGATTA TGTGGAGAAA	7680
AAAATAGTGG TTCAGACAAC GGGAAATCTG GTCACATATGA GTCGCTAATT AACCCATAAT	7740
TTACACACAT GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA	7800
TTGCTCAAAC TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG	7860
CTGTTCAAGT TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAAACT AAAGCTACGG	7920
TTGTAGAAAA ACCACTGAAA GATTTTAGAG CGTCTACGTC TGATCAGTCT GGTGGGTGG	7980
AATCTAATGG TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA	8040
CAGATGGTAA ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTGTAAAAAT	8100
TTTCTGGTAG CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTTACAGGC TGGGGAACAG	8160
ATGGTAGCAG ATGGTCTTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG	8220
AAAATGGCAC TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG	8280
TCCGACCACA CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC	8340
CAGATGGTTA CCGTGTAAT GGTAATGGTG AATGGGTAAA CTAGGCTCAG GCCATAGGTA	8400
AAGCATTCAT CTTACTTAGC AAAAAGAATG AACGATAAGA AAGAGGTTGA TGGCGAACAT	8460
TGGCCTCTTT TGATTTATAA AGATTGGATT CTGTGCGCCT CAATTCAGA CTTTCTATT	8520
GTAAGCTAAT ATTTTATAGC CCATTAAAAG CATAAGCGGT AATCTAATTT AAAAAATGCT	8580
GTAATTAGTC TGAAGTCCAC ACTTACTTGT TGAGATGTTA TCTCTGTTT TTATCGTTA	8640
AATTTACTGT ATTTTATATA GTATGCAGAA TATTTTAAAG TATATTTCAA TAGAAATTTC	8700
TATCGATTTA TTGTATAATG ATAAGTAATT GTTGAAAAGT ACTCAGAAAA TTCCATACTA	8760
TATTATTTTT ATGTTTATAC TTTTATGCTA TAAAATATAG ATTGATATAA AGAATATAGA	8820
AAAAGCGAGG TTAATATGAG CCGAAAAAGC ATTGGTGAGA AACGCCATAG TTTCTCGATG	8880
AGAAAGTTGT CAGTGGGATT GGTATCAGTT ACTGTATCTA GTTTCTTTTT GATGAGTCAA	8940
GGGATTCAAT CCGTATCGGC CGATAATATG GAAAGTCCAA TTCATTATAA GTATATGACC	9000
GAGGGTAAAT TGACAGACGA GGAAAAATCC TTGCTGGTAG AGGCCCTTCC ACAACTGGCT	9060

1091

GAAGAATCAG ATGATACTTA TTACTTGGTT TATAGATCTC AACAGTTTTT ACCGAATACA	9120
GGTTTTAACC CAACTGTTGG TACTTTCCTT TTTACTGCAG GATTGAGCTT GTTAGTTTTA	9180
TTGGTTTCTA AAAGGGAAAA TGGAAAGAAA CGACTTGTC ATTTTCTGCT GTTGACTAGC	9240
ATGGGAGTTC AATTGTTGCC GGCCAGTGCT TTTGGGTGA CCAGCCAGAT TTTATCTGCC	9300
TATAATAGTC AGCTTCTAT CGGAGTCGGG GAACATTAC CAGAGCCTCT GAAAATCGAA	9360
GGTTATCAAT ATATTGGTTA TATCAAACT AAGAAACAGG ATAATACAGA GCTTCAAGG	9420
ACAGTTGATG GGAATACTC TGCTCAAAGA GATAGTCAAC CAACTCTAC AAAACATCA	9480
GATGTAGTTC ATTCAGCTGA TTTAGAATGG AACCAAGGAC AGGGGAAGGT TAGTTTACAA	9540
GGTGAAGCAT CAGGGGATGA TGGACTTCA GAAAAATCTT CTATAGCAGC AGACAATCTA	9600
TCTTCTAATG ATTCATTCGC AAGTCAAGTT GAGCAGAATC CGGATCACAA AGGAGAATCT	9660
GTAGTTCGAC CAACAGTGCC AGAACAAGGA AATCCTGTGT CTGCTACAAC GGTGCAGAGT	9720
GCGGAAGAGG AAGTATTGGC GACGACAAAT GATCGACCAG AGTATAAACT TCCATTGGAA	9780
ACCAAGGCA CGCAAGAACC CGGTCATGAG GGTGAAGCCG CAGTCCGTGA AGACTTACCA	9840
GTCTACACTA AGCCACTAGA AACCAAGGT ACACAAGGAC CCGGACATGA AGGTGAAGCT	9900
GCAGTTCGCG AGGAAGAACC AGCTTACACA GAACCGTTAG CAACGAAAGG CACGCAAGAG	9960
CCAGGTCATG AGGGCAAAGC TACAGTCCGC GAAGAGACTC TAGAGTACAC GGAACCGTA	10020
GCGACAAAAG GCACACAAGA ACCCGAACAT GAGGGCGAAG cGGCAGTAGA AGAAGAACTT	10080
CCGGCTTTAG AGGTCACTAC ACGAAATAGA ACGGAAATCC AGAATATTCC TTATACAACA	10140
GAAGAAATTC AGGATCCAAC ACTTCTGAAA AATCGTCGTA AGATTGAACG ACAAGGGCAA	10200
GCAGGGACAC GTACAATTCA ATATGAAGAC TACATCGTAA ATGGTAATGT CGTAGAACT	10260
AAAGAAGTGT CACGAACTGA AGTAGCTCCG GTCAACGAAG TCGTTAAAGT AGGAACACTT	10320
GTGAAAGTTA AACCTACAGT AGAAATTACA AACTTAACAA AAGTTGAGAA CAAAAATCT	10380
ATAACTGTAA GTTATAACTT AATAGACACT ACCTCAGCAT ATGTTTCTGC AAAACGCAA	10440
GTTTTCCATG GAGACAAGCT AGTTAAAGAG GTGGATATAG AAAATCCTGC CAAAGAGCAA	10500
GTAATATCAG GTTTAGATTA CTACACACCG TATACAGTTA AAACACACCT AACTTATAAT	10560
TTGGGTGAAA ATAATGAGGA AAATACTGAA ACATCAACTC AAGATTCCA ATTAGAGTAT	10620
AAGAAAATAG AGATTAAAGA TATTGATTCA GTAGAATTAT ACGGTAAAGA AAATGATCGT	10680
TATCGTAGAT ATTTAAGTCT AAGTGAAGCG CCGACTGATA CGGCTAAATA CTTTGTAATA	10740
GTGAAATCAG ATCGCTTCAA AGAAATGTAC CTACCTGTAA AATCTATTAC AGAAAATACG	10800

1092

GATGGAACGT	ATAAAGTGAC	GGTAGCCGTT	GATCAACTTG	TCGAAGAAGG	TACAGACGGT	10860
TACAAAGATG	ATTACACATT	TACTGTAGCT	AAATCTAAAG	CAGAGCAACC	AGGAGTTTAC	10920
ACATCCTTTA	AACAGCTGGT	AACAGCCATG	CAAAGCAATC	TGTCTGGTGT	CTATACATTG	10980
GCTTCAGATA	TGACCCGAGA	TGAGGTGAGC	TTAGGCGATA	AGCAGACAAG	TTATCTCACA	11040
GGTGCATTTA	CAGGGAGCTT	GATCGGTTCT	GATGGAACAA	AATCGTATGC	CATTTATGAT	11100
TTGAAGAAAC	CATTATTTGA	TACATTAAAT	GGTGCTACAG	TTAGAGATTT	GGATATTAAA	11160
ACTGTTTCTG	CTGATAGTAA	AGAAAAATGTC	GCAGCGCTGG	CGAAGGCAGC	GAATAGCGCG	11220
AATATTAATA	ATGTTGCAGT	AGAAGGAAAA	ATCTCAGGTG	CGAAATCTGT	TGCGGGATTA	11280
GTAGCGAGCG	CAACAAATAC	AGTGATAGAA	AACAGCTCGT	TTACAGGGAA	ACTTATCGCA	11340
AATCACCAGG	ACAGTAATAA	AAATGATACT	GGAGGAATAG	TAGGTAATAT	AACAGGAAAT	11400
AGTTCGAGAG	TTAATAAAGT	TAGGGTAGAT	GCCTTAATCT	CTACTAATGC	ACGCAATAAT	11460
AACCAAACAG	CTGGAGGGAT	AGTAGGTAGA	TTAGAAAATG	GTGCATTGAT	ATCTAATTCTG	11520
GTTGCTACTG	GAGAAATACG	AAATGGTCAA	GGATATTCTA	GAGTCGGAGG	AATAGTAGGA	11580
TCTACGTGGC	AAAACGGTCG	AGTAAATAAT	GTTGTGAGTA	ACGTAGATGT	TGGAGATGGT	11640
TATGTTATCA	CCGGTGATCA	ATACGCAGCA	GCAGATGTGA	AAAATGCAAG	TACATCAGTT	11700
GATAATAGAA	AAGCAGACAG	ATTTCGTACA	AAATTATCAA	AAGACCAAAT	AGACGCGAAA	11760
GTTGCTGATT	ATGGAATCAC	AGTAACTCTT	GATGATACTG	GGCAAGATTT	AAAACGTAAT	11820
CTAAGAGAAG	TTGATTATAC	AAGACTAAAT	AAAGCAGAAG	CTGAAAGAAA	AGTAGCTTAT	11880
AGCAACATAG	AAAAACTGAT	GCCATTCTAC	AATAAAGACC	TAGTAGTTCA	CTATGGTAAC	11940
AAAGTAGCGA	CAACAGATAA	ACTTTACACT	ACAGAATTGT	TAGATGTTGT	GCCGATGAAA	12000
GATGATGAAG	TAGTAACGGA	TATTAATAAT	AAGAAAAATT	CAATAAATAA	AGTTATGTTA	12060
CATTTCAAAG	ATAATACAGT	AGAATACCTA	GATGTAACAT	TCAAAGAAAA	CTTCATAAAC	12120
AGTCAAGTAA	TCGAATACAA	TGTTACAGGA	AAAGAATATA	TATTCACACC	AGAAGCATTT	12180
GTTTCAGACT	ATACAGCGAT	AACGAATAAC	GTACTAAGCG	ACTTGCAAAA	TGTAACACTT	12240
AACTCAGAAG	CTACTAAAAA	AGTACTAGGA	GCAGCGAATG	ATGCAGCCTT	AGATAACCTA	12300
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TTAGCGATGG	ATAAATCAAT	CAATACTACA	GGAGACGGTG	TAGTTGAATA	CGTAAGTGAG	12420
AAAAATCAAAA	ATAACAAAGA	AGCATTTATG	CTAGGTCTTA	CTTATATGAA	CCGTTGGTAC	12480
GATATTAATT	ATGGTAAAAAT	GAATACAAAA	GATTTATCTA	CGTACAAGTT	TGACTTTAAC	12540
GGAAATAATG	AGACTTCAAC	GTTGGATACT	ATTGTCGCAT	TAGGAAATAG	TGGACTAGAT	12600

1093

AACCTGAGAG	CTTCAAATAC	TGTAGGTTTA	TATGCGAATA	AACTTGCATC	GGTAAAAGGA	12660
GAAGATTCAG	TCTTTGACTT	CGTAGAAGCG	TATAGAAAAC	TGTTCTTACC	AAACAAAACA	12720
AATAACGAGT	GGTTTAAAGA	AAATACAAAG	GCATATATAG	TCGAAATGAA	GTCTGATATT	12780
GCAGAAGTAC	GAGAAAAACA	AGAATCACCA	ACAGCCGATA	GAAAATATTC	ATTAGGAGTT	12840
TACGATAGAA	TATCAGCACC	AAGTTGGGGG	CATAAGAGTA	TGTTATTACC	ACTACTAACT	12900
TTACCTGAAG	AATCTGTGTA	TATTTTCATCG	AATATGTCTA	CACTTGCATT	CGGTTCTGAT	12960
GAAAGATATC	GTGATAGTGT	GGATGGAGTT	ATTCTTTTCTAG	GAGATGCCTT	ACGAACTTAT	13020
GTAAGAAATA	GAGTTGATAT	AGCAGCGAAA	AGGCATAGAG	ACCATTATGA	TATTTGGTAC	13080
AATCTTCTTG	ACAGTGCTTC	AAAAGAAAAA	CTTTTCCGTT	CTGTGATAGT	TTATGATGGA	13140
TTCAATGTAA	AAGATGAGAC	AGGAAGAACT	TATTGGGCAA	GGTTAACGGA	TAAAAACATC	13200
GGCTCTATTA	AAGAATTCTT	CGGACCTGTT	GGGAAATGGT	ATGAGTATAA	TAGTAGTGCA	13260
GGAGCGTATG	CGyAtGGAAG	TTTAACGCAC	TTTGTGTTAG	ATAGATTATT	AGATGCTTAT	13320
GGAACGTCGG	TTTATACTCA	TGAAATGGTT	CATAATTCGT	ATTCTGCAAT	CTACTTTGAA	13380
GGAAATGGTA	GACGTGAAGG	ATTGGGAGCG	GAGTTATACG	CACTTGCTTT	ACTGCAATCT	13440
GTAGATAGTG	TAAATTCTCA	TATTTTAGCT	TAAATACGT	TATATAAAGC	AGAAAAAGAT	13500
GATTTGAATA	GATTGCATAC	ATATAATCCG	GTGGAACGTT	TCGATTCGGA	TGAGGCGCTT	13560
CAAAGTTATA	TGCATGGATC	ATATGATGTA	ATGTATACAC	TTGATGCGAT	GGAAGCAAAA	13620
GCGATATTAG	CTCAAAATAA	TGATGTTAAG	AAAAAATGGT	TTAGAAAAAT	AGAAAAATTAT	13680
TACGTTCTGTG	ATACTAGACA	TAATAAAGAT	ACACATGCAG	GAAATAAAGT	CCGTCCATTA	13740
ACAGATGAAG	AAGTAGCTAA	CTTAACATCG	TTAAACTCAT	TAATCGACAA	CGACATCATA	13800
AATAGACGTA	GCTATGATGA	TAGTAGAGAA	TATAAACGAA	ATGGCTACTA	TACTATAAGT	13860
ATGTTCTCTC	CTGTATACGC	AGCGCTAAGC	AATTCGAAAG	GTGCTCCTGG	AGATATTATG	13920
TTTAGAAAAA	TAGCTTATGA	ATTACTTGCG	GAAAAAGGTT	ATCACAAAGG	ATTCCCTACCT	13980
TATGTTTCTA	ATCAGTACGG	AGCAGAAGCA	TTTGCCAGCG	GAAGCAAAAC	ATTCTCATCA	14040
TGGCATGGAA	GAGATGTTGC	TTTAGTGACA	GATGATTTAG	TATTTAAGAA	AGTATTCAAT	14100
GGTGAGTACT	CATCATGGGC	TGATTTCAAA	AAAGCAATGT	TTAAACAACG	TATAGATAAA	14160
CAAGATAATC	TGAAACCAAT	AACAATTCAA	TACGAATTAG	GTAATCCTAA	TAGTACAAAA	14220
GAAGTAACTA	TAACAACGGC	TGCACAAATG	CAACAATTAA	TTAATGAAGC	GGCTGCGAAA	14280
GATATTACTA	ATATAGATCG	TGCAACGAGT	CATACCCAG	CAAGTTGGGT	GCATTTATTA	14340

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AAACAAAAA TCTATAATGC ATATCTTCGC ACTACAGATG ACTTTAGAAA TTCTATATAT	14400
AAATAAGATT GTAGAGTTTC ATTGTTGAGT AGTGTTCCTT GTAAGGATGA GGAGTCAGAT	14460
GACAAATCGA CTCCTTTTTC TTATGGATCG ATGTAGAGAT TTGATTGAAT GCAGATTGCA	14520
GGAATCATCT TCAACTCATC AACGACCAAT GGTGACAAGG TGGATTTCAA TCCCACAGAA	14580
AATGTTGATT TGAGAAATAA CTTTGCTAGT CTAGTAAAAT AAATACAAAA CAATCCTAGA	14640
AGATTTTTC TGGGATTGTT TTTTGCTGAG TGGGATGCTT CAAGTTGTCT GGCTTGACTT	14700
TCTTGAGGGA AGTTATATAA TAGTTGTAAT AATTAG	14736

(2) INFORMATION FOR SEQ ID NO: 172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11770 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

ACAGGAAAGC ACGATAGCAA TCTCTTTGGA AGATTTAAAA AATATTCCTC AAAGTTTCGC	60
TGTTGCTTAC GGTGATACGA AAGTATCTTC GATTCTCTCT GTCTTGCGTG CTAATTTAGT	120
AAATCATTTG ATTACAGACA AAAATACAAT TTTAAAGTT TTGGAAGAAG ATGGGGATTT	180
GACTTTTAGA GAGATTCTAG GTGAGTGAAA ATGATAGACT GATTCAGTTT ATCGTTTTC	240
TTTTTAGTTG ATTGCACATT TGTGCTTATA TAAACAAAA TAGTTTATCT GTTGTTTTTG	300
GATTGACAAC TTTATTATGT AGTTGTATTC TATAGTTACA AAAGAAAATT TTAAAAATTC	360
AAATGAAAAA AGCTTTTAC ATAGTGAAAT GAGGAGGAAT TTATGGAAAT GATTGTTCCA	420
GATCAAATTA TCATGGGTTT AATTTTATAT GCTGGTGATG CGAAACAACA TATTTATAAA	480
GCGTTAGATT ACATAAAAAA TGGTACATGT GAACGGTGTG AAGAAGAAAT ACAGTTAGCT	540
GATGCAGCCT TATTAGAAGC TCATAATCTA CAAACAAAAT TTTTGGCACA GGAAGCGCT	600
GGTACAAAGA CAGAAATTAC AGCTCTCTTT GTTCATTCAC AAGATCATCT CATGACCAGT	660
ATGACGGAGA TTAATTAAAT CAAAGAAATT ATTAGTTTGA GAAAAGAACT TCATAAAAAA	720
TAATACTAGA GTATTATCAT TGTTATTAAC ATAGAGGAGG AAAACATAAT GGTGAAGATT	780
GGTTTGTTTT GTGCAGCAGG TTTTCTACT GGTATGCTTG TAAATAATAT GAAAATTGCA	840
GCGCAATCTA GTGGAGTTGA GGCAGAAATA GAGGCGTTTT CTCAGTCTAA ATTAGCGGAT	900
TATGCGCCAA ATATAGATGT TGCACTATTG GGTCCACAAG TTGCTTATAC ATTAGATAAA	960
TCAAAAGAAA TTTGTGATAA GTGTGATGTT CCGATAGCTG TTATCCGAT GATGGACTAT	1020

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GGTATGTTAG	ATGGGAAAAA	AGTATTAGAT	TTGGCCCTAT	CTTTGATTAG	TGGGTAAGAA	1080
AAGGAGATTT	ATTATGTCAA	AGATGGATGT	TCAGAAAATC	ATTGCACCGA	TGATGAAGTT	1140
TGTGAATATG	CGTGGCATT	TAGCTCTAAA	AGATGGGATG	TTAGCAATTT	TGCCATTGAC	1200
AGTAGTTGGT	AGTTTGTCT	TGATTATGGG	ACAATTGCCG	TTCGAAGGAT	TAAATAAGAG	1260
CATTGCTAGT	GTTTTTGGAG	CTAATTGGAC	AGAGCCGTTT	ATGCAAGTAT	ATTCAGGAAC	1320
TTTTGCTATT	ATGGGTCTAA	TTTCTTGTTT	TTCAATGCC	TATTCTTATG	CTAAGAATAG	1380
CGGAGTAGAG	GCTTTACCAG	CTGGAGTTCT	ATCTGTATCT	GCATTCTTTA	TTTTGCTAAG	1440
ATCATCTTAT	ATCCCTAAAC	AAGGTGAGGC	GATTGGGGAC	GCTATTAGTA	AAGTTTGGTT	1500
TGGAGGCCAA	GGAATTATCG	GTGCTATCAT	TATAGGTTTG	GTAGTAGGAA	GTATTTATAC	1560
CTTCTTTATA	AAGAGAAAAA	TTGTTATTAA	GATGCCAGAA	CAAGTTCCAC	AAGCTATTGC	1620
CAAACAGTTT	GAAGCAATGA	TTCCAGCATT	TGTAATTTTC	TTATCTTCTA	TGATTGTATA	1680
TATTTTAGCG	AAGTCATTGA	CTAATGGCGG	AACATTCATA	GAAATGATTT	ATTCTGCTAT	1740
TCAAGTCCG	TTGCAAGGTT	TAAGTGGATC	TTTGTATGGT	GCTATTGGAA	TTGCATTCTT	1800
TATATCATTT	TTGTGGTGGT	TTGGTGTTC	TGGGCAATCG	GAGTAAATG	GAGTAGTGAC	1860
AGCTCTGCTT	TTATCTAATC	TTGATGCTAA	TAAAGCTATG	TTAGCCTCTG	CTAATCTATC	1920
ATTAGAAAAT	GGTGCACATA	TTGTTACTCA	ACAATTTTTA	GATTCATTTT	TAATTCTATC	1980
AGGTTCAAGG	ATTACGTTTG	GTCTTGTAGT	TGCCATGCTT	TTTGCAGCAA	AATCAAAACA	2040
ATACCAAGCC	TTAGGAAAAG	TTGCAGCTTT	TCCAGCAATA	TTTAACGTAA	ATGAGCCAGT	2100
TGTATTTGGA	TTTCCGATTG	TCATGAATCC	AGTTATGTTT	GTACCTTTCA	TTCTTGTTCC	2160
TGTACTTGCA	GCTGTGATAG	TATATGGAGC	TATTGCAACA	GGTTTCATGC	AGCCATTCTC	2220
AGGGGTAACA	TTGCCTTGGA	GTACACCAGC	TATTTTATCA	GGATTTTGGG	TGGGTGGATG	2280
GCAAGGAGTT	ATTACTCAGC	TGGTGATATT	AGCGATGTCT	ACATTGGTTT	ATTTTCCATT	2340
CTTTAAAGTA	CAGGATCGTT	TAGCTTACCA	AAATGAAATC	AAACAATCTT	AGAGGTATTT	2400
GTGTGTTACT	GTTAAACTCA	CACATTGTGT	CTAAAAATTA	GAGAGTTAAA	ATTTTCTAG	2460
TTAAAAGCTT	GAAAATTTCT	ATAAAAATCG	GTATTATATT	TTCGAAAGAA	ATAAAAATAT	2520
TTTCGAAAGA	AAGGTGCTTA	CGATGGTAAA	TACAGAAGTA	GCAAGAACAA	CAATCAAGAC	2580
AGAATATTTT	GGCAGCCTTA	CTGAAAGGAT	GAACAAATAT	CGAGAAGATG	TTTTAAATAA	2640
AAAACCTTAT	ATTGATGCTG	AGAGAGCAGT	TCTAGCAACA	CGCGCCTATG	AACGATACAA	2700
GGAACAACCT	AATGTCCTAA	AACGTGCATA	TATGCTGAAA	GAAATTTTGG	AAAATATGAC	2760

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TATCTATATT	GAAGAAGAAT	CTATGATTGC	GGGAAATCAA	GCTTCTTCCA	ATAAAGATGC	2820
TCCTATTTTT	CCGGAATATA	CGCTAGAATT	TGTTCTCAAT	GAGTTGGATC	TTTTTGAAAA	2880
GCGTGATGGA	GATGTTTTCT	ATATTACAGA	AGAAACAAAA	GAACAACCTA	GAAGTATTGC	2940
TCCGTTTTGG	GAAAATAATA	ATTTACGTGC	TAGAGCTGGT	GCCTTATTAC	CTGAAGAAGT	3000
GTCTGTTTAT	ATGGAAACAG	GATTCTTCGG	TATGGAAGGT	AAGATGAATT	CTGGAGATGC	3060
TCACCTAGCA	GTTAACTATC	AGAAACTTTT	GCAATTTGGT	TTAAGAGGTT	TTGAAGAGCG	3120
GGCTCGTAAA	GCAAAAGTAG	CTCTAGATTT	AACAGATCCA	GCAAGTATTG	ATAAATATCA	3180
TTTTTACGAC	TCTATATTTA	TCGTAATCGA	TGCTATTAAA	GTATATGCAA	AGCGCTTTGT	3240
TGCTCTTGCT	AAAAGTTTAG	CCGAAAATGC	AAATCCTAAA	CGTAAGAAAAG	AATTACTTGA	3300
GATTGCAGAT	ATTTGCTCTA	GAGTCCCAT	TGAACCGCA	ACTACTTTTG	CAGAAGCTAT	3360
TCAATCAGTT	TGGTTTATTC	AATGTATTTT	ACAAATTGAA	TCTAATGGCC	ACTCTCTTTC	3420
ATATGGCCGT	TTTGATCAAT	ATATGTATCC	ATATATGAAG	GCTGATTTAG	AAAGTGGTAA	3480
AGAAACAGAA	GATAGCATTG	TTGAACGTCT	GACAAATCTT	TGGATTAAAG	CAATTACAAT	3540
TAATAAGGTT	CGCAGTCAAT	CACATACATT	TTCTTCAGCA	GGAAGTCCTT	TATATCAAAA	3600
TGTTACAATT	GGTGGACAGA	CTCGAGATAA	GAAGGATGCT	GTTAACCCAT	TATCTTATTT	3660
GGTATTAAAA	TCAGTTGCAC	AAACCCATCT	ACCGCAACCT	AATCTAACTG	TACGTTACCA	3720
TGCAGGTTTA	GATGCTCGTT	TCATGAATGA	GTGTATTGAA	GTGATGAAAC	TTGGTTTTGG	3780
TATGCCTGCA	TTTAATAATG	ATGAGATTAT	TATTCCTTCT	TTTATTGCAA	AAGGAGTATT	3840
GGAAGATGAT	GCTTATGATT	ACAGTGCCAT	TGGATGTGTT	GAAACGGCAG	TTCCAGGGAA	3900
ATGGGGCTAT	CGTTGCACAG	GTATGAGTTA	TATGAACCTC	CCTAAGGTTC	TACTTATCAC	3960
GATGAATGAT	GGAATTGATC	CGGCTTCGGG	TAAACGGTTT	GCACCAAGCT	TTGGTCGTTT	4020
TAAGGATATG	AAGAACTTTT	CTGAATTAGA	AAATGCTTGG	GATAAAACAC	TAAGATATTT	4080
GACACGAATG	AGTGTTATTG	TTGAAAATTC	TATTGATTTA	TCATTGGAAC	GAGAAGTCC	4140
TGATATTCTA	TGTTTCAGCAT	TGACTGATGA	TTGTATTGGT	CGTGGAAAAC	ACCTTAAAGA	4200
AGGTGGAGCA	GTATATGATT	ATATATCAGG	ATTGCAAGTT	GGAATTGCAA	ATTTGTCGGA	4260
TTCATTAGCT	GCAATTAAAA	AATTGGTGTT	TGAGGAAGAA	CGTATAAGCC	CAAGTCAGCT	4320
TTGGCATGCA	CTGGAAACAG	ATTATGCCGG	AGAAGAAGGT	AAGGTCATT	AAGAAATGTT	4380
GATTCATGAT	GCACCTAAGT	ATGGTAATGA	TGATGATTAT	GCTGACAAAT	TGGTTACTGC	4440
TGCTTATGAC	ATTTATGTTG	ATGAAATTGC	TAAATATCCT	AATACACGTT	ATGGAAGAGG	4500
GCCTATTGGA	GGAATTCGTT	ATTCAGGAAC	ATCTTCTATC	TCAGCCAACG	TAGGGCAGGG	4560

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ACGTGGAACA	TTAGCAACTC	CAGATGGACG	CAACGCGGGT	ACACCGTTAG	CAGAGGGTTG	4620
TTCACCATCA	CATAATATGG	ATCAACACGG	CCCTACATCT	GTTTAAAAAT	CTGTTTCAAA	4680
ATTACCAACA	GATGAAATCG	TAGGTGGGGT	TCTCTTAAAT	CAGAAAGTAA	ATCCTCAAAC	4740
GTTAGCCAAA	GAAGAAGATA	AATTAAAACT	AATTGCTTTG	TTACGAACAT	TCTTTAATCG	4800
TTTACATGGG	TACCATATTC	AATACAATGT	TGTTTCCAGA	GAGACGCTGA	TTGACGCTCA	4860
GAAACATCCT	GAAAAACACA	GAGACTTAAT	TGTTCTGTGT	GCAGGATACT	CTGCATTCTT	4920
CAATGTTCTT	TCTAAGGCAA	CCCAAGATGA	CATTATAGGA	CGTACTGAGC	ATACTTTGTA	4980
AAATAAAGAG	GTTCTTTTTA	TGGAATTTAT	GCTTGACACA	TTAAATTTAG	ATGAGATTAA	5040
AAAGTGGTCT	GAAATTTTGC	CGCTAGCTGG	GGTAACTTCA	AATCCCACTA	TTGCAAAAAG	5100
AGAGGGTTCT	ATTAATTTT	TTGAACGAAT	CAAAGATGTA	AGAGAATTGA	TTGGCTCTAC	5160
ACCCTCTATT	CATGTTTCTG	TGATTTCTCA	AGATTTTGAA	GGCATCTTAA	AGGATGCTCA	5220
TAAAATTCGA	AGACAAGCAG	GAGATGATAT	ATTATCAAAA	GTACCTGTTA	CTCCAGCTGG	5280
ATTACGTGCA	ATAAAGGCGC	TAAAAAAGA	GGGCTACCAT	ATCACTGCAA	CAGCTATTTA	5340
TACAGTTATT	CAGGGATTAT	TAGCTATCGA	AGCAGGAGCG	GATTACCTAG	CTCCATATTA	5400
TAATAGAATG	GAAAATCTGA	ACATTGATTC	AAATCTGTGC	ATTCTGCAAT	TAGCTCTTGC	5460
TATTGATAGA	CAGAACTCTC	CTAGTAAGAT	TTTAGCTGCA	TCCTTTAAAA	ATGTAGCACA	5520
AGTAAATAAT	GCTTTAGCTG	CAGGTGCGCA	TGCTGTTACA	GCAGGAGCGG	ATGTTTTTGA	5580
ATCAGCTTTC	GCCATGCCAT	CTATCCAAAA	GGCGGTGAT	GATTTTCTCG	ACGATTGGTT	5640
TGTTATTCAA	AATAGTCGTT	CCATTTAGAT	AGAGAGGAAA	TACATATGAG	AATTTTGTCT	5700
AGTCCTTCTA	GATATATTCA	GGGGGAAAAT	GCCTTGTTTG	AAAATGCCAA	ATCAATTTTG	5760
GATTTGGGAA	ATTGCCCTAT	TCTATTATGC	GATCAGTTGG	TTTATGATAT	TGTTGGAAAA	5820
CGATTTGAAG	ATTACCTACA	TAGGTATGGT	TTCCATATTG	TTCTGGCGCT	ATTTAATGGT	5880
GAAGCTTCTG	ACAATGAAAT	CAATCGAGTT	GTTGCCTTGG	CTGAGAAAGA	AAATTGTGAT	5940
AGTATTATCG	GTCTTGGTGG	GGGAAAGACG	ATTGATAGCG	CAAAAGCTAT	TGCAGATTTG	6000
ATTGAAAAGC	CTGTATTAT	TGCTCCAACA	ATTGCATCGA	CCGACGCACC	TGTATCTGCT	6060
TTATCTGTTA	TTTATACAGA	TGAAGGTGCA	TTTGATCATT	ATCTATTTTA	TTCTAAAAAT	6120
CCAGATTTAG	TTTTGGTTGA	TACAAAAGTT	ATTCACAAG	CCCCTAAGCG	TTTATTAGCG	6180
TCTGGTATTG	CAGATGGTTT	AGCAACTTGG	GTTGAGGCGC	GTGCGGTAT	GCAGGCAAAT	6240
GGAAAAACTA	TGTTGGGACA	ACAGCAAACA	TTGGCTGGAG	TTGCAATTGC	GAAGAAATGT	6300

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GAAGAAACGC	TGTTTGCAGA	TGGTTTACAG	GCTATGGCAG	CTTGTGAAGC	TAAAGTGGTG	6360
ACACCAGCAT	TAGAAAATAT	TGTTGAAGCT	AATACTTTAT	TGAGTGGTCT	AGGTTTGTAA	6420
AGTGGAGGAT	TAGCTGCGGC	GCATGCAATT	CATAATGGTT	TTACTGCATT	GACAGGTGAC	6480
ATTCATCATT	TAAACATGG	TGAAAAAGTA	GCTTATGGAA	CTTTAGTACA	ACTATTATTG	6540
GAAAATAGAC	CTAAAGAAGA	ACTTGATAAG	TATATTGAGT	TTTACAAAAA	AATTGGTATG	6600
CCAACAATC	TAAAAGAAAT	GCATTGGAT	CAAGTTGGAT	ATGATGATT	AATAAAAGTT	6660
GGTAAACAAG	CAACTATGGA	GGGTGAGACA	ATTCATCAGA	TGCCGTTTAA	GATTTGCGCT	6720
TCAGATGTTG	CTCAAGCTAT	TATCGCTGTA	GATGCCTATG	TAAATTCAAA	ATAACAATA	6780
AGGACTACTG	TTTCCAAAT	GGTAGCTTT	TATTGATCCC	TGTATTGAAT	TCTATAGAAG	6840
ATTGAAATAG	GATGAGAACA	AATCGATTGG	GAAAGTAAAA	TTAATTTCTA	TAAATGTTTT	6900
AGCAATTGTT	TCGTACTATT	TCAGATTCAG	TCTACTATAT	GTTCTTCATA	AATCAAAAAG	6960
CGACATAGGT	TGTCGGCTAT	TTATTGTGAA	TACATTAATT	AGCATTCAG	TTTATCTTC	7020
GGTCTAAAAT	AAGTATTTTG	TGCTATACGA	GATAAGCTTC	TTGACTTACT	CCTTGATTTA	7080
CTGCATAACA	ATGGGATAAA	AAGTGGGAGA	TAGAGCAATT	CATAGTCATC	AAAATTAATG	7140
AGATACAGTA	TACAGTTTTT	CCTTTAAACA	CATTTCAAAT	TCCCTCAAAA	ATGGTATAAT	7200
AGTAACATCA	CAAAATTGGA	GAGAGACCAT	GAGTTTTTAC	AATCATAAAG	AAATTGAGCC	7260
TAAGTGGCAG	GGCTACTGGG	CAGAACATCA	TACATTTAAG	ACAGGAACAG	ATACATCAAA	7320
ACCTAAGTTT	TATGCGCTTG	ATATGTTCCC	TTATCCGTCT	GGAGCTGGTC	TGCACGTAGG	7380
ACACCCAGAA	GGTTATACTG	CAACCGATAT	CCTCAGTCGT	TACAAACGTG	CGCAAGGCTA	7440
CAATGTCCTT	CACCCAATGG	GTTGGGATGC	TTTTGGTTTG	CCTGCAGAGC	AATACGCTAT	7500
GGATACTGGT	AATGACCCAG	CAGAATTTAC	AGCGGAAAAC	ATTGCCAACT	TCAAACGTCA	7560
AATTAATGCG	CTTGGATTTT	CTTATGACTG	GGATCGTGAA	GTCAACACAA	CAGATCCAAA	7620
CTACTACAAG	TGGACTCAAT	GGATTTTCAC	CAAGCTTTAC	GAAAAAGGCT	TGGCCTATCA	7680
AGCTGAAGTG	CCAGTAAACT	GGGTGAGGA	ATTGGGAACT	GCCATTGCCA	ATGAAGAAGT	7740
GCTTCCTGAC	GGAACCTCTG	AGCGTGGAGG	CTATCCAGTT	GTCCGCAAAC	CAATGCGCCA	7800
ATGGATGCTC	AAAATCACGG	CTTACGCAGA	GCGCTTGCTC	AATGACTTAG	ATGAAC TAGA	7860
TTGGTCAGAG	TCTATCAAGG	ATATGCAACG	CAACTGGATT	GGTAAATCAA	CTGGTGCCAA	7920
TGTAAC TTTC	AAAGTAAAAG	GAACAGACAA	GGAATTTACA	GTCTTTACTA	CTCGTCCGGA	7980
CACACTTTTC	GGTGCGACTT	TCACTGTCTT	GGCTCCTGAA	CATGAATTAG	TAGACGCTAT	8040
CACAAGTTCA	GAGCAAGCAG	AAGCTGTAGC	AGACTATAAA	CACCAAGCCA	GCCTTAAGTC	8100

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TGACTTGGCT	CGTACAGACC	TTGCTAAAGA	AAAAACAGGG	GTTTGGACTG	GTGCTTATGC	8160
CATCAACCCCT	GTCAATGGTA	AGGAAATGCC	AATCTGGATT	GCAGACTATG	TCCTTGCTAG	8220
TTATGGAACA	GGTGCGGTTA	TGGCTGTGCC	TGCCCACGAC	CAACGTGACT	GGGAATTTCG	8280
CAAACAATTT	GACCTTCCAA	TCGTCGAAGT	ACTTGAAGGT	GGAAATGTCG	AAGAAGCTGC	8340
CTACACAGAG	GATGGCCTGC	ATGTCAATTC	AGACTTCCTA	GATGGATTGA	ACAAAGAAGA	8400
CGCTATTGCC	AAGATTGTGG	CTTGGTTGGA	AGAAAAAGGC	TGTGGTCAGG	AGAAGGTAC	8460
CTACCGTCTC	CGCGACTGGC	TCTTTAGCCG	TCAACGTAC	TGGGGTGAGC	CAATTCCAAT	8520
CATTTCATTGG	GAAGATGGAA	CTTCAACAGC	TGTTCTTGAA	ACTGAATTGC	CGCTTGCTCT	8580
GCCTGTAACC	AAGGATATCC	GTCCTTCAGG	TACTGGTGAA	AGTCCACTAG	CTAACTTGAC	8640
AGATTGGCTT	GAAGTGACTC	GTGAAGATGG	TGTCAAAGGT	CGTCGTGAAA	CCAACACTAT	8700
GCCACAATGG	GCTGGTTCAA	GCTGGTACTA	CCTCCGCTAT	ATTGACCCGC	ACAATACTGA	8760
GAAATTGGCT	GATGAGGACC	TCCTCAAACA	ATGGTTGCCA	GATGATATCT	ACGTGGGTGG	8820
TGCGGAACAT	GCTGTACTTC	ACTTGCTTTA	TGCTCGTTTC	TGGCATAAAT	TCCTCTATGA	8880
CCTCGGTGTT	GTTCCGACTA	AGGAACCAT	CCAAAACTC	TTTAACCAAG	GGATGATTTT	8940
GGGAACAAGC	TACCGTGACC	ACCGTGGTGC	TCTTGTGGCA	ACCGACAAGG	TTGAAAAACG	9000
TGATGGTTCC	TTCTTCCATG	TAGAAACAGG	GGAAGAGTTG	GAGCAAGCGC	CAGCCAAGAT	9060
GTCTAAATCG	CTCAAGAACG	TTGTTAACCC	AGACGATGTG	GTGGAACAAT	ACGGTGCCGA	9120
TACCCCTTCGT	GTTTATGAAA	TGTTTATGGG	ACCACTCGAT	GCTTCGATTG	CTTGGTCAGA	9180
AGAAGGTTTG	GAAGGAAGCC	GTAAGTTCCT	TGACCGAGTT	TACCGTTTGA	TTACAAGTAA	9240
AGAAATCCCT	GCGGAAAACA	ATGGTGCTCT	TGACAAGGTT	TACAACGAAA	CAGTCAAAGC	9300
TGTTACTGAG	CAAATTGAGT	CTCTCAAAT	CAACACAGCT	ATTGCCCAAC	TTATGGTCTT	9360
TGTCAATGCT	GCTAACAAGG	AAGATAAGCT	TTATGTTGAC	TATGCCAAAG	GCTTTATTCA	9420
ATTGATTGCA	CCATTTGCAC	CTCACTTGGC	AGAAGAACTC	TGGCAAACAG	TCGCAGAAAC	9480
AGGTGAGTCA	ATCTCTTATG	TAGCTTGGCC	AACTTGGGAC	GAAAGCAAAT	TGGTTGAAGA	9540
TGAAATTGAA	ATTGTCGTCC	AAATCAAAGG	AAAAGTTCGT	GCCAAACTCA	TGGTTGCTAA	9600
AGATCTATCA	CGTGAAGAAT	TACAAGAAAT	CGCTTTAGCT	GATGAAAAAG	TCAAAGCAGA	9660
AATTGACGGT	AAGGAAATCG	TGAAAGTAAT	TGCGGTACCG	AATAAACTCG	TTAATATCGT	9720
CGTTAAATAA	CGAGTTTATT	AGCTCTATCT	GCCACCTTCA	ATAGTCCACT	GGACTATTGA	9780
AsCCAACTAA	ATTAGTTAAC	ATTGTTGTGA	AATAAGATAG	GAGTCCTTCA	GAGTAGAATC	9840

1100

TGGAGGATTT TTTGAATCTT CTTATGAAAG TATGATATAC TATGGGCAAC TATAAAGTTT	9900
GAAAAGTGAA ATAAGGAGAA TAAGATGCCA GTAAATGAAT ATGGTCAAAT GATTGGGGAG	9960
TCAATGGAAG CTTATACTCC AGGTGAATTG CCTTCTTTTG ATTTCTTAGA AGGGCGTTAT	10020
GCTAGGATAG AGGCTCTTTC AGTGGAAGAG CATGCGGAGG ATTTATTAGC TGTTTATGGC	10080
CCTGATACGC CTCGGGAGAT GTGGACCTAC CTCTTTCAGG AGTCAGTAGC AGACATGGAG	10140
GAACTGGTCA GCCTTTTAAA TCAGATGTTG GCTCGTAAGG ACCGTTTTTA TTATGCAATC	10200
ATAGACAAGG CAACTGGTAA GGCTTTGGGA ACTTTTTCCC TCATGCGAAT TGATCAGAAT	10260
AACCGAGTAA TAGAAGTGGG AGCTGTCACT TTTTCTCCAG AGCTCAGGGG GACACGGATA	10320
GGAACAGAAG CCCAGTATCT CTTGGCTTGC TATGTCTTTG AGGAGCTTAA CTATCGTCGC	10380
TATGAGTGA AATGCGATGC TCTTAACCTG CCATCCAGAC GAGCAGCGGA ACGTTTGGGA	10440
TTTATTTATG AAGGAACCTT CCGTCAGGCA GTGGTTTATA AGGGGCGTAC AAGAGATACG	10500
GATTGGTTGT CTATGATTGA TAAGGACTGG CCTCAAGTCA AAGCTCGATT GGAAATATGG	10560
TTGCGTCCTG AAAACTTTGA TAAAAATGGA CGACAGCACA AGAGCTTGAG AGAACTTTAA	10620
GAGGTGTTGA GATGATTACT ATTAAAAAGC AAGAAATTGT CAAGCTAGAG GATGTTTTGC	10680
ATCTCTATCA GGTGTCGGT TGGACAAACT ATACCCATCA AACAGAGATG CTGGAGCAGG	10740
CCTTATCTCA TTCATTAGTA ATTTATCTGG CACTTGATGG TGATGCTGTG GTGGGCTTGA	10800
TTCTGTTGGT TGGAGATGGT TTTTCATCAG TTTTGTGACA GGATTTGATT GTTTTGCCTA	10860
GCTATCAGCG TCAAGGGATT GGTAGCTCCT TGATGAAAGA GGCTTTAGGA AATTTTAAAG	10920
AGGCCTATCA AGTCCAGCTG GCGACAGAAG AGACAGAAAA AAACGTGGGA TTTTATCGTT	10980
CTATGGGCTT TGAAATCTTA TCCACCTATG ACTGTACAGG AATGATTTGG ATAAACAGAG	11040
AAAAATAAAA AAACCTGTTT GTTCTTAAGC AAAGTTTAAG GATGGTCTAG TATCATATAG	11100
TCATTAAATA AAGACCTCCT AACTTTATTT AATAAAATCC TAAACTTTTT TCATCACAAT	11160
CTCCTAATGA AGCCACCCAA TCAGGTGGCT TTTTGTGCGT ACGACGGGCA TGTCGTATAT	11220
CTGAGGTGTA AGTCCTCAGC CTGACTATCG TGAGGTAGCA GGGAGAGGAA GGGATAGCGA	11280
AATCGTGGCT CTACGAACAG GAACGTGATA GTAAGGCGTA TATAGCGGAT AAGGAGGCTT	11340
CAAACTCTAA AGTCCAAAAA GGTAGTCGTA ACCTATATGT GTAAATCACG AGAGTAATTG	11400
AATTCGGAAT AAGGTTTGTG TGAAAAAGAT AAATCTTTCT AGAGTCTAAA GACTCTGCGT	11460
CAGATTTTCT ATTTTCACTG TAACCTTTTA ACGTCCTCAT ATCTTGATATA AACGAGGAAA	11520
GATGTACGAC TTATCCCGTG AGGTTTCATG AGCGCTGAAA GCGTAGTAAC AACGAATCAT	11580
GAGAAGTCAG CCGAGCCCAT AGTAGTGAGG AAACCTCCGT AATGGAAGTG GAGCGAAGGG	11640

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GTGAATACTC AAACAGTCTG GGGAGAGACT GTTTGAGGTC TGTGCTAGA AAGAGAAAAC	11700
GACAGATCGA AGTAATCCTA CTTCACTTGT GTCTGTAAAA TGAGTGGTCT GATAGAAGT	11760
GACTTTGAGG	11770

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAAACTA CTTTCTTAGT ATAACACTTT CAGAATCATT GTCAATAGAA ATGACTTGAT	60
TTTTTCAATT TTTTCAAGCT ATTTCCAAGG GTTGTAATAAT CGTCCCTGAT TCTGCAAGAT	120
AAGTAGTAAA CTAAGTACTA AAAACAAGGT TGCCAAGAGC AAGGTAATAT AGTCTCCTTT	180
TTTCAAGGCC TGATAACTAT ACCATGTGCG TTTTCTCTCT TTTCCCAAAGC GGCGAACTCC	240
ATGGCAGTCG CAATGGTATC AATGCGTTCT AGCGAGCTAA AAATCAAGGG CGTAATAATG	300
AGCAGATTGC CTTTGATTCT TTGCATAAGA GAAGCTTTCT TGGATAATTC CATCCCACGC	360
GCCTCCTGAG ACATCTTGAT AGTAAAGAAT TCTTCTGCA AATCTGGAAT ATAGCGCAAG	420
GTCAGGCTGA CAGAATAAGC AATCTTATAG GGCACACCAA TTTGATTAA ACTGGAAGCA	480
AACTGACTAG GATGGGTTGT CATCAAAAAG ATAATAGCCA GAGGAATGGT GCAAAGATAC	540
TTAATGGCCA AATTAGCAG ATAAAAGAGC TCCTGGCTGG TTAGAGTGTA GACACCGATT	600
CCCTGCCAAA TCACACTTCT CTCTCCATAA AGTCCAACCC CATACTCGGG AGAAAAGAGA	660
TAGACCATCA AAACGTTTAA AACGGCAAAT ATCGTCGCAA AAACGGCTAC AAAGGAAACA	720
TCTTTAAAGC GAATTTCTGA TAAATAGAGG AGAAAGACTG AAAAGATGGC AATCAGCAAG	780
AGCATTCTGG TATCATAGCT AATCATGGCC GCCAATGATA CCAGAATGAA AAAGAGAAGT	840
TTCCCAGCTC CTGACAAGCG ATGAATCACA GTATCTCTAT GCTGGTAACC GATTAATTTA	900
GCTTGCATCC CTCTCTCCTT TCTTTGTAAA ATGCCGTTAA ATCCAGTGGA TCCACATCTA	960
GTTTCTTAGC CAAGTTAAAG ATGGAGGTTT CTTTGTAGAT GGCTTTTACT AACAGCTCAG	1020
GATCGCTCAA CAGACTGGCT GGAACAGTAT CGGCAATCAA TTCTCCATCC ACCATGACAA	1080
GGACCCGGTC TGAATAATCC AGCATCAATT GCATATCATG GGTAAATCATG ACAATGGTAT	1140
GCCCTTTTTC ATGTAACCTC TCGAGAAATT CCATAATCTC AGTATAGTTC TTCTGATCTT	1200

1102						
GACCTGCAGT	CGGTTTCATCT	AGGAGAATAA	TTTCAGCTCC	TAAGACCAAA	ATTGAAGCAA	1260
TGGTGACACG	TTTTTCTGA	CCAAATGACA	GGGCAGAAAT	AGGCCAATTA	CGGAATTCAT	1320
AAAGTCCACA	GATTTTCAAG	GTTTCATATA	CTCTCGTTTC	AATTTCCCTTC	TCATCCACAC	1380
CTCGCAAACG	GAGCCCTAGA	GCCACCTCAT	CAAAAATCAT	ATTGGTTGAA	ATCATTTGAT	1440
TAGGATTTTG	TAGCACATAT	CCTACTCGTT	CCGCCCCTC	TGCAACAGAA	TCGCCTTTTA	1500
TATCCTGTTT	TTCCCAAAGA	TAGCGTCCTT	CCGTCTGAAT	AAAGCTACTT	ATAGCCTTGG	1560
CTAGAGTTGA	TTTCCCTGCT	CCATTTTTC	CGACAATAGC	AATCTTTTCA	CCCTTTTTAA	1620
TATCTAAATG	TAGGGATTTT	AAAATCGGTC	TATCATCATA	AGAAAAAGAT	ACTTCCTCTA	1680
GTCTAAAGAG	TGACTGCAAT	GCTGGGGTTT	CTTTTGCCAG	TTCATTCTGC	AACTGAACCT	1740
GACCTTTTGA	GATAGACAAG	TTATCCAGAT	TCGCTAATTG	TTCTTCCTTG	ACTAAGTCCA	1800
CACCTAATTG	ACGGAGAGTC	GTTAGATAAA	GGGGTTCTCG	AATTCCA'TTT	TGAGTCAATA	1860
AATCAGTCGC	AAGCAACTGG	TCAGGGCTCC	CATTAAAAAG	GATACGACCA	TCGTTTATCA	1920
AGACAATCCG	ATCCACAGGG	CGATGCAGAA	CGTCCTCCAA	ACGGTGCTCG	ATAATAAGAG	1980
TCGTCGTCCC	CTCTTCCTTA	TGAATCTGGT	CAATCAATTC	GATAATATCC	TGACCTGACT	2040
TGGGATCTAG	ATTGGCGAGT	GGCTCATCAA	ACAAGAGAAT	CGGACTTTCA	TCAATCAAGA	2100
CACCAGCCAG	ACTGACTCGC	TGCTTTTGTC	CACCTGACAA	ATCCTGAGGA	CGCTGATCCA	2160
GTAAAGGAAG	AAGGTCCAGC	TTTTCAGCCC	ATTTATAAAC	ACGACCTTTC	ATCTCATCTA	2220
GGGCTGTCAC	ATCATTTTCC	AGAGCAAACG	CCAAATCTTC	TGCCACAGAC	AAGCCAATAA	2280
ACTGCCCATC	TGTATCCTGC	AAAACGTGTC	TAACCAGATG	AGACTTATCA	TAGATGCTCA	2340
TATCAAAGGC	TACTTGACCC	TTTATCAAAA	ATTCTCCATA	TGTCTGACCC	TTGTAAATAT	2400
TGGGAATAAT	CCCATTCAAA	CACTGACCCA	AGGTAGATTT	ACCTGACCCA	GATGGTCCAA	2460
CAATTAAGAC	TTTCTCTCCC	TTGTAAATGG	TCAAGTCTAT	CCCTTGCAAG	GTCGGTTCTT	2520
GTTGTGTTTC	ATACCGGAAA	GAGAAATCCT	TCCACTCAAT	TaTAGCTTCT	TTCATCTIAC	2580
TCTCTTCATT	CGCTTCTTAG	ACTTCTATTT	TATCATAAAT	CAAGCCCTTC	TTGCAGTCTC	2640
TCCTCTTAAA	ATCTTAGCGC	CAAAAAGATT	CCTATCCTAG	CTTACTTGCC	TAACCTAATCT	2700
ATAAACATCG	AAAAAGACTA	GTTGCCCAGC	CTTCCCCATC	ATTTTATACT	CTTCGAAAAT	2760
CTCTTCAAAC	CACGTCAGcT	TCGCCTTGCC	GTAGGTATGG	TTACTGACTt	CGTCAGTTTC	2820
ATCTACAACC	TCAAAACCAT	GTTTTGAGCc	TGCTTCGTCA	GTTCTATCCA	CAATCTCAAA	2880
ACACTGTTTT	GAGCAACtGC	GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	2940
TAGTCCTTTT	TCAAACCTCC	TGCACGAGTT	TGGGTTCCTG	CATAGGCAAG	TAAGAGAAGA	3000

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GTTCCTGCAA TAGCTACAGA TACACCATTG GCAATTCCCG CAACAATCCC TTGTGCAAAT	3060
ACTTTTTCTG CCGCTTCTTG ATAAATCACA ACATCTCCAA GTGGTGCCAA GACACCCCAA	3120
ACAAGGGCAT TTGCAAGTAG TTGAATGAGA TTAATAATAA GAATATCTTT CCAGTCAAAA	3180
ACACCATTGA TCACGCGAAC GTACTTTCTA AAAAGTCCCA CAACTAAACC AAAGAGTCCG	3240
CTAGCGATAA TCCAAGTCCA CCATAGACCA TAACCAACAA GAGAGTCCTT GATTGCATGA	3300
CCAATCAACC CGACAAGCAA ACCGATAATC GGTCACAAAA TAATAGAAAG TAGCGCTTGT	3360
ACCGCATACT GAAGCTGGAT GCTTGTATTT GGAACAGGGG TTGGAATGTT GATCATCCCG	3420
ATGACGACAA AGAGGGCAGC GCCAATTCCG ACAGCAACAA CTGTGTTAAT TGTAATTTTG	3480
ATTTCCATAC TATTCTCCTA TTTTATCCTT CTATTTTCTT TATTTCAATG GTCCAAGATG	3540
AACCGACACC TACATTATAG GCCTTGCCAA AGGAACCTTG GTTGATAGCC AAACCTAAAC	3600
GATAGAGAGA GTTGATGTAA AGGATGGGTT GCCCAATTCT CACATCTGCA AATGATTTGC	3660
CATAGACAACT CTGATTTTGA TAGACCAGCA TATCAGCATG ATAGATGGTC ACTTCAAAAC	3720
GATCACCAAA TTCTGGTTCC AGCTTGTAAG ATTCTTCCCG TGTGATAGAG GTCCAAAGCG	3780
AACCGAAACG CACATCCAGA ATATCAATGG CTCCCTTCAC CAGATGATCT TCTATGATGG	3840
TCGCTACGAC TGGAAGCTCT ACAATCTGTT CCACACTGAG CTCTGGCCCT ACTTCCTCAA	3900
AAGTAATGTG ACCACTGGCC AGTTTAGCAC CAGTATAGGC ATAGACATCA CGACCGTGGA	3960
AGGTATAAGA ATGCTCTGTG TTTTGACGCC TATTGGCCAC CTCAGAAATC TCACGAATGG	4020
CTACAATGCC AACGTGTTTC TTGATAAAGG AAAGCGTCCC ATTATCTGGC GTGACAATGT	4080
ATTGATTTTT TGCACTCTTG GCAACTACAC TCTTACGTTT CGAACCGACA CCTGGATCGA	4140
CAACCGATAC AAACGTCGTT CCCTCAGGCC AGTAATCCAC CGTCT	4185

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2069 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

TGATAGAGTT AAAGCCGCTG AGTCATTCAA TCCATCTCCA ACCATCAAAA TAGTGTGACC	60
TGCTTTCTGC AGTTTCTCTA CTAACCTCAA TTTCCCATCA GGTTCAGT CTGTATAGAC	120
CTGATCAAAG GGCAAATCTT TGAATAATTC CTCTGTCCTA ATCAAGGTGT CTCCTGTGTC	180

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CAGAATCAAT TTTT ^y CCCCCT GTGCCTTAAG TTTATCCAAG GCTGTTTTTG CTTCTTTTCT	240
CAAAGGAGTA TGAATGCAGA ACATTCCAAT CAATTCATTT TGATAAGCCA AGAATAAGAG	300
ATTGTAGTGA CTCTTGACT CTTCAATTAA AGCATTTTGT TCTGAACTGA TATGAATCTG	360
CTCATCCTGC ATCAAGACAT AATTCCCAAT AAGAACTGGT TGGCCATCTA TATGAGATTT	420
GATCCCCCTG CTTGCGATAT ATTGGAGTTT CCCATGCATT TCCTCATGTT CAATTCCCTC	480
TATCTCAGCT TGCTTGACGA TGGCATTAGC AATAGGATGA TAAATGTGTT CCTCAAGACA	540
GGCACTGATT CTGAGAATAT CTTCTCACT ATAGTCTCCA AAAGGTAACA CTTTTTCAAC	600
TATAGGATAA CTAGTTGTGA TTGTTCTGT CTTATCAAAC AAGAAAGTAT CAACTTCCAG	660
ATATTTCTCC AGAACATCTC CATCCTTAAT CACCATTTCA CGGTTCAACC CTTCTTGAT	720
AACTGTCAAA TAAGCTACAG GAGTAGAGAT TTTCAAAGCG CAGGAGAAAT CGACCAATAG	780
GAAAGAAATA GCCTTAGAAA AAGAACCTGT CAATAGGTAA GTCAGCCCAG CCCCCAAGAA	840
ATTATATTTG ACGACTTTAT CCGCCATCTT GATGAAATAG CGTTGTTTCG TTTTCTTGTT	900
TTCTTCAGAT TTCTTCATCA ACTCAATCAG CTGTAAAATA CGGCTGTTCA TCTGATTATC	960
TGTTACACGA ATGCGTAACT CTCCAGTTTC TAATACTGTA TTTGCACAAA CCAAATCAGA	1020
CTCTCTTTTT TCAACTGGAA AACTCTCTCC TGTCAGGAA CTTTCGTTGA CCATACCTAA	1080
ACCTGAAACT ACTTGTCAT CAAACAGAAT TTCATTTCTT TGAGATAAGA TCAAGACATC	1140
TCCTATTTGA ACATCGGAAC TCTTGATACT AACAACCGTA TCGCCCTGTA CTAGGAATAC	1200
ATCGCTCTCT TTTGCAAGAA GACTCTGTTC TAAATCTGTT GCAGTTTTTT TCAAGGACCA	1260
CTGATCTAAA TGATTCCCCA AATCAAGCAT AAACATGATA TTGCTAGCTG TCTTGGATTG	1320
GTTCATAAAC AAAGACAATA AAATAGCCGA ACAGTCCAAG ACTTCCATCG TTAGT ^y CCTT	1380
ACGCGCTAGT GTTTGATAGG CTCTCTAAT ATAACCCAAA GCCTGATAAC AAGTCCATAT	1440
ATAGCGAATA GGATACGGCA CAAAAC ^t ACG AAAAAGTACA CGCTTAACCG CTGCACCTGA	1500
AACAATAGAA TAAGCACTCT CTTCTCTACG AATGGGAAGA GTCATCAACT CAGAACTTT	1560
CCCTTTATCA ATTCTTTT ^t A AAAAGGCTTC TGCATTATCT AATACAGAAA AGCCTTCTTT	1620
TATGCGTAGA GTAAAGTGCT GTTGATCCAT GTAAACTGG ATAGACTCAA TCCCCTTTTC	1680
ATCTCTCGCC AAGGAACGAA GATAGTCTTG AATATCCAAG GTAAGTGAAA AAGAAGATGA	1740
TAGTCGGATA TGTGGTATC CTCTATGTAG CACTTTAAAA GACATATTAT TCACCTATAA	1800
GGCTATCTAA TTGCTCTTCT TTTTCTCTT GCTCGTACAA ATATTTGGCA TCTTGCAAGA	1860
CATCGTCTCC ATGTTGCTTC ACAACAGAAA CAGATGCATC TAGCTCGTCT TTCAACTTGT	1920
AAGCCTTAGC CAAAGCTTTA GAATAACCTT TTTTAGCTTC CTTACTTGCT AAGATTTTCA	1980

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AACCAAGGGT ACCAAATGCG ACACCACCCA AAAATAATGA AGATTTTTC GCAACTTTTG 2040
 CAACGGTTAA TACTTCTTTT AACATAGGG 2069

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4597 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AAATCTTGCG CAATAAGCT CATCTCCATC TCCCGATTGA AACAGTCACT CCCC GGACTG 60
 TTTCAACGTC CCAAGACATA ATCTTAGGCA GATTTCTAAA ATTACTCA AAGTGGAAGT 120
 CATTGAGCTT TCGAATGACA GTTGAAGTTG AAATGGCCAG CTGATGGGCA ATATCGGTCA 180
 TAGAAATCTT TTCAATTAAC TTTTGCGCAA TCTTTTGTTT GATAATACGA GGAATTTGGT 240
 GATTTTCTT GACGATAGAA GTTTCAGCGA CCATCATTTT CAAGCAATGA TAGCACTTAA 300
 AACGACGTTT TCTAAGGAGA ATTCTAGTAG GCATACCAGT CGTTTCAAGG TAAGGAATTT 360
 TATAGGGTCT TTAATGTCTA GTAATTTTGT GATAAAATGT AATTGTTCCA TATGATTCTT 420
 TCTAATGAGT TGTTTTGTCG CTTTTCATTA TAGATCTTAT GGGACTTTTT TTCTACCCAA 480
 AATAGGCTCC ATAATATCCA TAGGGAATTT ACCCACTACA AATATTATAG AGCCCAAAGT 540
 TTTAGGTCGC TTGATAATAT GCGTTTTTTG AATTTTATAG ACTGCTCGTT TAAACTCTAT 600
 TTACTTCGTA CCTTCTGGAG CGAGACGGAA TATTAGTCAC ATACAAAATG AGTACTATTA 660
 GGATTTTATT TTCATGTACA ATTTCAGCCA GTCTTGTTAT AATCAGCCTA TAGGAATCAA 720
 GGAGGTGACT CTTATGGCTG TTTTGTGTC TTTGGATGGA ATTGTGGTAG AAGTCCTTGA 780
 TGTCTTTTCT TCTTTTAATG GGGATAGTGA GTTTTCTTG TGTATAGCAT TTTGAATCTG 840
 GAATAGGACG CCATGACTGC TAAAAGATTT CTATAAATTA ATTTGATTTT CCTAATCAAT 900
 TTGTTTCATAT CTTATTTTCAT TCCACTATAA ACGTCTTAAA GACAAGAGTC AGTTTGTTAT 960
 GGAACGCTCT CAGTTCGAGG AGATGTTCCA ACTTCAAAGT AGTCGCTTGA CGACGCAAGA 1020
 AAAATTACAA TTGTTTACCT CTGTGTTTGC TGGCCGTTAT GATGTTTATG CTAAGAATTT 1080
 TATCAATGAA CAAGGGAAAA TTCAGTATTT TCCTTCCTAT GATTATGGTT GGAAGCAGTT 1140
 GCCACCTGAA AAACGGAGTT TCCAGACATT GACGAACTCC GTTTTGAAAT CTCATTTTCG 1200
 TGGGGAGGCA GCTATCGGTA TCTTTCCTAT GCACTTAGAT GATAGCTGTT ATTTTTTGGT 1260

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ACTGGATTTG GATGAAGGAG ATTGGAAAGA AGCTGGTTTA ACCATTCGAA GAATAGCCAG	1320
GGAACGCCAG ATGGAAGCCC ATTTAGAGAT TTCTCGTTCG GGTACGCGAC TCCATATTTG	1380
GTTCTTCTTT GAGGAAGCGA TTCCGAGTCG AGAGGCTCGC TTGTTTGGAA AGAAACTGAT	1440
AGAACTGGCA ATGCAGGAAA GTATGCAACT GTCCTTTGAT TCTTTTGATC GCATGTTTCC	1500
AAATCAGGAT GTCCTTCCTA AGGGGGGATT TGGAAATTTG ATTGCCTTGC CTTTTC AAGG	1560
AGAAGCTTAC CATCAAGGGC GAACGGTCTT TGTGGATGAA CAGTTTCAGC CTTATGAAGA	1620
CCAATGGAGG TATCTACAAG AAATTCAGAG GATTTCAACT GCTAAAGTGG CACTGTTAAT	1680
CCAAGAGGAG TTAGGCAAGC AAGAATTGGA TAAGGAGTTG AAGGTCGTTT TATCCAATAT	1740
GATCCAACTT GAAAAATCGT CTGTGACATC CAAGGCACTT TTTTCTTGAA AAATATGGCT	1800
TCCTTTTCTA ATCCCGAATT TTATAGTAGA TTGAACTAG AATAGTACAC CTCTGCTTCT	1860
AAAACATTGT TAGAAATCGA TTTGACTTTC CTGATCGATT TGTCTCTGTA TTATTTCAAT	1920
TTACTATATT TAAAGCAGGC TATGCGACAG CCAACCTATC AAATTCCTGA GAGAATGTAT	1980
TTATTTGGAG AATCCGATCA TTATTTATGG TTGCCAAGAG GTTTGCTGTA TCCATTGCAA	2040
GATAAATTTA AGCAGGTATC TGTGGAAGAT AGGAGAAAGG TACAAAGGTC TATTAGCGTG	2100
GAATTTAAGG GAGAACTCAC TTTTGAGCAA GAGTTAGCCC TGTCAGATAT GACTTCTAAA	2160
GAAAATGGTT TACTTCATGC GGAGACTGGT TTTGGGAAGA CCGTTT TAGG TGCTGCTCTT	2220
ATCTCTGAAC GGAAAACAAA AACAATTATT CTAGTCCATA ATAAGCAACT CTTAGACCAA	2280
TGGCTAGATC GCTTAAACTG CTTTTTGACT TTCGAAGAGG AGGAGGCTAT CCGTTATACG	2340
GCATCAGGTC GTGAAAAGGT AATCGGCTAT GTTGGGCAGT ACGGTGGGAC TAAGAAATGG	2400
CTGAGTAAAC TGGTTGATGT CGTTATGATT CAATCTCTAT TTAAGTTGGA AAATAGTCAA	2460
AGTCTTTTGG ATGAGTATGA GATGATGATT GTGGATGAGT GTCATCATGT CTCTGCCTTG	2520
ATGTTTGAAA AAGTTGTTGC TCAGTTTAGA GGGAAGTATC TTTACGGTTT GACGGCTACG	2580
CCTGAGCGTA AGAATGGTCA TGAGCCTATT GTTTTTCAGA GAATTGGTGA GATACTCCAT	2640
ACTGCTGATA AGAGGGAAAC GGATTTTAAA CGGCAATTGC AATTAAGATT CACTTCTTTT	2700
GGTCATTTGG AAATTGAAAA GACCAAAGCA AGTAATTTTA TACAGCTTAG TGATTGGATT	2760
GCTACTGACT CAGTGAGGAA TCAGATGATT CTCAAGGATA TTCTAGCCCA AGTGGCAGAA	2820
GGACGGAATA TCTTGTTTTT AGTTAATCGA ATTCAACAGA TAGATGTCTT TGAAAAATTA	2880
TTGAAAGAGA AAGAGGTTGA TGACTGTTAC ATTATTAGCG GAAAAACCAA AGTCCGAGAG	2940
AGAACGAGTT TACTGGAGAC GTTAGAACAG TTAGATAAAG GGTTTGTTTT GTTGTCTACT	3000
GGAAAATACA TTGGCGAAGG TTTTGACTTA CCTCAGTTGG ACACGCTTAT CTTGGCAGCA	3060

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CCCTTTTCTT GGAAAAATAA TTTGATTTCAG TATGCAGGTC GGATTCATAG AAAC TACAAG      3120
GATAAGTCTT TGGTGCGTAT TTTCGATTAT GTGGATATTC ATGTTCCCTTA TTTAGAAAAAG      3180
ATGTTTCAGA AACGACAAGT AGCTTATCGA AAGATGGATT ATCGTGTCAT CGAGGGTGAG      3240
GAGAAACAAT TCGTTTATGT TGATAGTAGA TATGAGAAGG TGTGAGAGA GGACTTAGCA      3300
GGGGAAAGAC AGGAATGTCT GCTTATTTTA CCTTATGTGC ACCAGACAAA ACTGATGAAT      3360
TTTCTAAAAG AATTTAGGAT TAGTCAAATT GAGATATGTA TACCAGAGAC GGTGCAAAAT      3420
AAAGCATGGC TAGACCAGTT GAAGAGCCAG AAAATTAAAG TGTCTTTTAC TCAATCAAAA      3480
ATAGTAACGC CTATTCTTTT GGTGAATAAG ACTATTGTTT GGATGGTGC AATGCCATTA      3540
TTAGGGAAGG TAGATGAGAT GACCATATTA CGTTTGGAAAT CAGCTAGTAT AGTTTCTGAA      3600
CTAGTGGCAG GTTTCAGATA GAGAAAATTT TTA AAAATTT CTATGTATGA TTTTCATTTC      3660
TTTAGTGAGA CTGTTGCCAT TATCACATTC GAATCACACA AAATAAAAAA A'TTTTATAA      3720
GTACTTGACA AATAGATTGA AATATCATAA AATAAAACG GTTACAGAGT TATTAATTAT      3780
TTAAGCTTCA TGTCACCATT AAAAATTGAA ATAAAAGGAT GTTATCACTA ATACAAGTGA      3840
GCAGGAACCT ATTTAATCAC ATCAGAAGAA GTTCTTGAT GTTTTAAAGT AGGTCCTTT      3900
TATTTTAAAA GGGAAATTTT ATGATCATAA AACGAATACT AAACCACAAT GCCGTAATTG      3960
CGCAAAGTAA AAAAGATATC GATATTCTTC TTTTGGAAAG GGGAATAGCT TTTGGAAGAA      4020
AAACTGGAGA TAAAGTAAAT CCAATTGATA TTGAGAAAAG TTTTTCCTC AAAAAAGAG      4080
ATAATATGAC CCGTTTTACA GAGATGTTTA TTAACGTCC TTTGGAGTTG GTGTACATCA      4140
CCGAAAAAAT AATTAACCTA GGTAAAATAA CATTTGGGTAA TAATTTTGAT GAAATTATCT      4200
ATATTAATTT AACGGATCAT ATTTCTTCGA GCATAGAACG TTATAAAGAA GGGATTATTA      4260
TTTCGAATCC CCTACGCTGG GAAATATCGA AATATTATAA AGAAGAATTT GAACTTGGA      4320
AAAGGGCTTT ACAAATAATA AAAAAAGAGT TAGGTATTGA ACTTCCAATT GACGAAGCTG      4380
CATTCATAGC GCTACATTTT GTTAATGCTA ATTTAGAAAA TAATTTTCAA GAGTCGTATA      4440
AAATCACTGA AATAATTATG GGAATTGAGA AAATCATTCA AGATTTCTAT TGTACTGAGT      4500
TTAACCAAGA TTCTATTGAT TATTATAGAT TCATAACTCA TATGAAATTA TTTGCCCATC      4560
GCTTGGTTGA GAATACAAC TATTGTGACG ATGATGA      4597

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(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

1108

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

CGGCTTATTT ACTACTTGTT CCATCATATA TGGAATATGC ATGAAACCTG CTCTCATATT	60
AGGGAATTTT TTATCCACTA AATAAGAGC TTGGTACATC AAATGATTGC AAACAAAGGT	120
TCCTGCACTA TTGGATACAA CTGCCGGAAG TCCCTGTTTT TTGATAGCTT GTACCATCGC	180
TTTGATAGGT AAACACTATA AATAGGCCGA TGCTCCATCA ATACGAATCG GTGTATCAAT	240
TGGTTGATTG CCTTCGTTAT CAGGTATGCG AGCATCATCT TGATTAATAG CCACTCGTTC	300
AGGTGTTAAG CCGGTCCTGC CGCCTGCTTG TCCAATACAA AGTACAGCAT CTGGTTGATA	360
TCGTAATATT TCTGCCTCTA AAACCTCTGA CGACTTATAA AAAACCGTTG GAATTTCTAC	420
CCAGCGAACT TCAGCCCCAT TAATCTCAGA TGGTAATAAT TTTACAGCCT CCAAAGCTGG	480
ATTAATCTTT TCACCTCCAA AAGGATTAAA ACCTGTAACC AATATTTTCA TTTTATTTTC	540
CTTTACTAAA ATGCGAGAAA GTACATTAAG AATATGTGAA TAACAATCAT TACTAGAGCA	600
ACACCTGCTT GAGCCTTTAT AACGCCATTC TGATCTTTCA TATCCATCAA TGCTGCTGGT	660
AGAGCGTTAA AATTAGCAGC CATTGGGGTC AATAAGGTCC CACAATAACC TGCTGTCATG	720
GCAAGAGCAC CAGCCACAAT TGGATTAGCT CCCAGAGCAA ATACAAAGGG AACTCCAACA	780
CCTGCTGTAA TAACGGTGAA TGCTGCAAAA GCATTTCCCA TAATCATTTG GAATAGAACC	840
ATTCCAAGAA CATAGGCCAA AACTCCTATA AAGCGACTAT CTGAAGGAAC AATACCGCTA	900
ATCAGATGAG AGATAACATC ACCAACACCT GCTACAGTAA AAATAGCCCC CAAAGCCCCCT	960
AATAATTGAG GAACAATCCC ACTTGTTGAA ACTTGCTGAG TCATTCGATT ATTTTCTGAT	1020
AACAGACTCT TAGGGTGAAT ATTGGTAATC ACAAGAACAG AAATTGTAGC AAACAAGGCG	1080
GCAAGGCTAA TCGAAATCTT GCTAAATTCT GGAATCATTT GCGCTAAGAC CAACGCAAGT	1140
ATTGCCATCA GCATAACTGG AATAAAAAAT TTATTTTTC AACTGTTAGA TTCAATATTG	1200
GCTTTCATTT CATCTAAGGA TGGCAAGGTT CCGATACGGA CTTGCTTAAA CAATGTTAAC	1260
AGCGATAATA GGATTACAAT AATACCAATA CTCATATTTG GCATATAGGA ACCACCTATA	1320
AACGTAATAG ACAATAGAGT CCAAAATGCA GATGTCCCAA GTCGAACTGG GTTTGTTTTA	1380
TCTTTATAAC TACAATAGGC TGTATGGAGA AATTGACAAC CAATCACAAT ATAGGTCAAC	1440
TCTAATAGTT GCTTTGCCAA CTCTGTCATT TTTGTTCTCC TCCCCTAGTC TTTTGTGATA	1500
TCAATTTTTT ATCAAATAAA TAATTATAAA TCCCCACTAC AATAAGTGTT ATAACAGCAA	1560
CAATAATAGA TGTAGAAGCA ATCCCTGCAT AATTGCTTTC ATAGCCTAAC TGATCTAATG	1620

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TTCCCCCTAT CAAGAGGACT CCCCCAGCAC CTACAAACGT ATTTTGAGCA AAGAAATTTTC	1680
CAAAATTTTC ATTCGCAGCC GCACGCGCTT TTATTGTCTC ATCTTCAACC TCTGTTAACT	1740
TTCTACCTAA TTGAGACTCT GCAGCTGCTT CTCCCATAGG TTGAACCAAA GGTCTGACAA	1800
ACTGAGGGTG TCCTCCTAGA CGAATTGAAA AGAAACCAGC TAACTCTCGA ATAAAGAAAT	1860
AAACTGTATA GAAGTTTCCA ACTGTCAGAC CTTTAATCTT TCGAATCAAA TCGATTGATC	1920
GTTGCTTGAG TCCAAAGGTT TCTGACAGCC CCACAAGAGG CAAGGTAACC ATAAAAATCG	1980
TGAGCACTCG CTGATTGCTA AATTCCTTTTC CCAAAATCTC CAAAATTC ACGAGAGAAA	2040
CACCTGAAAC TAAAGCTGTA ACCAAACCAG CTAAGACTAC TGTGCAATT GTATCAAATT	2100
TTAAATAAAA ACCCACAACA ATGATTGCTA TTCCTATTAA TCTAATCCAC TCCATATCAA	2160
ACTCCTTTAT ATTCAAAATG ACAGTATTTT TAAATTTTA TCAAGATCAA TACCATTCCCT	2220
TATTTAATGT GTTTTCTAG TTCTTTTGG TATTTGCTAT TGGATTCCAA TTTTCTTTT	2280
TGCCATTTTT TAAAAACCTC GTTATATTCT TTGTTGTAA CAATATCTTT TTGCAATTTTC	2340
ATTCTTTTAA AGATATATGG ATCCCCCTTA ATACCAACTT GTGAGTATGG TTTTGAGAAT	2400
GGTACTACGT TACTTACAAC TGGAGAACCA CCAGATGAAG CTGTTGGCAT CAATAATGAA	2460
CTATCTGTCG ACCAAGCTTG AGCTTTGGCA TATTTTTCAT ATCTTTTCTC TAGGTCAGTG	2520
GTCTCAGAAA CAGCATCTTC TAACAATTTT TTATATTTAT CCAAACCAGG TTTAGCTACA	2580
ACATCCTTAT CTTTTCCTTT CGTAATACCA AGGTGTTTCA TGGCAGAACC AGATTTTGGA	2640
TCTATAATAT TCAAGTGAGA CGCTGGATCT TGATAGCTTG GAGCCCATCC TGTACTGTTC	2700
AAATCATAGT CTTTTTGAGA AGGAGCAACA TTGCCGTATT TATCATTTTC CATCAAACCA	2760
TCAATAACAT TTCCAATAAC GTCTGTCCTC GATGTTGCG TCGCTATACT GTAGCCCAAT	2820
GATGCTGGAT CTACTGCATA GACATAAGAA AATGTTGTCG GTGCATCTGC TTCTTTATCA	2880
GTTTTTCCAC AAGCCACTAA AATAGCTGAC GTGCTCAGGA CCACTCCTGC TGTAAAGAGC	2940
CACCTTTTCT ATTTTCATAA GAATCTCCTT TGGTTTATTT TAATCTACTT TTACAATCCA	3000
ACCTTCTGGC GCTTCAATAT CGCCAACTG AATACCCGTC AATTCATTAT ATAATTTACG	3060
CGTCACAGGA CCTACTTCTG TTTCCTATA GAATACATGG AAATCATCAC CATGTTGAAT	3120
ACCTCCAATT GGAGAAATAA CCGCTGCTGT ACCACAGGCA CCTGCCTCTA CAAAACGGTC	3180
AAGATTATCA ATTGGAACAT CACCCTCAAT AGGAGTTAAT CCCAAGCGAT GTTCTGCCAA	3240
ATAAAGCAAG GAATACTTGG TAATAGATGG CAAGATAGAT GGAATCAATG GTGTTACAAA	3300
TTCAATTATCA GCTGTAATTC CAAAGAAGTT AGCTGATCCG ACTTCTTCAA TCTTTGTATG	3360

1110

AGTTGATGGG TCCAGATAGA TAACATCTGA GAAATGACGT GACTTGGCCA TTTTTCCTGG	3420
TAAGAGACTT GCAGCATAGT TTCCACCAAC CTTAGCCGCA CCTGTACCAT TTGGTGCTGC	3480
ACGGTCGTAC TCATCCTGAA TCAAGAAGTT GGTGGGACC AAACCACCTT TAAAGTAATT	3540
TCCAACGGC ATAGCAAAGA TGGTGAAAAT GTACTCTTCT GCCGGTTTTC CCCCATAAT	3600
ATCTCCGACA CCAATCAAAA GAGGGCGAAG ATATAAGGTT CCACCTGTTC CGTATGGTGG	3660
TACGTATTCT TCATTGCGAC GGACAACTGC TTTACAAGCT TCTACAAACA TGTCTGTCGG	3720
AACTTGTTGGC ATCAAGAGAC GGTCACATGT ACGTTGCAGA CGTTTAGCAT TTTCATCAGG	3780
ACGGAACAGT TGAACACTGC CATCCTTAGT ACGATAAGCT TTCAAACCTT CAAATGCTTG	3840
TTGTCCATAG TGAAGACTTG GAGAAGACTC TGAATATGC AAAGTTGCAT CCTCTGTAAG	3900
CTCTCCTTGA TCCCATTGTC CATTTTTGAA ATGAGCAAGA TAGCGATAAG GTAATTTTCAT	3960
ATAGGAAAAA CCGAGGTTTT CCGG	3984

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8703 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TATCTAATTA TTGGTTTTTA TCGCTGACCT TGGCTATTGT TGGGGTTGTT TTACCCTTGT	60
TGCCTACAAC ACCTTTCCTT TTGTTGTCTA TTGCTTGTTT CTCCAGAAGT TCCAAGCGAT	120
TCGAAGATTG GCTTTATCAT ACCAAGCTCT ATCAAGCATA TGTAGCTGAT TTTCGTGAGA	180
CCAAGTCTAT TCGCGTGAA CGAAAGAAAA AAATCATCGT CTCTATCTAC GTCTTGATGG	240
GAATTTCTAT TTATTTTGCA CCTCTTTTAC CAGTCAAAAT CGGTCTGGGT GCTTTGACCA	300
TCTTTATTAC TTATTATCTC TTCAAGGTCA TTCCAGACAA AGAATAGTTA AAACAGTAGT	360
TATTTGCCTT GATAAAATTG AAAGCATATT CATAACAATA TGATATAATA AAATTGAAGT	420
AATATTCAAG GAGAATCAAA TGATTTACGA ATTTTGTGCT GAAAATGTGA CTTTACTTGA	480
AAAAGCGATG CAGGCTGGAG CTCGTCGGAT TGAAGTCTGT GATAATCTAG CAGTTGGTGG	540
GACAACACCC AGCTATGGAG TGAATAAGGC AGCGGTTGAA CTGGCAGCTA ACTACGATAC	600
AACCATCATG ACCATGATTC GGCCACGTGG TGGTGACTTT GTCTATAATG ACCTAGAAAT	660
TGCTATCATG CTAGAAGACA TTCGTTTGAC TGCTCAGGCT GGAAGTCAAG GGGTTGTATT	720
TGGAGCTTTA ACTGCTGATA AAAAGTTGGA TAAGCCTAAT CTGGAAAAGT TAATTGCTGC	780

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ATCAAAAGGA	ATGGAAATTG	TCTTTCACAT	GGCCTTTGAT	GAAC TAAGTG	ATGAAGATCA	840
AGCGGAAGCT	ATTGACTGGC	TCAGTCAAGC	CGGTGTCAC	TATCCTAA	CTCGTGCTGG	900
TGTGTCTGGC	GACTCCTTAG	AAAAACGTTT	TGTTCACTAT	CACAGAATTT	TGGAGTACGC	960
TAAAGGTAAA	ATTGAAATTC	TACCAGGTGG	GGGGATTGAC	CTTGAAAACC	GTCAAACCTT	1020
TATCGACCAG	GTGGGGGTAA	CACAATTGCA	TGGTACTAAG	GTTGTTTTTT	AAAAAATAGA	1080
AAGGAACTGC	TAGCTTTGGG	TAGCAGTTTT	CACCTATGTT	TGAAATTTTT	AAATCCTATC	1140
AATTTAATCA	AGAAAAGGCT	CATGATTATG	GTTTTATAGA	AAATAGCGAA	GTCTGGACAT	1200
ATAGTTGCCA	GATTTTGCAA	GGTGACTTTG	TCATGACTGT	GTCCATCACT	GCTGATAATG	1260
TGAACTTTCA	AGTCTTTGAC	CAAGAGACTG	GTGACCTCTA	TCCTCACGTT	TATATGGAAA	1320
GCATGAGGGG	AAGTTTGTGC	GGAAATGTCC	GTGAGGCTTG	TCTGGAGATT	CTTTACCAGA	1380
TTCGGAAGCG	TTGTTTGTAT	GTGCAAGATT	TTATCTGTCA	TCAGACTAAG	CGTATCATGA	1440
CTCAAGTTCA	GGAAAAGTAT	GGAAACCAGT	TGGAGTATCT	GTGGGAAAAA	TCGCCTGATA	1500
CAGCTGTATT	GCGCCATGAA	GGCAATCAAA	AGTGGTATGC	CGTCTTGATG	AAAATCTCTT	1560
GGAATAAGCT	GGAAAAGGGC	AGAGAAGGAC	AAGTGAAGC	AGTCAACCTC	AAGCATGACC	1620
AAGTAGCTAA	TTTGCTTTCA	CAAAAGGGGA	TTTATCCAGC	CTTCCATATG	AGCAAGCGCT	1680
ACTGGATTAG	TGTGTCCCTT	GATGATACTT	TATCAGATGA	AGAAGTACTG	GAATTGATAG	1740
AAAAAAGTTG	GAAC TTAACC	TCTAAAAAAT	GAAATATTTT	AATAATTTTC	ATGAACTTTC	1800
AATTAGCTAA	ATATTCTTTA	CTGAAGAGAT	TTTTAGAAAA	TATAGGATTT	ACCACACTAG	1860
AGGAATATGG	TGCCATCTTC	AAATACCTGA	TTGAGAATGT	CAAGACGGAT	CGTCAGATCA	1920
TCTATTCGCC	TCACTGTCAT	GATGACCTCG	GAATGGCAGT	GGCAAATAGC	CTTGCTGCTG	1980
TCAAGAATGG	TGCAGGACGT	GTTGAAGGGA	CTATCAATGG	TATTAGGGAG	CGAGCTGAAA	2040
ATGCTGCTTT	GGAAGAAATT	GCAGTGGCTC	TCAATATTCG	CCAAGATTAC	TACCAAGTAG	2100
AAACCAGTAT	TGTCCTAAAT	GAGACCATCA	ATACGTCAGA	AATGGTTTCT	CGCTTCTCTG	2160
GTATTCCAGT	TCCTAAAAAC	AAAGCCGTCG	TTGGTGGCAA	TACCTTCTCC	CACGAATCTG	2220
GTATTCACCA	AGATGGAGTC	CTTAAAAATC	CTCTCACTTA	TGAGATCATC	ACACCTGAAT	2280
TGGTTGGTGT	TAAGATTCTG	CTTGAAAAAT	TATCTGGTCG	CCATGCTTTT	GTTGAGAAAC	2340
TGAGAGAATT	GGCCCTAGAT	TTTACAGAAG	AGGATATCAA	ACCACTCTTT	GCTAAGTTCA	2400
AGGCACTGGT	CGATAAGAAG	CAAGAAATCA	CAGATGCAGA	TATTCGAGCT	TTGGTAGCTG	2460
GAACCATGGT	TGAAAATCCA	GAAGGCTTCC	ACTTTGATGA	TTTACAACCT	CAAACCTCATG	2520

1112						
CAGATAATGA	CATTGAAGCG	CTCGTTAGCC	TAGCCAATAT	GGATGGTGAG	AAAGTCGAAT	2580
TTAATGCGAC	AGGGCAAGGT	TCCGTTGAAG	CAATCTTTAA	TGCTATCGAT	AAGTTCTTTA	2640
ACCAATCTGT	TCGTTTGGTG	TCCTACACTA	TCGATGCGGT	AACAGATGGA	ATCGATACCC	2700
AGGATCGGGT	TTTGGTCACT	GTTGAAAACA	GAGATACAGA	AACCATCTTT	AATGCAGCAG	2760
GGCTTGATTT	TGATGTGTG	AAGGCTTCTG	CTATTGTCTA	TATAAACGCT	AATACCTTTG	2820
TTCAAAAAGA	GAATGCAGGT	GAGATGGGAC	GCAGTGTTTC	TTACCACGAT	ATGCCTAGTG	2880
TGTAAGGAG	AAGGCTATGG	CAAAGAAAAT	AGTAGCTCTA	GCAGGAGACG	GAATTGGCCC	2940
AGAAATCATG	GAGGTTGGTT	TAGAAGTTCT	GGAGGCTCTA	GCTGAAAAAA	CAGGTTTGA	3000
CTATGAGATT	GACAGACGAC	CGTTCGGAGG	TGCAGATATT	GATGCAGCAT	GACCTCCCTT	3060
ACCTGATGAA	ACCCTTAAGG	CAAGTAGGGA	AGCAGATGCT	ATCCTACTAG	TAGCTATCGG	3120
TAGTCCTCAG	TATGATGGAG	CAGTGGTTCG	CCCTGAACAA	GGCCTGATGG	CTCTCCGTAA	3180
GGAACTCAAT	CTTTACGCTA	ATATTCGTCC	TGTAAAAATC	TTTGACAGTC	TCAAGCATTT	3240
GTCACCACTC	AAACTGGAAC	GAATTGCTGG	TGTAGACTTT	GTCGTGGTGC	GTGAATTGAC	3300
AGGCGGGATT	TACTTTGGAT	ATCATATTCT	TGAAGAGCGC	AATGCGCGTG	ATATCAACGA	3360
CTATAGCTAT	GAGGAAGTGG	AGCGGATTAT	TCGCAAAGCC	TTTGAAATTG	CAAGAAATCG	3420
CAGAAAAATC	GTTACTAGTA	TCGATAAGCA	AAATGTTCTA	GCGACCTCAA	AACTCTGGCG	3480
GAAAGTAGCT	GAGGAAGTCG	CACAGGATTT	CCCAGATGTA	ACCTTGGAAC	ATCAGCTGGT	3540
AGACTCAGCT	GCTATGCTTA	TGATTACCAA	TCCTGCTAAG	TTTGATGTTA	TTGTAACGGA	3600
GAATCTTTTT	GGAGATATTT	TATCTGATGA	ATCAAGCGTC	TTATCTGGTA	CACTTGGGGT	3660
TATGCCATCA	GCCAGTCATT	CTGAAAATGG	ACCAAGTCTC	TATGAACCTA	TTCACGGTTC	3720
AGCACCTGAT	ATTGCAGGTC	AAGGAATTGC	CAATCCTATT	TCCATGATTT	TATCAGTTTC	3780
CATGATGTTG	AGAGATAGTT	TCGGACGTTA	TGAGGATGCA	GAGCGTATCA	AACGTGCTGT	3840
TGAGACAAGT	CTGGCGGCAG	GAATTTTAAC	GAGAGATATA	GGAGGTCAGG	CTTCAACAAA	3900
GGAAATGACG	GAAGCTATTA	TTGCAAGGTT	ATGAAGTTAG	ACGAAAAAAT	TACTCTAGTC	3960
CTTTTGATTT	GGAATGTCAT	CATTTTCTTG	ATTTATGGTA	TTGACAAATC	TAAGGCAAGG	4020
AGAAGAGTTT	GGCGCATCCC	TGAGAAAATC	TTACTTATTT	TAGCCTTTAC	TTTTGGTGGT	4080
TTTGGTGCCT	GGCTAGCAGG	AATCATCTTT	CACCACAAGA	CTCGAAAATG	GTACTTTAAA	4140
ATAGTTTGGT	TTCTTGGGAT	GGTGACCACA	CTAGTAGCCT	TATATTTTAT	TTGGAGGTAA	4200
TGGATGGCAG	GGTCTTCGAG	GGAATACGCT	GCTTGGGCTC	TAGCGGACTA	TGGTTTAAAG	4260
GTCGTGATTG	CAGGATCTTT	CGGTGACATT	CATTACAATA	ATGAACCTAA	TAATGGCATG	4320

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TTGCCAATCG	TTCAGCCTAG	AGAGGTTAGA	GAGAACTAG	CCCAGCTAAA	ACCAACCGAC	4380
CAGGTAAC TG	TGGACTTGGA	ACAACAAAA	ATCATCTCAC	CAGTTGAAGA	ATTCACCTTC	4440
GAGATAGATA	GCGAGTGGAA	ACATAAACTC	CTAAATAGTT	TGGATGATAT	CGGTATTACC	4500
TTGCAGTATG	AAGAGTTGAT	TGCTGCTTAT	GAAAAACAAC	GACCAGCCTA	CTGGCAGGAT	4560
TAGAAAAAAT	AGAAAAGGAG	ATATAGTAAA	CTGAAATAAG	ATGTAAACAA	ATGAATTGGA	4620
GCTTAACATC	CATTTCCAGC	AATTTT TTAG	AACTACAGT	GGACTATTCT	GGATTCAACA	4680
CATTATAAAA	TTATGACAAA	ACACATTCAC	AAGAAGGCTA	CGACATTTTA	AAAGGTGAGG	4740
GCGGATGTAT	CGTTTGCCCT	ACTAAAGTTG	GTTACATTAT	CATGACCAGT	GACAAGGCAG	4800
GACTTGAGCG	TAAGTTCGCA	GCCAAAGAAC	GTAAGCGTAA	CAAACCAGGT	GTTGTTCTCT	4860
GCGGTAGCAT	GGATGAACTT	TGCGCTTTAG	CGCAACTCAA	CCCAGAAATT	GAAGCATTCT	4920
ACTAAAAACA	TTGGGATGAA	GATATTCTTC	TTGGTTGTAT	CCTTCCTTGG	AAACCAGAAG	4980
CCTTTGAAAA	ACTCAAAGCA	TACGGGGATG	GCCGTGAAGA	ACTTATTACT	GATGTACGTG	5040
GTAAGTAGCTG	TTTTGTTATC	AAGTTTGGA	AAGCAGGTGA	ACAATTGGCT	GCCAAGCTTT	5100
GGGAAGAAGG	TAAAATGGTC	TACGCCTCAT	CTGCTTCAAT	GACAAAACGA	TTGAAACTCG	5160
CTATGAGCAA	GGTGTAATGG	TGTCTATGGT	CGATAAGGAC	GGCAAAC TCA	TCCCAGAACA	5220
AGGAGGAGCA	CGTTCAACTT	CACCAGCTCC	AGTTGTGATC	CGTAAAGGGC	TTGACATTGA	5280
TAAAATCATG	ATGCACCTGT	CAGATACTTT	TAACTCATGG	GACTACCGTC	AGGTTGAGTA	5340
TTATTAGGAT	AGAGAAGAAG	TCTAGTGTTA	TGAGATATTA	AAGCTCCTAA	CACTGGGCTT	5400
TTGTTTAGAA	TTTCTTTTCT	TTTTCTATAG	GATATGGTAT	TCTATGTAGA	AAATATATGT	5460
TAATAAGTAA	TGCCAATATT	TAAACATCAT	TAGTAAAAGG	AGTTAGATTG	ATGAATAAAA	5520
GAAAAGTTAG	TTTAGAAGAT	TTTTATAAAT	GGTATAGTCT	AAATAAAGAA	GAGTTATTAA	5580
ATAAGGCAAC	TGTTGGTGAA	AAGTTTAATG	ATAAATTAAA	AGAAGAGTTT	CTCCAGGAAT	5640
GGCCTTTGGA	TAGGATTTTA	ACAATGTCAA	TCGATGAATA	TGTAATAGGA	AAGGGACAGC	5700
AAAATAAGTC	TTTATGCTAC	GCTCTTGAGA	AGGGAAAATA	CAAAAATCTA	TTTCTTGGA	5760
TTTCTGGTGG	CTCAGCTTCA	AAATTTGGTA	TTTATTGGAA	TAAAAAACA	AACAAATATA	5820
AAGATCAAGC	TAATAATGAG	ATTTCAGAGT	TGGATCAGCG	ATTTTCAAAA	TTAAAATCAG	5880
ATTTGTATGA	AATTATCAAA	GAAGGTATTC	GTTTTAACTT	TGAAAATCCT	ATTTTGTGATA	5940
TGAAAAGATC	AACAAATGAA	TTTATTGGTC	GTTCTGCTAT	GGTGACAAAA	TTACTTTGTA	6000
TCTATACTGA	GGGAGATCCT	TTCTTTGGTG	TAAATATTAA	TAGTCAGAAA	GAATTTTGGA	6060

1114

ACCACTTTTGT TTCTCAGACA AATCAAGGTG GACCTTATCT GCAAAATCAT AAAATAATTG	6120
AACTGGTGTC CAAAACCTAT CCTGAGTTGG AGCCATCGAA ATTAGGAACT ATGCTTTTTG	6180
AGTATTCTAA GCTTTTATG GAAAATAAGG AAGACAATAG TACAATGGAT TCATCAAACA	6240
ATTTTCGTCA TCAATTAACCT CAATCTCTAT TAAAGTCTCC AAACCTCATC CTCCGCGGTG	6300
CTCCTGGCAC GGGAAAACT TATCTTGCTA AAGAAATTGC TAAAGAATTA ACGGATGGCA	6360
ACGAAGATCA AATCGGATTT GTACAATTC ACCCATCATA TGATTATACG GATTTTGTAG	6420
AAGGTTTAAG ACCAGTATCA AATGGGGATG GAGCTATGA GTTTAGGCTA CAGGACGGTA	6480
TTTTTAAAGA TTTTGTCTAG AAAGCAAAAG AAACCCAATT GATTGGAGGA CAAGATAATT	6540
TTGATGAGGC TTGGGATTCT TACTTAGAAT ATATAAATGT TGCTGAAGAA AAAGAATATA	6600
TAACAAAAAC ATCTTACTTA TCTGTTAATA GTAGACAAAA TTTGTCTAGTA AATTATGATA	6660
GTGGTGTTCC AGGATGGTCA CTACCTAGCA AATATGTTTA CGAGTTGTAT AAAGATAAAA	6720
ATTATAATAA GCAAGAATAC TACAAAAGTG GTGAAAAAAC TGTCTAGAA ACATTGAGAA	6780
AGAGATTTGG TTGAAAGAC TATGTTTCCC CAACAGAAAT TGATACTGAT AAGAATTTTG	6840
TCTTCATCAT CGATGAGATC AATCGTGGGG AGATTTCTAA GATTTTTGGC GAACTCTTTT	6900
TCTCTATCGA CCCCGGCTAT CGTGGTGAAA AAGGAAGTGT TTCTACCCAA TATGCAAATC	6960
TACACGAAAC TGATGAAAAG TTCTATATCC CCGAAAATGT TTACATCATC GGAACATGA	7020
ATGATATTGA TCGTTCAGTG GATACCTTTG ATTTTGCTAT GCGTCGTCGT TTTCGTTTTG	7080
TTGAAGTTAC TGTCGAGGGT CAAGCTGGCA TGTGGATAA AGAGTTGAAT ATCCATGCAG	7140
AAGAAGCAAA AATTCGTCTA AGAACTTGA ACGCTGCTAT CGAAAATATT CAGGAATTAA	7200
ACAGTCATTA TCATATTGGA CCAAGTTATT TTCTTAAGTT GAAGGATGTA GATTTTGACT	7260
ATGAATTACT CTGGTCTGAT TATATTAAGC CTCTCCTAGA AGACTACTTG CGAGGTCTTT	7320
ATGATGAGGT TGAAACTTTG GAaACTTTGA AAAAAGCATT TGATCTGACA AATAATGAGC	7380
AAAAAGATCA GGCAGTAGCT GATGACAATG AAGGCGATGA AAACGATGAT GCGGATTACT	7440
GATAATCAAC ACAAGATTAT TAAAGAAAAA TTTGTTGAAG AATATCCTAA ACTAAGCAAT	7500
CCTCTTTTAG ACAGAACCTT GGAAAGTCTA TCCCAAGATG AACGTATTTT CATTTTTCCTA	7560
AATGATTwGA CTCATACTCC TGATTTGGAT AAGGACCAA AGATTTTGA AACAGTCAAT	7620
CAGAAAATCA AGACAGGGAA CGTGATTGGT TTTCTTGGAT ATGGTCAGGA AAGATTAACG	7680
ATTTCTCTAC GATTTTCTGA TGAGAGTAAT GACCACTTT TGCATTATCT CTTAAACAAG	7740
GTTCTTCATA TCAATCTCAC TAGTTTAGAT GTTGCTTTGT CTCGTGAAGA GAGGCTTTAT	7800
CAACTTTTGG TGTATCTCTT TCCCAAGTAT CTACAAGCTG CTATTCGAAA AGGTCTTTAT	7860

1115

AAGGAATATC ATCGATTTTC TCATAACGAC AGTCATGTTA AGGGAGTGAT TGATGTAAGA	7920
AACCATCTCA AGAAAAATCT TCCTTTCACG GGAAATATTG CCTACGCAAC GAGAGAGTTC	7980
ACCTATGATA ATCCCCTCAT GCAGTTGGTC CGTCACACTA TTGAATACAT TAAGAATCAG	8040
AAAAGCATTG GTCAAGGGGT ACTAGATAAT CTCTCAACTA GTCGTGAAAA CGTATCTGAA	8100
ATCGTGCGTG TAACGCCCTC TTATAAACTA GCTGATCGTG CTAAGATTAT TCGGGGAAAT	8160
CAATCTAAAC CTATACGTCA TGCATACTTT CACGAGTACA GAAACTTACA AGAACTTTGT	8220
CTGATGATCC TAAACCAAGA AAAGCACGGT TTAGGGTATC AAGATCAAAA AATCTATGGT	8280
ATTCTCTTTG ATGTTGCCTG GCTTTGGGAA GAGTATGTTT ACACCTTGTT GCCAAAAGGT	8340
TTTGTACATC CCAGAAATAA GGATAAGACG GATGGAATTT CAGTATTTTC TGTGGGAAA	8400
CGAAAAGTAT ATCCAGATTT TTATGACAGA GAACGAAAGA TTGTTCTAGA TGCAAAATAT	8460
AAAAAAGTGG AATTGACTGA AAAAGGAATC AACCGTGAGG ACTTATTTCCA GCTGATTTCC	8520
TATTCTTATA TTTTAAAAGC TGAGAAGGCT GGACTGATTT TTCCTAGTAT GGAGCAGTCA	8580
GTAAATAGTG AAATAGGAAA AGTAGCTGGC TATGGAGCTC AATTGAAGAA GTGGTCTATT	8640
CGAATCCCTC AGAATGCCTC ATTCTATAGT ACATTTTGTA AAATGATGGA AAATTCAGAA	8700
GAG	8703

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

CATCACCAGT TTTAGATGGC TTAAACAGTG AAATTATTGC TTTTAATCTT TCTTGTTTCG	60
CTAATTTAGA ACAAGTACAA ACAATGTTGG AACAGGCATT CAAAGAGAAG CACTACGAGA	120
ATACGATTCT CCATAGTGAC CAAGGCTGGC AATATCAACA CGATTCTTAT CATCGGTTCC	180
TAGAGAGTAA GGGAATTCAA GCATCCATGT CACGTAAGGG CAACAGCCAA GACAACGGTA	240
GGATGGAATC TTTCTTTGGC ATTTTAAAT CCGAAATGTT TTATGGCTAT GAGAAAACAT	300
TTAAATCACT TAACCAATTG GAACAAGCCA TTATAGACTA TATTGATTAT TACAACAATA	360
AGAAAATTAA GATAAACTA AAAGGACTTA GTCCTGTGCA GTACAGAACT AAATCCTTTG	420
GATAAATTAT TTGTCTAACT GTTTGGGGC AGTACACAAG AAAGCGCTT AAAACAGTA	480

1116

GACCTTTTCA	TAAGGTTTCGC	TTGATGTACC	AAGATGAGGC	TGGTTTCGGT	AGAATCAGTA	540
AACTGGGATC	TTGTTGGTCT	CCAATAGGAG	TAGGTCCACA	TGTCCATAGT	CACTATATAC	600
GAGAATTTTCG	CTATTGTTAT	GGAGCTGTTG	ATGCCCATAC	AGGCGAATCA	TTTTTCTTAA	660
TAGCTGGTGG	ATGTAATACT	GAGTGGATGA	ACGCCTTTTT	AGAAGAGCTT	TCACAAGCTT	720
ATCCAGATGA	TTATCTTTTA	CTCGTTATGG	ACAATGCTAT	ATGGCATAAA	TCAAGTACCT	780
TAAAGATTCC	GACTAATATT	GGTTTTACCT	TTATTCCTCC	ATACACACCA	GAGATGAACC	840
CATTGAACAA	GTGTGGAAAG	AGATTCGTAA	ACGTGGATTT	AAGAATAAAG	CCTTTCGAAC	900
TTTGGAAGAT	GTCATGAATC	AACTCCAAGA	TGTCATACAA	GGATTGGAGA	AGGAGGTGAT	960
AAAGTCCATC	GTAAATCGGA	GATGGACTAG	AATGCTTTTT	GAAAACAGAT	GAGTATAAAA	1020
TTGAATTGCT	TATAAAAAAG	CTCCATACAC	TGGATGTGTA	TAGAGCAATG	GGGCTTTATT	1080
TGATATAGAG	TTCTTGGTTT	TTTAGGACAA	TTTCTCGGAT	ACTTGCAAAC	TTTTTAAGTT	1140
TTTTGATTTT	TTCTGGATGA	GTGACGAGAG	TGATAACATA	ACCTTCCTTG	CCCATACGAC	1200
CAGTACGGCC	AGCACGGTGT	GTGTAGGTTT	CGCTATCTCT	AGGAATATCA	AAGTTTACGA	1260
CACATTCTAG	GCTATCGATA	TCAATTCCAC	GAGCCAAAAG	GTCAGTTGCA	AGAAGCAGGG	1320
TTAGTTGGTT	ATCTTTAAAC	TTTTCTAAGA	TGATTTTTCT	AAATTTAACA	TTAACATCAC	1380
TAGCGAGGGA	AACAGCCAAT	ATATCACGAT	ACTGTAGTTT	TCCTCGGCA	TTCCCAAGGT	1440
CTGACAGGCT	ATTGAAGAAG	ACTAGACCAC	GGAAATCCTC	TACATGAGCC	AGTTTTCGTA	1500
GCATATCCAC	TCGATGACGT	TGGTCTACCT	GCATGTAGAA	ATGCTGGATA	TTGTCCAATT	1560
TTTGATCAGA	GAGATCAATA	GTGCGTGTAT	TCGGCACAAT	CTTTTCTTGG	TCAAAC TTGG	1620
TCGTGGCACT	CATGTAGACC	AGTTGGTGGT	CACGAGGTGC	GTAGTGAGTG	ATTTTTTCTA	1680
CAAAGTGAAT	CTGAGAATCA	TCTAGTAATT	GGTCAAATTC	ATCCAGGATG	ATGGTTTCCA	1740
CATTCAATCAT	CTTGATTTTT	TTAAGTTTAA	TGAGTTCAAA	GATACGGCCA	GGAGTTCCAA	1800
TCAGAATTTT	TGGCCCTTTT	TTAAGACGTT	CAATTTGTCT	TTTCTGACTT	GAACCTGAAA	1860
GGAAGAGTTG	AGCAGTCAAT	CCGATAGCTT	CTGCCCACGT	TTTACATACA	TCAAAAATCT	1920
GTCCAGCAAG	TTCCGTATTT	GGTGCTAGAA	TCAAGAGTTG	TTGGGCTTTT	TTCTTTTGTA	1980
GTCTGAGAAG	ACTTGGTAGG	AGATACGCTA	GGGTCTTACC	AGTTCCGGTT	TGGCTCACTC	2040
CTAGGAGGTT	TTCTCCAGCA	AGAAGGGGCT	CAAATAGTTG	AGTTTGAATG	GGGGTGAATT	2100
CTTGGAACCC	GAGTTGGTCA	CTCAGTTCTT	GCCATTCACT	CGGTAGTTTG	GTTTTCATTT	2160
TTCTGCCTCA	AATCTAATGC	CAGCAGTCTG	GCGCATGGTA	TATAGTAGCT	CATGAACAGA	2220
GCCTGCATCA	TACAGCCAAG	TTTGGTAGAG	ATTCAGATCT	GGTTGCTGGA	TCATGTGTGC	2280

1117

AAATGCAGCG	ACTTCCTCAG	TCATCGTATG	AGGAGCCTGT	TGGATAGGAA	GCTGGACTTG	2340
ATTTCCCTTG	TGGTCGGTAA	AAATAGCTGA	GCGAATATGC	TCAATCGTGT	TGAGAGTCAA	2400
GGTTCCATCT	GTTGTATAAA	TCTCGCAAGG	AAGATTGGAA	GTGATGTTTT	TTCCAGCCTT	2460
GATGTGAACT	TGATAGTCTG	GGTAGAAGAG	GATACCATCT	CCATTTAGGT	CAATGCTATT	2520
GTCAAGCTGT	TGAGCATGGT	AAGTCGCGTC	ATTGGCTTTT	CCAAAAAGAC	GAACAGCAGC	2580
ATAGAGGGGA	TAAATCCCCA	AATCCATGAG	GGCTCCACCA	GCAAAACGGT	CTGAAAAGAC	2640
ATTTGGTGTT	TGTCCAGCCA	ACAAGTCAGG	CATCTTGGAA	GAGTATTTGG	CATAGTTGAA	2700
ATCTGCTCCT	AACACTTGCT	TATCTGCTAA	AAAGTTTTTG	ATAGTAGTAA	AGGCTTTCTC	2760
GTGGTAATTA	CGAGCTGCTT	CAAAGATAAA	ACAGTTATTT	TTTTCAGCTG	TTTGAATCAA	2820
ATCAAACCAT	TCTTGTGGTT	GAGAGACAGC	TGGCTTTTCG	AGAATAACAT	GTTTACCAGC	2880
AGACAAGGCA	GCTTTTGCCCT	GAGCAAAATG	TAAGGAGTTT	GGACTGGCGA	TATAGACTAA	2940
ATCAAAGAA	GATTTGAAGA	AGACTTCTAA	TTGATCGAAT	AGTTGGATAT	TCTGATAGCG	3000
AGAAGCAAAG	GTGCTGCAG	TTTCTAGTTT	TCTAGAATAG	ATTGCGACCA	GTTGGTATTC	3060
TCCACTGGTA	TGGCTGCTT	CTATGAAATG	ATGGCTGATA	GCGCCAGTTC	CGATGACACC	3120
TAATTTTAGC	ATAAATACTC	CTTTTCCGAT	TTTAAATCCT	TCTTTCATTA	TAACATAGAT	3180
AGACGGGACT	ATCCAACAGA	GAGGAGAAAA	TTTCAAATAA	GCTATTAGCT	TTCTTTTCCG	3240
AATAAATAGA	TAGAAGCATA	GAATCTAGCA	AACCTAGATT	TAAAAATGTG	CTATAATAGA	3300
AGGAGGAAAA	GGAGGATTCT	CAGACATCTA	GGTATCAGCC	CAACTAATGA	TTTGTCAATT	3360
TATCCGCGAT	ATGCTGGACT	TGCCAGCAAA	AAATGTGACG	ATTTTGGAGG	GAAGTAACAT	3420
TCACGTCTTG	CCTTCCATGC	CCTACTCAGC	GTAAGATTTC	TATACTAGTA	TAGACGTCTT	3480
GGCGGAGTTA	GATAATGGAA	TCCAAGTTAT	CATCGAAATT	CAGGTTCATC	ATCAGAATTT	3540
TTTCATCAAT	CGCCTATGGC	CTTATCTGTG	CAGTCAGGTT	AATCAAAACC	TAGAAAAAAT	3600
TCGCCAACGT	GAAGGTGATA	CCCACCAGAG	CTACAAACAA	ATCGCACTAG	TATACGCTAT	3660
CGCAATTGTC	GATAGTAATT	ACTTCTCAGA	TGACCTAGCT	TTTCATAGTT	TTATAGTAAA	3720
ATGAAATGAG	AACAGGACAA	ATCGATCAGG	ACAGTCAAAT	CGATTTCTAA	CAATGTTTTA	3780
GAAGTATAGG	TCTACTATTC	TAGCTTCAAT	CTACTAGAAA	TTCCATAGAT	AGAAAACTAC	3840
ATAATCTCTA	CAGATACGGA	TGTTGGAGTT	GATGTAAGAT	GCTTTGGCTT	GCTAGAGGAA	3900
TTGTGGATTG	CCAAATTGTA	TCATTGAAAT	TATTGCTCAA	ATTTGTTATG	ATATAAATAT	3960
GAATAAAAGT	AGACTAGGAC	GTGGCAGACA	CGGGAAAACG	AGACATGTAT	TATTGGCTTT	4020

1118

GATTGGTATT TTAGCAATTT CTATTTGCCT ATTAGGCGGA TTTATTGCTT TTAAGATCTA	4080
CCAGCAAAAA AGTTTTGAGC AAAAGATTGA ATCGCTCAAA AAAGAGAAAG ATGATCAATT	4140
GAGTGAGGGA AATCAGAAGG AGCATTTTCG TCAGGGGCAA GCCGAAGTGA TTGCCTATTA	4200
TCCTCTCCAA GGGGAGAAAG TGATTTCCCTC TGTTAGGGAG CTGATAAATC AAGATGTTAA	4260
GGACAAGCTA GAAAGTAAGG ACAATCTTGT TTTCTACTAT ACAGAGCAAG AAGAGTCAGG	4320
TTTAAAGGGA GTCGTTAATC GTAATGTGAC CAAACAAATC TATGATTTAG TTGCTTTTAA	4380
GATTGAAGAG ACTGAAAAGA CCAGTCTAGG AAAGGTTTAC TTAACAGAAG ATGGGCAACC	4440
TTTTTACTT GACCAACTGT TTTCAGATGC TAGTAAGGCT AAGGAACAGC TGATAAAAGA	4500
GTTGACCTCC TTCATAGAGG ATAAAAAAT AGAGCAAGAC CAGAGTGAGC AGATTGTAAA	4560
AAACTTCTCT GACCAAGACT TGTCTGCATG GAATTTTGAT TACAAGGATA GTCAGATTAT	4620
CCTTTATCCA AGTCCTGTGG TTGAAAATTT AGAAGAGATA GCCTTGCCAG TATCTGCTTT	4680
CTTTGATGTT ATCCAATCTT CGTACTTACT CGAAAAAGAT GCGGCCTTGT ACCAATCTTA	4740
CTTTGATAAG AAACATCAAA AAGTTGTCGC TCTAACCTTT GATGATGGTC CAAATCCAGC	4800
AACGACCCCG CAGGTATTAG AGACCCTAGC TAAATATGAT ATTACAAGCG GGGT	4854

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TAAACAGGTG TTAGGTGCTC TAACTATTA AAATTCTAAG GAAATAAGGC TACTTTTTCT	60
GGGTCTTGTT CATAGTAGGT GTGGTTCTTT TTTTCGAGTG TAGCCCATAG CTTTGAGCGC	120
ATAGTGGATG GTAGTTGGAT GACAGCCAAA TTCAGAAGCT ATTTTCAGTCA AATAAGCAAC	180
TGGATTGTCA GTAAGATAGT TTTTAAGTCT ATCTCTATCA ACTTTTCTTG GTTTTGTTCC	240
TTTTTACTTG TGGTTTAGCT CTCCTGTTTT CTCTTTTAGC TTTAACCAGC CATAAATGGT	300
ATTACGTGAG ATTTGGAAAA CGTGTGATGC TTCTGTTATA CTACCTGTTC GCTCACAATA	360
AGAGAGAACT TTTTACGAA AATCTATTGA ATATGCCATA AGAAGATTAT ACCACATTGT	420
GTACTATTTT TGGTTCATTT TACTATATTT CTTAACACTT AGAAATAATA AAACAAATTA	480
AATATTATTT CTAAATATTT GAAAATAACA TCTATTTGTA TTATACTATC TTTGAGGTAA	540
CTATTATGAA CTATATCAAA AGACCACATT ATTTAGATTT TTTAAGAAAA CATCGTGACC	600

1119

GACCAATCAT CAAAGTTGTG AGTGGAGTTA GACGAGCTGG TAAATCTGTG CTTTTTCAAC	660
TCTATAAAGA GGAGTTACTA GCAACTGGGG TAGACGAGGA TCAGATTATA TTCATCAATT	720
TCGAAGATTT GAGTTACTAT GATCTGCGAC ATTTTCAAAC ATTATTCGCT TATATAAAAG	780
ATCAATTAGT TAGCAAGAAA ACATACTATA TCTTTTTAGA TGAAATTCAA TATGTTGAAA	840
AATTTGAACT GGTAGCAGAT AGTCTATTCA TCTTAGCAAA TGTAGACCTC TATTTGACTG	900
GATCTAACGC CTACTTTATG AGTAGCCAAT TAGCAACAAA CTTGACTGGT CGGTATGTTG	960
AGATAGAGGT TCTTCCTTTG TCATTTGAAG AATATCTATC AGGTCAATCT CTCACAGAGA	1020
ATCTGAATAC AACAGAAATT TTAAACAATT ATCTCTTTAG TGCTTTCCCT TACTTATTGC	1080
AAACATCATC TTACGATGAA AAAATTGACT ATCTCAGAGG AATATATAAC TCCATACTGT	1140
TAAATGATAT TGTCACTAGA TTGGGAAAAC CAAATCCTAC TATTATTGAG CGCATTGTCC	1200
GAACCCCTCT CAGTAGTACA GGTAGCTTAA TATCAACAAA TAAGATTGCG AATACCCTAG	1260
TCAGCCAAAA TGTTTCAATA TCCATAATA CTTTGAAAA TTATTTGACA ACTTTGACAG	1320
ATAGTTTACT TTTTATTCC GTTCCACGTT TTGATGTAAA AGGTAGAGCA TTATTGCAAC	1380
GTTTAGAAAA ATATTATCCC GTTGATTAG GTTTACGACA TCTCTTATTA CCAGACCAGA	1440
AAGAAGACAT TAGGCATATC TTGGAAAATA TGGTATATTT GGAATTGAGA CGTAGATATT	1500
CACAAGTATA TGTTGGTAAT TTAGATAAGT ATGAGGTTGA TTTTGTGTGT GTAACGTATC	1560
TTGGCCACTA CGCTTATTAT CAGGTCACTG AAACAACACT TGCTCCAGAA AACTAGAAA	1620
GAGAACTTAG ACCACTAGAA GCCATTAAAG ATCAATTCCC TAAATATCTA TTAACAATGG	1680
ATACGATTCA GCCAACAGCC AATTACAATG GAATCGAGAA GAAAAGCATT ATAGATTGGT	1740
TACTAGAAAA ATAGATAAAT ATAAATCATA CAGCTAATTA GATTTGCAAC AGTCTGTTAT	1800
CAATGATTCT ACCCAAATCC TAACAAGATA TAGTGAATTT CGAATACGCT ATATAATACG	1860
GACACTTGAA AATAGAAATT GGGGATGAAA GGGGATCTAT AATTTCTGGA AGTACTATCA	1920
AAAATTAATA TCATAGTCTT ATTAGAGAAT AGCATCACCC ACTTTCTCAA ATAAGATTAA	1980
ATTGTAAC TG AATTATAATG AAAAAGAGAC TGAGCAATCA GTCTTTAAAA TCAGAAAAGC	2040
GCATAGTATC AGGTATTGAA CAACCTTGAT AATATGCGTT TTATTATGGA AATATTTGCT	2100
TCATTTTCTC CTGAAATAGA GCTTTTGCTA TCCTATTTT CTCTATTCT AATGATTTAC	2160
TTCAACTTCT TACCTCTTGG GAAAAA	2186

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3236 base pairs

1120

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GTCACACGTT TGACTTCACG TATTTTCATAA GTATAAACTT TATTTTTATC GGTAGATAA	60
ATCTTCATGC CATTTTTAGC ATTATCTAAA GGAGAAAATA ACATTTTATT AGCATTATCA	120
ACACCAAAGA TATGGTGACT AGCTAGACTA TAATTTTCCTT CTCCCATTAC TTGCTCGCGT	180
TTCATTGTAC CAGCTCCGTA GAAGAGATTA ACATTATCAA GTCCTTTAAA AATCGGCAAA	240
TTCATTTCCA ATTCAGGAAT TGCAATTCCC CCAATAACTG GTAATTTTGT AGCATCCCAT	300
TGAGAAGTTA GAACAGCTTC CGAAGAGATA GCTTTGACAG AATCAAAGTC AAAATTGCCT	360
TCTGTATCCT GATTTTCTTC TAATTTTCTT TTTGATACCT GGCTAACTTG ATACTTATTG	420
GTATTCCAGA CTATGAAAAT ATTTTGAATT TGAGTATTAA AAATCAAAGC CAGTGACAGT	480
AATATCAGAA ATCCTGCTAG GATATTTGTC AGCAGATTTT TTCGCTTGTT TTTCTTTTTA	540
TTATTTTITT GAGACATTAT GCTTCACCTT CTGTTTCGTT TTCTGTCCCA ACTTCTTCTT	600
TTTCTGCCAC CGCAACCGTT GTGAAAGTCA CTATCTGAGC ATCTTGATCC AGGCGCATTA	660
CTTTAACTCC CATAGTTGCA CGTCCTGTTT GTGAAATATT GGCAAGATTG GTTCGAATCA	720
TGACACCTGT ATCAGTGATA ATCATCAAAT CCTCATCCCC TTGAACAGTC ATAAGACCGG	780
CCAGCAAGCC ATTTTTTTCG GTAATTTTAG CTGTCTGCAT TCCCTTACCA CCACGACCTT	840
TTGTTGGGTA TTCAGTAGCG ACTGTACGCT TACCATATCC TTTTCTGTG ATAATAAGAA	900
CCTCATCTTG ATCAGTAATC AAGCTGGCAC CAACAACGTG GTCTCCTTCA CGAAGGTAA	960
CACCTTTCAC ACCAGTGGCG ATACGGCTCA TACCACGAAC GGCTGATTGA TTAAAGCGAA	1020
CTGCATAACC AAAGTTGGTA CCAATGATAA TATCCATATC TCCTTCTGCC AACAAGACAT	1080
TGATTAACTC ATCTTCATCC TTAAATTCA GCGCTTTGAG ACCATTTTGA CGAATATTGG	1140
CAAATCCTT AACACTGGTT CTCTTCACAA TACCGTGACG GGTGTAAAAG AAGAGATAAG	1200
CATCATCACT GCGATCAGAC TCAACATTGA TAACCGTCTG AATACTTTCG TCTTCATCCA	1260
ATTTCAAGAG ATTGACTACT GGTAGCCCTT TGGCAGTCCG ACCATACTCA GGAATTTTAT	1320
AACCTTTAAG ACGATAGACA CGTCCCTTGT TTGTGAAGAA GAGCAGATGA TCATGGGTGC	1380
TAGTTGACAC TAACTCACGA ACAAAGTCAT CATCTTTCAC TCCCGTTCCT TGGACACCAC	1440
GACCCCCACG TTTTGTAGCA GTGAACTCGT CCTGATCCAA ACGCTTAATG TAGCCTCTGT	1500
TAGAAAGGGT AATCAAGACA TCCGATCTT CAATCAAGTC CTCATCCTCG AGACTCAAGA	1560

1121

CCTGTCCAAT	CATCAACTCT	GTACGGCGCT	TATCAGAAAA	TTTACGTTTA	ACTTCATCCA	1620
ATTTCGTCTTT	GATAATTGGA	GAAACACGTT	CAGGCTTAGC	AAGAATATCT	GCTAAATCCG	1680
CAATCAGAGC	CAAGAGGTCA	TCATACTCAG	ATTGAATCTT	ATCGCGTTCC	AAACCTGTCA	1740
AACGACGAAG	ACGCATATCA	AGGATAGCTT	GACTTTGACG	TTCAGAAAGC	TTAAACTTGC	1800
TCATCAACTC	AGCTTGAGcT	TCCGCATcCG	tTTCACTAGC	ACGGATGATA	CGAATCAyTC	1860
GTCGATATGG	TCTAGCGCAA	TCAAGAGACC	TTCTAAGATA	TGAGCGCGCG	CTTCCGCTTT	1920
TTCCTTATCA	AAACGTGTAC	GACGAACAAC	CACTTCTTTT	TGGTGCTCGA	TATAAGCATC	1980
CAAAATCTGA	CGAAGAGACA	AAATTTTCGG	TATACCATTT	TGGATAGCGA	GCATATTGAA	2040
ACCAAAATTG	GTTTGCAATTT	GGGTCAATTT	GAAGAGGTTA	TTGAGAATAA	CATTGGCTGA	2100
GGCGTCGCGC	TTGACTTCAA	TAACAAATCG	AACACCTTCA	CGGTTTGACT	CATCACGTAC	2160
TGCTGTGATA	CCCTCAATGC	GTTTTTCCTG	AACCAAGCGA	ACAATATGCT	CATGCACCTT	2220
GGTTTTATTG	ACCATGTAAG	GAAATTCTGT	TACAACGATA	CGCTCACGAC	CAGTCTTAGT	2280
CGTTTCAATC	TCTGTACGAG	AACGTAGGAC	AATCGAACCT	TTACCTGTTT	CATAAGCCTT	2340
ATGGATACCT	GATTTCCCCA	TGACAAGAGC	ACCAGTTGGA	AAATCTGGTC	CAGGCAAGAC	2400
TTCCATCAAG	TCCTTGGTAG	TCACTTCAGG	ATTATCCATG	ACCAACTTCA	CTGCATCAAT	2460
gGTTTCAACC	AGATTATGAG	GTGGAATATT	GTTTGCCATC	CCAACCGCGA	TACCAGTTGC	2520
TCCATTAAAC	AAAAGGTTTG	GAAAACGCGC	TGGCAAGACC	AAGGGTTCCT	GTTTCATTGGC	2580
ATCATAGTTA	TCAACGAAAT	CAACTGTATT	TTTGTTGATA	TCACGAAGCA	TTTCCAGAGC	2640
AATCTTGCTC	ATACGTGCCT	CGGTATAACG	TTGAGCGGCA	GCACTATCTC	CATCCATGGA	2700
ACCAAAATTC	CCATGACCAT	CTACAAGCAT	GTAACGGTAG	CTCCACCATT	GAGCCATACG	2760
GACCATGGCT	TCATAAATAG	AGGAATCCCC	GTGTGGGTGA	TATTTACCCA	TGACATCCCC	2820
TGTAATACGA	GCAGATTTTT	TATGGGGTTT	GTCTGGGGTC	ACACCCAATT	CATTTCATTCC	2880
GTAGAGAATG	CGACGGTGAA	CAGGT'TTTAA	GCCATCTCGA	ACATCAGGAA	GAGCTCGCGC	2940
TACGATAACA	CTCATGGCGT	AGTCGATAAA	ACTTGCCTTC	ATCTCCTTTG	TCAGATTGAC	3000
ATTCACTAAA	TTTTTATCCT	GCATTAATAA	ATGCCTCATT	TCACAATTAG	TAAGTAACAA	3060
CATTATACCA	TAAATTCCTA	TCTATTTTCAG	CCTCTAAACC	ACTAAAACGT	TTACATCGAG	3120
AACTATAAGG	CATATTCGTG	ACAAAGTTTT	TTAAAAGTGA	TAGAATGAAG	TTGTCTAGGG	3180
AAAACCCCTA	ATAGAATAAG	GAGATGGTTA	nACAATGACT	CTGACTAACA	CACAAA	3236

(2) INFORMATION FOR SEQ ID NO: 181:

1122

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8651 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

AGGTCCTGAA GTATTGGAAC AGGAAGGTCA AGAGTTTGTG GAACATTTC AAAAACTCTT	60
GGAGTCAGTT GAAGTAGTAG CCATCTCAGG TAGTCTGCCA GCTGGCCTTC CAGTTGATTA	120
CTATGCGAGC TTGGTAGAAC TTGCTAATCA AGCTGGCAAG CATGTAGTCT TGGACTGCTC	180
AGGTGCAGCA CTTCAGGCTG TTCTTGAATC ACCCCATAAA CCAACAGTCA TCAAACCAAA	240
TAATGAAGAA TTGTCTCAGC TTCTTGGAAG AGAAGTTTCT GAGGATTGG ATGAATTAAA	300
AGAAGTACTT CAAGAACCTT TGTTTGCAAG GATTGAATGG ATTATCGTTT CACTTGGTGC	360
CAACGGTACT TTTGCCAAAC ATGGTGACAC TTTCTACAAG GTAGATATTC CTAGAATTCA	420
GGTGTTAAAT CCTGTTGGAT CTGGAGACTC TACTGTGGCA GGAATTCTT CAGGACTTCT	480
TCACAAAGAA TCGGATGCAG AATTACTCAT CAAGGCAAAT GTCCTTGGTA TGCTCAATGC	540
TCAAGAAAAA ATGACTGGTC ATGTCAACAT GGCCAACTAT CAAGCTCTAT ATGATCAATT	600
AATAGTAAAA GAGGTATAAA ATGGCTTTAA CAGAACAAAA ACGTGTACGC TTAGAAAAAC	660
TTTCTGATGA AAATGGTATC ATCTCAGCTC TTGCATTTGA CCAACGTGGT GCTTTGAAAC	720
GCCTCATGGT TAAACACCAA ACAGAAGAAC CAACTGTGGC CCAAATGGAA GAACTTAAAG	780
TCTTGGTAGC AGATGAATTG ACTAAATATG CTTCATCTAT GCTTCTTGAC CCTGAGTATG	840
GACTTCCAGC AACTAAAGCT CTTGATGAAA AAGCTGGTCT TCTCCTTGCT TATGAAAAAA	900
CAGGTATATGA CACAACAAGC ACAAACGCT TGCCAGACTG CTTGGATGTT TGGTCTGCAA	960
AACGTATTAA AGAAGAAGGT GCAGATGCAG TTAAATCTT GCTTTACTAT GATGTAGATA	1020
GCTCAGACGA ACTCAATCAA GAAAAACAAG CCTACATCGA ACGCATCGGT TCTGAGTG/G	1080
TGGCTGAAGA TATCCCATTC TTCCTTGAAA TCCTTGCTTA CGATGAAAAA ATTGCGGATG	1140
CAGGTCTCTGT AGAATACGCT AAAGTAAAC CACACAAAGT TATCGGCGCT ATGAAAGTCT	1200
TTTCAGACCC ACGCTTTAAC ATTGATGTTT TGAAAGTTGA AGTTCCTGTT AACATTAAAT	1260
ATGTTGAAGc kTCGCTGAAG GTGAAGTAGT TTATACACGT GAAGAAGCAG CAGCCTTCTT	1320
CAAAGCGCAA GATGAAGCAA CGAACTTGCC ATACATCTAC TTGAGTGCTG GTGTATCAGC	1380
TAAACTCTTC CAAGATACTC TTGTATTTGC TCATGAATCA GGTGCCAACT TTAACGGAGT	1440
TCTTTGTGGC CGTGCTACAT GGGCAGGATC AGTTGAAGCT TACATCAAAG ATGGTGAAGC	1500

1123

AGCAGCTCGC GAATGGtCGC ACAACTGGAT TTGAAAACAT TGACGAACTC AACAAAGTTC	1560
TTCAAAGAAC AGCAACTTCA TGGAAAGAAC GCGTGTAAGA AAGTCCTCCT AGTTTAGGAA	1620
CATGAATCTA AAAAAATTTA AAAAAAGTTG TATGTAAAGG CTTACAAAAT AACTTACTTG	1680
TGCTATACTT AAATCACAAAG TTAATATGAA TTAGAAAGTA ACTATATGAA GTATAATAAA	1740
AATAGGATAT AGTTTATTTT ACGAGCTAGG AAGGAAAAAT ACGGAAACAA TATTGCCAGA	1800
ATAAACTATA TTTAGATGCA CATTTCATTC ATTGTTTAT AAAAGGAGAA GATAAACGGC	1860
TACTAAAAAG AGTTTTTAAAG CGTTAGTTGT AGGACTAGGT ATTGTTTCAA TATTCTTATC	1920
AGCCTTACCT ATGGTTAGTG GTTCTGTATT TGCAGATAGT GCCCTAACTA CAGTAGATAA	1980
AGCAAATGAT ATTGTTTGA ATGTTGATGG GAATAAATTT TATAATGTTT CGGTTTCAGA	2040
AGATATTGTA AATGCTGGTC AAATTTTGA AGATTATTTT TATGTAGATA AATTTGGAAA	2100
TATAAAITTA AAAGGCACTC CTGAAGAGTT AGCAAAAAAT ATTGGTATTT CTGTACAAGA	2160
AGCAAGTTTG ATGTATGGAG CTGTAAAAGA GTTACCCAAC GTTTACGAAA GAGGTCCTGT	2220
AGGTTTTCGT TTCAATCTTG GTCCTCAAGT GAGGGGATG GGTGGCTGGG CTGCTGGAGC	2280
TTTCGCTACT GGATATGCTG GATGGCATTT GAAACAATTT GCGGTTAATC CTGTTACATC	2340
TGGATTTGTT GCTGTAATAA GTGGTGCGAT TGGCTGGGCT GTAAAACTG CTGTAGAAAA	2400
TTATTGGACA GTTGCTGTAG CTACAGTAGA AGTGCCGTTT GTGAACCTTG TTTACACCAT	2460
AGATTACCT TAGAGGTAT TTCTTTATGA ATCATTTCTT TAAAAAATA ACTGTATTTT	2520
GTTTTATAGT TTCTTGTTT CTTTGTATAT TAGACTTAAT GAATTTTAAA AATGTAGCTA	2580
CTTTTTTATT TTTCTGTCTT CCTGTTTTTG TTTTGATTTA CAAAAATAA TAAAAACAGA	2640
GCCTCTGTTT GATGAATTTT AGAACATAGT TAAGTTTAA AAAAAAGTTGT ATGTAAAGGT	2700
TTACAAAATA ACTTACTTGT GCTATACTTA AATCACAAAG TAATACAAGG TGAGTGTTAC	2760
TAAGTAATAT TAGGCATGAT CACAGGTGAA TTAGAAATCA GCTGATTTTC TAGTTCATTT	2820
GTGGTCATTT TTTGTACTTA TATACCTTTA AGATATAAAA GGAGGTTGAC ATGTATCGAA	2880
TTCTAAATCC AATGAATCAC AATGTCTCGC TTGTCAGAAA TGATAAGGGA GAAGAGGTGA	2940
TTGTAATTGG TAAGGGAATT GCATTTCGAA AGAAGAAGGG GGATTTGATT GCTGAAAATC	3000
AGGTTGAGAA AATCTTTTCG ATGAAGACCG AAGAGTCCAG AGAAAACTTT ATGGCTCTTC	3060
TCAAAGATGT TCCGCTTGAT TTTATCACAG TGACCTATGA AATCATTGAT AAGCTATCAA	3120
AGAAATATCA TTATCCGATT CAAGAGTATC TCTATGTAAC CTTGACAGAT CATATTTACT	3180
GTCTTATCA AGCTCTAACT CAAGGAAGGT ACAAGGATAG TAATCTGCCA GATATTTCCG	3240

1124

CTAAGTATCC	TGTCGCTTTT	CAAATCGCAA	ATGAAGCTTT	TGAAATTTAC	CGTCAGAAGC	3300
TAGCAGATCA	TTTTCTGAG	GACGAAATTA	TTCGGATTGC	TTATCATTTT	ATTAATGCTG	3360
AAGGTGAAAA	TGAAGTGGAA	CTTGTGGAGT	CGATTGATAA	GAGGAAAGAA	ATTCTCAGGA	3420
ATGTGAAGA	AGTTTAAACG	GAATATGCAA	TTCAACGAAC	TAAAAAGAAT	AACCATTTCT	3480
ATGATCGCTT	TATGATCCAT	TTGAATTATT	TCTTGGATTA	TTTAGACAGA	TCTAGAGATG	3540
ATAACCAATC	ACTTCTGGAT	ATGGAAGATC	ATATTAAACA	ATCCTATCCA	AAAGCCTTCG	3600
AGATTGGTTC	CAAGATCTAT	GATGTGATTA	CGCAACATAC	GGGTCTTGAT	TTGTATAAAA	3660
GTGAACGAGT	TTATCTAGTT	CTACATATCC	AACGTTTATT	GTCATAAAAA	TTTATTTAAA	3720
ACTATATAAG	GAGAATTCTA	TCATGAATAG	AGAAGAAGTA	ACATTGTTAG	GTTTTGAAAT	3780
CGTAGCCTAT	GCTGGCGATG	CTCGTTCAAA	ACTATTGGAA	GCCTTGAAGG	CTGCTGAAGC	3840
TGGTGATTTT	GAAAAAGCGG	ACGCTCTGGT	AGAGGAAGCT	GGTAGCTGTA	TTGCAGAGGC	3900
TCACCACGCG	CAAACAAGTC	TATTGACTAA	GGAAGCTTCA	GGTGAGGACT	TGGCTTATAG	3960
TGTAACCATG	ATGCATGGCC	AAGACCACTT	AATGACAAC	ATCTTGTTAA	AAGATTTGAT	4020
GCATCATTTA	ATTGAACTCT	ACAAGAGAGG	AGTTCAATAA	TGAATAAACT	AATGCATTT	4080
ATCGAGAAAG	GAAAGCCTTT	CTTTGAAAAA	CTATCTCGTA	ATATCTATCT	TCGTGCTATT	4140
CGTGATGGTT	TCATTGCAGG	TATGCCTGTT	ATTCTCTTCT	CAAGTATCTT	TATCTTGATT	4200
GCCTTTGTAC	CAAACCTATG	GGGCTTTAAA	TGGCTGTATG	AAGTTGTAGC	CTTTCTGATG	4260
AAACCTTATA	GCTATTCTAT	GGGTATTCTG	GCTCTCTTGG	TAGCTGGTAC	AACAGCTAAG	4320
TCATTGACTG	ACTCAGTAAA	CCGGAGCATG	GAAAAAACCA	ATCAAATCAA	GTATATGTCA	4380
ACATTGTTGG	CAGCAATTGT	TGGTTTGTGG	ATGTTGGCAG	CTGATCCTAT	CGAAAGTGGT	4440
CTAGCTACTG	GATTCTTGGG	GACAAAAGGT	TTGCTTTCAG	CCTTCCTTGC	TGCCTTTGTT	4500
ACTGTAGCCA	TCTATAAGGT	TTGTGTTAAG	AACAACGTCA	CTATTCGTAT	GCCTGACGAA	4560
GTTCCACCAA	ATATCTCACA	AGTCTTTAAA	GATGTGATTC	CATTCACCTT	ATCTGTTGTT	4620
TCTCTTTATG	CTCTTGACTT	ATTAGCACGT	TATTTTGTGG	GTTCTAGTGT	GGCAGAATCA	4680
ATCGGTAAAT	TCTTCGCACC	ACTCTTCTCA	GCAGCAGACG	GATACCTTGG	TATTACCATT	4740
ATCTTTGGTG	CCTTTGCCTT	CTTCTGGTTT	GTTGGGATTC	ATGGTCCATC	TATCGTTGAA	4800
CCAGCTATCG	CAGCTATTAC	CTATGCCAAT	GCCGAAGTTA	ACTTGAACCT	TCTCCAACAA	4860
GGGATGCATG	CAGACAAGAT	TCTTACTTCT	GGTACACAAA	TGTTTATCGT	TACCATGGGT	4920
GGTACAGGTG	CGACATTGGT	CGTTCCATTT	ATGTTTCATG	GGTTGACAAA	ATCGAAACGT	4980
AACCGTGCAA	TCGGACGTGC	TTCAGTAGTT	CCTACCTTCT	TCGGTGTA	TGAACCAATC	5040

1125

TTGTTTGGTG CACCTCTTGT TTTGAATCCA ATCTTCTTCA TTCCATTTAT CTTTGCTCCA	5100
ATTGCAAACG TATGGATTTT CAAATTCTTT ATTGAAACTC TTGGAATGAA CTCATTCACT	5160
GCTAATCTAC CATGGACAAC TCCAGCTCCA CTAGGTCTAG TTCTTGGAAC TAACTTCCAA	5220
GTGCTATCAT TCATTCTTGC TGCCCTTCTA ATCGTGGTTG ACGTTGTCAT TTACTATCCA	5280
TTCCTTAAGG TCTATGATGA ACAAATTCCT GAAGAAGAAC GTTCAGGTAA GTCTAATGAT	5340
GAATTGAAAG AAAAAGTTGC TGCAAAC TTC AACTGCAA AAGCGGATGC TATTCTTGAA	5400
AAAGCGGGTG TCGATGCAGC ACAAATACC ATCACTGAAG AAACAAATGT CCTCGTTCTC	5460
TGTGCAGGTG GAGGAACAAG TGGTCTCCTT GCAAATGCTT TGAATAAGGC AGCAGCAGAA	5520
TACAATGTCC CTGTGAAAGC AGCAGCAGGC GGCTATGGTG CTCACCGTGA AATGTTACCA	5580
GAGTTTGATC TTGTTATCCT TGCCCTCAA GTTGCTTCAA ACTTTGAAGA TATGAAAGCA	5640
GAAACAGATA AGCTCGGTAT TAACTAGCG AAAACAGAAG GCGCTCAATA CATCAAATTA	5700
ACTCGTGATG GAAAAGGTGC TCTTGCATTC GTACAAGCGC AATTCGATTA AGGCTAGAGA	5760
CTCTGAAATA GTCTCCATC GTTACGGAAA TCGCTATGGC GAATTCCTA TTATTAATTC	5820
GTCGGTAAAA AGATATCGTT TTTACCTCCT CATGTCACAA TTCGGTGA CT TGGTACAAGA	5880
AGTGAGATGG AGAAGGATGG CTCACTGACT CCTCTCCTCT CACTTTTACT TTATTTAAAT	5940
CAAGAAATAG GTGAAAAAAA TGACAAAAAC ACTTCCAAAA GACTTTATTT TTGGTGGCGC	6000
AACAGCTGCT TATCAAGCAG AAGGTGCTAC ACATACTGAT GAAAAAGGAC CAGTTGCTTG	6060
GGATAAATAT CTTGAGGATA ACTACTGGTA CACTGCCGAA CCAGCTAGTG ATTTTACAA	6120
TCGATATCCA GTTGACCTCA AGCTAGCAGA AGAGTATGGT GTCAATGGTA TTCGAATTTC	6180
TATTGCTTGG TCACGTATTT TCCCAGCTGG TTACGGCCAA GTAAATGCTA AAGGTGTTGA	6240
GTTTTATCAT AATTTATTTG CAGAGTGTCA CAAACGTCAT GTTGAGCCTT TTGTAACTCT	6300
TCATCACTTT GACACGCCAG AAGCTCTCCA CTCAAATGGA GACTTCTTAA ACCGTGAAAA	6360
TATCGAACAT TTTGTAGACT ACGCTGCCTT CTGTTTTGAA GAATTTCCAG AAGTAAACTA	6420
TTGGACAACC TTTAATGAAA TTGGACCAAT CGGTGATGGT CAATATTTGG TTGGGAAATT	6480
CCCTCCAGGT ATCCAGTACG ACCTTGCCAA AGTCTTTCAA TCACACCACA ATATGATGGT	6540
GTCTCATGCA CGCGCGGTAA AATTGTACAA AGAGAAAGGC TATAAAGGGG AAATTGGTGT	6600
TGTTACGCC CTGCCAACTA AATATCCTCT AGATCCTGAA AATCCAGCAG ATGTTCTGTC	6660
AGCTGAGTTG GAAGATATCA TCCACAATAA ATTCATCTTA GACGCAACTT ATCTAGGTCG	6720
CTATTCAGCT GAAACCATGG AAGGTGTCAA CCATATCTTA TTAGTCAATG GTGGTAGTTT	6780

1126

GGATCTTCGT	GAAGAAGATT	TTACAGCATT	AGAAGCTGCA	AAAGACTTGA	ATGATTTCCT	6840
AGGAATCAAC	TACTATATGA	GTGACTGGAT	GGAAGCCTTT	GATGGAGAAA	CTGAAATTAT	6900
CCATAATGGT	AAAGGTGAAA	AAGGAAGCTC	TAAGTATCAA	ATCAAAGGTG	TTGGTCGTCG	6960
TGTAGCTCCT	GACTATGTAC	CACGCACGGA	TTGGGATTGG	ATTATCTACC	CTCAAGGTTT	7020
GTATGACCAA	ATCATGCGTG	TGAAGAAAGA	TTATCCTAAC	TACAAGAAGA	TTTACATCAC	7080
TGAAAATGGT	CTCGGCTATA	AAGATGAGTT	CGTTGATAAC	ACTGTTTACG	ATGATGGTCG	7140
TATTGATTAC	GTGAAGCAAC	ACTTGGAGGT	TTTATCTGAT	GCGATTGCAG	ATGGAGCTAA	7200
TGTAAAAGGT	TACTTCATTT	GGTCATTAAT	GGATGTCTTC	TCATGGTCAA	ACGGTTATGA	7260
GAAACGTTAT	GGTCTCTTCT	ACGTAGATTT	TGAAACTCAA	GAACGTTATC	CTAAGAAATC	7320
AGCTCACTGG	TACAAGAAAG	TAGCGGAAAC	TCAGATTATA	GACTAGTAGA	ATTAGTCATT	7380
AGATATAGAA	TTTTAGTGAG	TCAAAAAGAT	GTTCAAAGAT	TTTATCCAAT	CTATTTATGA	7440
AAAAAAGTTT	ATATTATAAA	TTTCGAAAAA	TGCTCTCAAA	TACCGTGTTT	GACGAGTGAA	7500
GAATTGAAAA	GTCTTGAAAA	ATGGTATGTC	TCGACTGGTA	AAGAATGGAT	TTGTCATTCA	7560
GATGATGAGC	TGGAAGAATT	TAAAAATCTA	TTTTTAAATT	TTATCAATCC	TGAAGAATGG	7620
GATACTATCT	CCTTTGATTC	AGATTTTATG	CCGTTTCAAC	AATCGTAACC	AATTTCTCAA	7680
AAAAGTTAAA	TCTTATATTT	AGTACTCTGT	AAAACCTCTA	TCTAATCACG	TTGCTTATAC	7740
TCAATGAAAA	TCAAAGAGCA	ACTTTAAACT	AGGAAGCGAG	TCGCAGATTT	CTCAATGCAT	7800
AGCTTTGAGG	AATTGGGCAA	AAAGTCTTTG	ATATAGAAAA	ACGCATAGTA	TCAGGTGTTT	7860
CAACACCTGA	TACTATGCGT	TTTATGTGGG	GAAGATTTAC	TTTTTTTCTT	CTGAAATTGA	7920
GTTGTTACCC	AGGCTCTTTC	AGTTTATTAA	GGCTTGATGA	CTTTAATGTG	TTTAGATAGC	7980
TTAAAAAGGA	TTGAATCACT	TAGTTTAGAA	TCTGAAACAA	TAGTATCAAG	ATTTGATACA	8040
TTATAAAAAG	TATAAAAATC	AAACTTATTG	AACTTGCTAT	GATCTGCGAG	TAAATATTTT	8100
TTATTAGAAT	TATTTAAAGC	GATGCGTTGA	GCCTCTCCCT	CTTCCTCGCT	AAAAGTAGCT	8160
AGAGCTCCGT	TTTGAATACC	ATTACAGCTA	ACGAAAGCTT	TAGAAAATTG	GAGATTAGAG	8220
AGATTTTGTA	GGGTCAATGT	ACCAACAAAA	GCACCTGTAA	TATCGCGATA	ATTTCCACCT	8280
ATTAAAAATCA	AATCTGTTAA	TTTTTCGTTG	CTTAAAAATCA	GAAAAACAGG	TAGACTGTTG	8340
GTTACGACGC	GGATATGTTC	AATAGGCAAC	TCACGCGCAA	AAAACCTCTA	TGTTGTTTCCT	8400
GGTCCAATGA	AAATAGTTTC	TCTTCTCTCT	ACTAGACTGC	CTGCAAAATG	GGCTATTTCT	8460
TGTTTTTCTG	CCGTTTGGAG	GGCTTGTTTT	TCAATATTTG	ATCGCTCATT	AGTCAAAAGG	8520
GAGTTGGTTC	GAAGTTTTTC	AGCTCCACCA	TGCACACGAA	TCAGCAAATC	TTTATCAGCT	8580

1127

AATTCCTGTA AATAGCGCCT TGCAGTCATA TCTGAAACGG CTATTTTCGTC CATAATCTGT 8640
TTAACTGTTA T 8651

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3786 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

AATCTCCAAT CAGTGCCACT TCAGCTACAA AGAAGAGGAG GATAATAACT CCGTTCACAA 60
 GGACAGACAA GAATAATTGA TAGAAGGAGT CGGTTTCACT TGCTTGACTT GGTCTTGTA 120
 TGATWTGGAG ACTGGCAAGC AGAATGATTC CAATGCTAAT CACACACAAG AGGGCTGTAA 180
 ATCGTAGGCT ATCAAAGAAA GCAAAGAAAC TAGCAATAGC AGTGAGGAmG ATTGGAATTG 240
 CCAAGAGTTG ACTATATTGT TGGAGAACCT TGTCTAGCGT CCAGTCCTTT TCCTGGTGGA 300
 TAAATCGTCT CACAACGAAA CTACCCAAGA GGAATGAAAA GAAGAAGAGT GTTGTCGCTA 360
 CTAGGATAGA GATGATAGAA AAAAGAGTTA AAGGAGCTAG CTGCTCAGGG AAGCGACTGT 420
 TAATGCTTGC TATATGTCCA TAGTAAGCAT GTTTGATGTG ATAGATACTA AAGAAAAAGG 480
 AAGATGCAGA AAACAGAATG AGCAAGAGAA AGGCTGTGTA ACTGTGTGTG ATACTTGTTT 540
 CCAACTTACT TGTAGGAGAT TTGATCGCTT CCACTAGCCA AGACCAAAAA TCAAGCACTT 600
 GCTCTTTCCA TTTATCCCTA GATTTTGGAG CTTGGTCGGG GATATAAGGA CTTTCTAAAG 660
 ATTTACTGAT AAGAAGTGGC TCTTTCGTGG TTGCTTTTGT CTGAGGAAGA GCTTCTTGGC 720
 TCTCTTCAGC TATAGTGA CT TTTCTGTTT CTTTAGAAAG GTCTGGCTCT TCTTCAGTAG 780
 AATTAGATGC CTTCTTTTCT TCTATTCTTG TTCTCGCTTC ACTGTCTTCA GGAGCTTCAA 840
 TTTTCTCTTC TTGCTGGCTT TCCAATTCGA CTTAGCTTG AGGGACTTCC TCCTCTAACT 900
 GAGTATTTTT TTCAATTGGT GTATCGAGAT CGGCTATCGT TTCTTCAGCC TTGTCTGCAA 960
 CCTCTTGAGC TTGCTCTTCA GGCTTGTTCT TGCTTGTTGT TTTTACAAAA TCATTACTTT 1020
 CAAACCATTC TTGTTTCATG GTAGAACCTC CTTTTTAGTT AGATAAATAT GTTTCCATAG 1080
 TAGCAAATGT AAGCGTTTTT GTCAACGTCT GCTTGGTGTG GATATTAGAT CAATATTATC 1140
 ATCAGATCTC GCAATGAGTT GATCCTTGAC ATCGGTTTTT TCAGTTTGTG AAGGGTTGCT 1200
 TAATCCGTA CCTCTTGATT CAGGCTTTTC TCTGTGAAT TGGAAGATAG AACCATAGTT 1260

1128

GCTTGAGATG	TCCCAGTTAA	TTCGTTGGCT	TTCTTTCTGG	TCTAGGATGA	TTCTGAGATA	1320
ATCTTTGGCA	GTCAGTTCAA	CCTTGCCATG	GACTTGGATA	TTTTCAGCGT	GGAAGTGATT	1380
CTCTGTTGAC	TCTAGCTGAC	TATCTGTAAG	AACTGTATCA	AAGATATTAA	CGATATTGGG	1440
CGTGTTGAGT	TTACTGTTTT	TGATACGACT	TCCTTCAATT	CGGAGGATAT	AGCTGTTTGT	1500
ATTGAGGGTC	GCATTTTCAA	GGCTAGCATT	TATGATGGTG	GTTTGTCCGC	GATTGGCTGA	1560
GATGTTGATC	CCTTTTAGAG	TTCTCCCTTT	TGGTAGTCGG	AGAATAACTT	CTTCAAAACG	1620
ACTAGAGTAG	CTACTTGCGA	TATGAAGAAT	CCCACCAATT	CCAGAAGAGA	GAAACGGAGT	1680
TTCAGACAGT	TTCTTATCAG	TGAGACTCAG	AGTTCATCG	TTCTGATTGG	TGATAAGATC	1740
ATGGTGAGCA	GAAAGAGATG	GATGGTAAGA	AATGTGGATT	TGATCATCGA	AAGAGTCTGT	1800
GATGGTGAGC	GTGTGTTGGT	GGAGAGTAAT	TTCTAGGTTT	TCGACTTCCT	TGCCAAAGGT	1860
TAGCTTTTCC	GTACGGCTAT	CATAGACAGG	TTCTTTGGAC	ATGGAAAGTA	GGCTCTTAAT	1920
CCCGTCAGAT	TGGATACCTA	CAAAAAGCAG	GATAAAGCCG	ATAACGGTAG	TCACCACACC	1980
AAAGATGAGA	AATCCTTTTG	TCCATTTACG	CATGCTGATT	ACCTCTCTTT	CCTTTTTTAA	2040
GAACAAATTG	TACCAGACGA	ACAATGAGTA	GACCGAAGAA	GCGAGTTGCA	TAGGAAATGC	2100
CAAGTAAAAC	TAGCGAAGAA	GCACCGATAG	CCAGTAAACC	AGAACCAAAA	ATCAAGATAA	2160
AGGCTGATTT	GGCTTGGGCG	AGGACAGTGA	AACTTTCAAC	TAAAAATAGG	AATCCGCCGA	2220
TGATACCCAG	TATGGAAACT	GCAAAGAAAG	CCAGAATGAC	AGTCAAAGCG	GCTACAAGAA	2280
TTGCGAACAG	GGTCACGAGG	ATGGCGATTG	CCAGAGGAAT	GCCGATAGGT	GCTGCAAGGA	2340
GGGCTAACAA	GGCGATATGT	AAAATTTGTC	GGTTATTTTT	TTGAGCGGGT	GCTTCATTGA	2400
TTTTTTTATC	GAGAAGATTG	GATAGAACTT	CGTGGGCCGC	TTCTTTGGGA	GTCCCAAAC	2460
TAGCGATGAG	TTCTTCTTCT	CCTTCGACTC	CAGCATCGTC	AAAGAGCTCT	CTGAAATAGT	2520
CCATGGCTTC	GATACGGTCA	GCTTCAGGTA	GTTTCTTGAG	ATAGAGTTCT	AGCTGAGTCA	2580
GGTATTCAGT	TCTTGTCATG	GCGGATACTC	CCTTCTATGA	TGCCATTGAT	GGTGTCTGTA	2640
TAGAGTGCCC	ATTCATCTTT	TAGGGTCAAG	AGCTGCTCTA	TACCACCGTT	TGTCAAGGAG	2700
TAGTATTTGC	GCATGCGACC	TTGGAACCTC	CTAGAATAGG	TTGTCAGAAA	GCTATTGCCT	2760
TCCAATTTTT	TGAGAATGGG	ATAGAGTGTG	GATTCTTTGA	TATTAGCGAT	CAGCTTAATG	2820
GTTTGGCTAA	TCTCATAACC	ATAAGAATCA	CCCTGCTCCA	GTACAGCCAA	GATGAGAAAT	2880
TCAATCAAGG	CAGAGGATGT	TGGAAAGTAC	ATGGGAAACC	TCCTTTTCTA	ATGTGTAAGA	2940
TTTTTATATA	TAATTTTCT	ACACATACAT	TGTACATCTA	AAAGAAAGCC	CTGTCAAGAG	3000
AAATGTGTAA	AATTTTTATA	TATAAAAAAC	TTCTAGCTAA	AACTAGAAGT	TTAAAGGATC	3060

1129

TTATCCGCTC TGTCCACTGT AAAGAGGGCC ACAGTCATCA GGATATCGAT GAGCAAGAGG	3120
GCAGCTACAG ATGGTACCCA AGAGTGGAAC AGGTCAAAAC TGTAACCAA GAGGGTTGGC	3180
CCAAAGGCTG CTAGGATATA GCCTCCTGTT TGAGATAGGC CGGACAATTG GGCTGTCTTT	3240
TCAGGGGCGC TTGTCTTGAG TGAAAAGTTG ACCATGAGAT AAGGGAAGAG GGCCTGGTT	3300
GCGGTTCCGA TGAGGAGATG GATGGCAAGC CAGTAAATGA AATTATTGAT TGGGAAAAAG	3360
AGCATGGAAG TGCCGACCAC ACCAGCTAGT GAAACCAGAG TGAGCATGAG CTGACGGTTG	3420
CGAGTAGATA AACTGGTTGT CAGGCTTGGG ATGGTCATTG AAAAAGGAAT GCTAATCAGA	3480
GATAAGATAG AAGTCAGCAA GCCAGCTTCG TGAAGTGGATA GACCTGCATG GATAGACATG	3540
GTAGGTAACC AGGTCATGAC GGTGTAAAAG ATCAAGGATT GAAAACCTGA AAAGATAATA	3600
ATTGCCCAAA CCTGTTTATT ACGCATGACC TTTATTTGAC TTTTGTGTTT GGTGTGTGGA	3660
GCTAGTCTAT GATTATAGCG GTGATTTGGG AGCCAGACCA AAAAAGTTGC TAGACAGAGT	3720
AACGTGAGGA GAAGGATAAG TCCTTTCCAA GAACTGGCTT GTGTAATGGG CACAGCTAGA	3780
TAGGAA	3786

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3054 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TCAGCTAAAA AACATTGCTA AATTGATTGA AGCTGGTGCT ACACATTCCG ATTCAACTTC	60
TCACACGGCG ACCACCAAGA ACAAGGTGAG CGTATGGCAA CTGTAAACT TCGGAAAAA	120
ATTGCAGGTA AAAAAGTTGG TTTCCTTCTT GATACAAAAG GACCTGAAAT CCGTACAGAA	180
TTGTTCGAAG GTGAAGCTAA AGAATATTCA TACAAAAC TGAAAAAAT TCGTGTGCA	240
ACTAAACAAG GAATCAAATC AACTCGTGAA GTGATTGCGT TGAACGTTGC TGGTGCTCTT	300
GATATCTATG ATGATGTTGA AGTTGGTCGT CAAGTTTGG TTGACGATGG TAAACTTGGT	360
CTTCGTGTGG TTGCTAAAGA TGATGCAACT CGTGAATTTG AAGTTGAAGT TGAAAACGAT	420
GGTATCATCG CTAAACAAAA AGGTGTGAAC ATCCCTAACA CTAAAATTCC TTTCCCAGCT	480
CTTGCTGAAC GCGATAACGA CGATATCCGT TTCGGTCTTG AACAAGGTAT CAACTTCATC	540
GCAATTTTCAT TCGTACGTAC TGCAAAAGAT GTGAACGAAG TTCGTGCAAT CTGTGAAGAA	600

1130

ACTGGAAACG GACATGTTCA ATTGTTTCGCT AAAATCGAAA ACCAACAAGG TATCGATAAC	660
TTAGATGAAA TCATCGAAGC AGCTGATGGT ATTATGATTG CTCGTGGTGA TATGGGTATC	720
GAAGTACCGT TCGAAATGGT TCCAGTTTAT CAAAAAATGA TTATCAAGAA AGTCAATGCT	780
GCAGGTAAAG TTGTTATCAC TGCAACAAAC ATGCTTGAAA CAATGACTGA AAAACCACGT	840
GCAACTCGTT CAGAAGTATC AGATGTATTC AACGCTGTTA TCGACGGAAC TGACGCTACA	900
ATGTTGTCAG GCGAGTCTGC AAACGGTAAA TACCCACTCG AGTCAGTAAC TACAATGGCT	960
ACAATCGACA AGAACGCTCA AGCTCTTCTT AATGAATACG GACGTCTTGA TTCAGATTCA	1020
TTTGAGCGTA ACTCTAAGAC AGAAGTAATG GCTTCTGCTG TTAAAGATGC TACTAGCTCA	1080
ATGGATATCA AATTGGTTGT AACTCTTACT AAGACAGGTC ATACTGCACG TTTGATTTCT	1140
AAATACCGTC CAAATGCTGA CATCTTAGCA TTGACATTTG ACGAATTGAC AGAACGTGGC	1200
TTGATGTTGA ACTGGGGTGT TATCCCAATG TTGACAGATG CTCCATCTTC AACTGACGAT	1260
ATGTTCGAAA TCGCTGAACG TAAAGCGGTA GAAGCAGGTC TCGTTGAGTC AGGCGATGAT	1320
ATCGTTATCG TTGCTGGTGT GCCAGTAGGA GAAGCTGTTT GCACAAACAC AATGCGTATC	1380
CGCACAGTAC GTTAAGAAAA ATATAAAAACTATCATATC CAGCTTTAGA GCTTGTGTGA	1440
TAGGCTTTTT GTATAGAGGG TAAGAAATAG GCAAACTTT CATAATGGAT TGATACTCTT	1500
CGAAAATCTC TTCAAACCAC GTCAGCGTCG CCTTACCGTA TATATGTTAC TgACTTCGTC	1560
AGTTCTATCT ACAACCTCAA AGCAGTGCTT TGAGCAACTG CGGCTAGCTT CCTAGTTTGC	1620
TCTTTGATTT TCATTGAGTA TGAAATAAGA TATGCACAAA TTGATTAGAA AGTCAAATGA	1680
ATTCTACAA ATGTTTtagc AATCGTAATG TACTTGTCTA GATTGATCT GATATATTTT	1740
CGATTTAATG ATATGGTATT TAAAACCTCC AAAGTAGCTT ACTCCATTCT TTTACTTACG	1800
TGAGTGTA TAGTTATTTAC TGTTTtagCG TTTTGTGT CCACCTAAC CATTATAGCA	1860
TTCTTCTCAG CTAGTGTACT AAGGAGTGTG TGCCTGAAAA TATGGGAAC TAAAGGGCTGG	1920
TTTATCGGTT TCTCTAGTTT AGTATTTGCC TTTTGCAAAG TGATCTTAAA TGCCTTTCTC	1980
TAAATTTACA TATCACTATT GTTTAACAAA ATCTAATCTA TTTTAGGTCA CTTATTTCTT	2040
TTTTGAAATG TAGAATGAAC TTTTTCAAAG TTTTTCGAAT CTTTAAAAAT CTGTTTGCTT	2100
TATATCGCCA TTCTCCCCC TTTTTTAATT CTCCCTATAT AGCCTGACAG CTTTCCCGAT	2160
GGTACGAATA TGGTTGCTTT CGTCTAGGTG GATGTCGGGG TATTCGGGAT TGAGTTTTTT	2220
TGAGGCAGCC TTGGCGGAGT TTCTTGACAT AGTTAGTGCC GTCTACTTGG AAGATGCCGA	2280
TGGTATTATA GTCAATCTGT GGGGTATTCT TGATAAATAG GTAGTCGCTG TTTCTTATCT	2340
TTGGCTCCAT GGAATTGCTG ACGACATAAG CGATTGGGTC GTAGTCGTCT GGGATAATGG	2400

1131

AAACTCCATA TCTAAATCGT TGTCTGTCAT CGAGCGGCTA CCTGCAGAGA TAAACTACCT	2460
AACACGAGAG TAAGTAGTCT GTCTGTAGTC GTCCAGTCTG ATGATTTTTA CGATACTTCG	2520
TTTTTCTGAT CATAAGTTG CCTCTCGGCA TAGGTCAGAA CTTTACCTTG TCTGGGTGGT	2580
TCCCGTTGGT CGTAGATAGA TTGGATATCG CTAGGAGAAT CCTTTTGAAC TGGAGGAAAG	2640
AGGGCATCGA TCAAGCTACT GAATACTTTA ACTAAGTCAA ATATAGTATT TTTCTTAGTA	2700
GACCTAACCC TTTTTCATA ATTTCTAATG GTGTTTTTAC TTATACCTAT CTTAGTACCC	2760
AATTCTTATT GAGTCCAACC ATTACTAGTC TATATTGTTT TATAGTTGAT TGAGTTTGGG	2820
ATAGTACGCT GTAGCTGCTA AAACATTTCT AGAAATTAAT TTGACTTTCC TAATAGAGTT	2880
GTTTCATATCT TATTTCAATC TATTATGTTT TTCACCTCTA ACAATCGCAA TCTCTTCTTT	2940
ATCCATGAAT GAAATCGCTT TCTATTTTGG TAAGTAAAGC ATAACACGAA ATCCACGAAA	3000
ATGAAAACCT TTGTGTGTT TTCGTAAAAA ATTTGTTGAC AGAGCACGAA ACGC	3054

(2) INFORMATION FOR SEQ ID NO: 184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1590 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TGTGATTTTC yGAAAATTTG GTAAAATATA TCTTAATCAT TTTCAGGAGG AAAAAATTT	60
GACAAGATAT CAGAATTTAG TAAATGGAAA ATGGAAATCA TCTGAACAAG AAATTACGAT	120
TTATTCACCA ATCAATCAAG AAGAATTGGG TACAGTTCCA GCCATGACTC AGACTGAAGC	180
TGATGAGGCT ATGCAAGCTG CGCGTGCAGC CCTGCCAGCA TGGCGAGCTT TATCAGCAGT	240
TGAACGTGCG GCTTATTTGC ATAAACAGC AGCTATTTTA GAACGCGATA AGGAAGAAAT	300
TGGTACTATC CTTGCCAAAG AAGTAGCAAA AGGGATTAAA GCAGCAATTG GAGAAGTAGT	360
GCGTACAGCA GACTTGATTG GTTATGCTGC TGAGGAAGGT CTCCGTATCA CTGGACAAGC	420
AATGGAAGGT GGTGGTTTTG AGGCAACAAG TAAAAACAAA CTGGCTGTTG TCCGTCGTGA	480
ACCAGTTGGT ATCGTGCTAG CGATTGCTCC CTTTAATTAT CCAGTTAATT TATCTGCTTC	540
TAAAATTGCA CCTGCCTTGA TTGCAGGGAA TGTGGTCATG TTTAAGCCAC CAACACAAGG	600
TTCCATTTCT GGA CTCTTGT TGGCTAAAGC ATTTGAAGAA GCAGGGATTC CGGCAGGTGT	660
TTTCAACACC ATTACAGGTC GTGGTTCAGA AATTGGGGAT TATATCATTG AGCACAAAGA	720

1132

AGTCAACTTC ATCAACTTTA CAGGTTCAAC TCCTATTGGA GAACGTATTG GTCGTTTAGC	780
TGGTATGCGT CCTATCATGT TGGAAGTTGG TGGGAAAGAT GCAGCTCTTG TACTAGAAGA	840
TGCAGATTTG GAACATGCTG CCAAGCAAAT TGTTCGCGGA GCCTTTAGCT ACTCAGGACA	900
ACGTTGCACG GCCATTAAAC GTGTCATTGT TCTCGAAAGT GTAGCAGATA AATTAGCTAC	960
TTTGCTTCAG GAAGAAGTTT CTAAATTAAC AGTTGGTGAT CCATTTGACA ATGCTGATAT	1020
TACACCTGTT ATTGACAATG CTTACGCCGA CTTCATTTGG GGCTTGATTG AGGATGCACA	1080
AGAAAAAGAA GCTCAGGCTC TTACACCAAT CAAACGTGAG GGCAATCTTC TCTGGCCAGT	1140
GCTTTTGTGAC CAAGTTACAA AAGATATGAA AGTGGCATGG GAAGAGCCAT TTGGTCCTGT	1200
TTTACCAATC ATTCGTGTGG CTAGTGTAGA GGAAGCTATT GCCTTTGCCA ACGAATCTGA	1260
ATTCGGCCTT CAATCATCAG TCTTTACAAA TGATTTCAAA AAAGCCTTTG AAATTGCTGA	1320
AAAAGTTGAA GTAGGTACAG TCCACATTAA TAATAAAACC CAGCGTGGTC CAGATAATTT	1380
CCCATTCCCTT GGTGTCAAAG GTTCTGGAGC TGGAGTGCAA GGAATTAAAT ATAGCATTGA	1440
AGCGATGACA AATGTCAAAT CCATTGTTTT TGATGTGAAA TAACGTGTAA AACCAGGAAA	1500
TTGTTTTCCT GGTTTTATTT TTTTGCTATA AAATAATAAT AATTATAGAA AAAATACGAA	1560
CTTTTGGTA TTATAATAGA TTGAAACCGG	1590

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4848 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

CCTGCAGTTG TCAGACCTGT AATTTTCTTT TTATCTGTAA TAAGAATCGT TCCAGCGCCT	60
AGAAAACCCA CACCTGATAT AACTTGAGCT CCTAATCGTG TAGGATCTCC TGTCCCAAAT	120
TTATAAGATA CGTATTCATT CGTCATCATA ATCAAACATG CAGCTAGACA AACAATACTA	180
TAAGTTCGGA TGCCTGCAGG CTGGGATTTG CTCCTCTCTCT CTAAACCAAT TATACTACCA	240
ATGACTACTG ATAAAACAAT CCTGACAACT ATTTCAATAT TTGATAACCC AAGACTAGTG	300
GCTGTCATGA TTATTTCCCTT ACTTTACGCC CCGGTCTTTG TGTGAAGTAT AATACCGTTC	360
CAGAAATAAT CATCAGAACA ATTGATATAA CAAATACCAG AGCTTGTCGA TTAGATGTTG	420
CTGTTTCATC ACCTGCAGAT CGAATCGTAA TACCTAATGG TTGAGCTAGG GGATGGTAAA	480
GGAATACAGA TAAGTCGAAG TCAGTTAATA AAGAGTTAAA GTTTAAAGCA ATAACAGAGA	540

1133

GAACAACCGG	TAAAAATAAT	GGAATGATAA	CCTTCATCAT	AGTATAAAAA	GGTGAAGCAC	600
CCATACTTCT	TGCTGCATCT	TCCATCTCAT	CATCAACACT	AAATAAAATA	GCACGTACCA	660
TTCTATAAGA	AAATGGGATT	TTTACAACCTA	TATATGCAAT	AAGTAGAATT	ACCAAACCTAC	720
CTACCAAAAT	CTGATTC AAG	ACAAGAAATT	GTGGCTGATT	AAAAGTAAAT	AATAAACTTA	780
CTGCTAAAAG	TGTACTTGGT	AGTAACCAAG	GAAGTAGAGC	ACCATATTCA	AATAAGAAAT	840
CAAAACGAGA	TTTATGTTTT	CTGACAACAC	GAGCAAATAC	AACTGCGAGA	ATTGTTGCTG	900
TTGTGCGAGC	AATAATAGAA	TAAATAAAGC	TGACCAAGAA	TGGAGAGAAT	GCCGCACTAT	960
TACTAAAGAA	TAAGCGATAA	TTTTCTAAAG	TAAAGTTTGA	TAATGTTAAG	TTACCTGTTT	1020
GAATTGCAAC	TGGATCTGTA	AATGAGTATA	ATACTATAAA	AATTAGTGGA	AGCATGAAAA	1080
CTGTGAACAA	TCCATATGCT	ACAATGTGAG	CAATGATATT	CCAAGGCTTA	GACGCAATTT	1140
TTTGTTTTTT	AAGAGGCGCT	TTAGTCTTAG	AGATAGAAAT	ATAATTTCCA	CCTTTTTCTA	1200
TCTTATTCAT	GATAGTAAGC	AAAATTGTAG	TGCAATACC	TAAAAATAAT	GCAAGTAGGG	1260
CAGCTAAATC	ACGAGAATTC	CCCATCCCTG	CAAATGTAAT	AATCATTGGA	TTTATAGTTT	1320
GAAATCTCTT	ACCACCAACA	ATCATGGGTG	CTGCTACTGC	AGATAAACCA	CTAAGAAAAA	1380
CCATAATAGT	AAGTGCAAAT	AGAGTTGGAA	TTAAGGTTGG	TAACACTACT	TTTCGGAAAA	1440
CAGTAAATGG	TTTTGCTCCC	ATATTTCGAG	CAGCCTCAAT	AGTGTGATAG	TCAACGCTTC	1500
GAATTGTATT	TGTTAAAAAC	AATGTATGAT	TAGCAGTTCC	TGAAAATGTC	ATAATGAATA	1560
AGACTGCACC	ATACCCAATA	AACCAGTTAG	GGTCTAAAGA	AGGGATAACA	TTTTGTAAAA	1620
ATTTTGTAAT	CAATCCATAA	GGACCATAGA	CAAATTTATA	TCCAGTCGCT	AAAACCACTC	1680
CTCCATAAAT	TAAAGAGGTC	ATATAACCTA	ATTTTAAAAAT	TTTAGCACCT	TTAATATCAA	1740
AGTACTCTGT	AAATAGAACA	CAAAGAATAC	CTACGACATT	AACTGTAATA	ATGAGTGAAA	1800
ATGCTAACTT	AAAAGTGTTC	ATAATACTCT	GAAGTGCCCT	CTGAGATTTT	AGAACACGAT	1860
GTACAGCATC	AAGGGAAAAT	TCTCCTCCTT	TTACAAATAC	ATTCACTACT	AGATCAAAGT	1920
TTGGATAAAT	AATAAATGTT	ACTAAGAACC	AGATTAAACC	TAAACGAATA	AGCCAATCTT	1980
TTAAATTTAA	TTTATGACGC	ATACTGCACC	TCCTTAAAAAT	TGCAGAACGT	CTGATGGTGT	2040
GATAAATAAT	TCCACACTTT	CTCCGACAGA	TCTAATAGCA	GCCTGACTAT	CAATACTTGT	2100
TACATTAAGA	ATCTGACTTT	CAGAACTTTT	TATTGTATAG	TGAATTGTAA	CTCCAGAAAA	2160
CTCAACATCA	ATAATTGTCC	CTTTTAGAAT	AAAATCTTGT	TCAGTTTCAC	GATTGAATCG	2220
AACTTCTCT	AATCGAATGT	ATCCTTTTTT	ATCCTCTAAG	AAAACGCTTG	TATTTTTCAA	2280

1134

TAATACTTCG	TGGACTGTTT	CATCGGTCAA	AACATTAATA	TCTCCAATAA	AATCACATAC	2340
AAATTCAGTT	TGAGAATTAT	GATAAATCTC	TACTGGTGTA	CCGACCTGTT	CGATGTATCC	2400
ATTGTTAAAG	ACTGCAATTC	TATCAGATAA	AGTCAAGGCT	TCCTCTTGAT	CATGAGTAAC	2460
ATATAAAGTA	GTAATACCTA	ACTCTTTTGT	AAGTCTTTTC	AACCTCTTTC	TCAAATCTAC	2520
ACGTAATTTT	GCGTCAAGGT	TTGACAATGG	TTCATCTAGA	CAAAGAATTT	TAGGTTCAAG	2580
AACCAGAGCA	CGAGCCAATG	CTACCCCTTG	TTGTTGACCC	CCAGATAATT	CTGATACATT	2640
ACGCTGTAAC	TGTTGATCAG	AGATCTTAAT	TTTTGTGCGC	ACTGCTGATA	CTTTAGCTTT	2700
AATAACATCT	GGAGCTACCT	TCTTAACCTT	TAAACCAAAT	GCAATATTAT	CAAAAACAGT	2760
CATAGTTGGA	AATAGCGCAT	AAGATTGAAA	TACAATACCA	ATTCCACGCT	TTTCAGGTTC	2820
CAAAATGAGTG	ACATCTGTTC	CATTAACCTC	AATACTTCCT	GATGATGGAT	CTAGAAAACC	2880
TACCAATGCT	CTCAAAGTAG	TTGATTTACC	ACATCCTGAA	GGCCCAAGAA	ATGTAAAAAA	2940
TTCCCCTTCA	TGTATATCTA	AATTCAGATT	ATCAATTGCA	ACAAAATCAC	CATATTTAAT	3000
TTGAATATTA	TCAAATTTAA	TCATCTCACT	AACTCCCTCT	ATTACTAAAC	CAAAGCCTC	3060
TCTTTATTTT	TTCCATAAAT	TTAGAAATAA	TAGAGAGACT	TGGACATAAA	AATTAACCTC	3120
TATTTCTTAT	TGTACGTATT	CTAATTCAGC	TTTTTCTACC	CATTCATCCA	AATGCTTTCC	3180
AACAGCTTCC	CAGTCAATAT	TTTGTGGTTT	CACTTGATCA	ACAAATTTCT	TCGTATCTTC	3240
AGGTAGATCT	TTGAGGGCAT	CTTTATTTCG	AGGAATAGAT	CCAAAGTTCT	TACTATATTC	3300
TACTTGAATT	TCTGATTGAC	CAAACCAATC	AATAAATTCT	TTAGCTAACG	CTTGTTTTTT	3360
ACTAGTGCTT	AAAACCATAG	TTTGTTCAGT	TACAAATGGT	ACACCAATCT	CAGGAGTCAT	3420
AACTTTGAAA	ACAACATTTT	GTTCTTTTTG	TCCAACATAAT	GCACCAGAAC	CCCACATCAT	3480
TCCATATTGT	ATTGGATCTT	CTTTGTCTAA	CATCTTAACA	ATTGAACTTT	CTCCCTTTTG	3540
AAGAGTGTAT	GCATTTTTC	AATATTCTTT	TGCTACTTCC	CAACCTTTTT	CGGAAACACC	3600
TAATTCACCT	TTATCATCAA	GGTATCGAAC	TAAGATACTT	GCTAGAATTG	CCCGTCCTGT	3660
ACCTCCTTGA	AGACCAGAAA	TTGAATATTT	ACCTTTATAC	TTACTACCTA	ATTCAGTCCA	3720
ATCTTTAGGC	ATTTCTTTTA	CATCAGGCGC	CCCAATTAAA	ACTAATGGTT	GAACAATCAC	3780
AGGATTATAA	TAATTATCTT	TATCTGATAA	AGATTGATCA	ATTTTATCTA	ACCATTTAGG	3840
CTTGTAATGT	ACTAGTAATT	TTTGATCTCT	AATTTTATTT	GAATCAACAG	CACCAATTCC	3900
AAATACCATA	TCTGCAACTG	CATTATTCTT	CTCAGCAATA	ACACGGTCTG	CTAATTGAGC	3960
GCCAGCGATA	TCAACCATTT	TTATATTAAA	ACCAGCTTCT	TTTGCTTTAG	CAGTTAACCA	4020
ATCACCACGA	CCATTTGAGA	CTGAGTTCGA	ATAGATAACT	AATTCCTGAC	TTTTATCAGC	4080

1135

TTTTTCTTCA GATGAAGAAG CAGTCGTAGA ATTTGAACCT CCAGAGCAAG CAGCAAGTGT	4140
AGTAAGAGCA ACTCCCGTTG CAAGTACAGT AGACCAAACCT TTCATTTTTT TCATGATAAG	4200
TTCTCCTTTT TTATTATTTT ATTTAAATTT TTCGTGATAT GGAACAAATT GTCTCATATC	4260
TTCAAATACA GTATAGTCAA TACGGTTTAC AGTAATAGTT GGAATCTTCT CTAATAAAAT	4320
TTCAAGTTAAT TCTGCTCTGA CTTTAGTAAA CTCTTCTTCC TCCTCTTCGG TTAGAGGAAT	4380
CCGAAGATAC CCAATTGAAA TATGGAATTG ATATCTATCA TGATTAGGGA AACAAACACC	4440
TGCTTTTTCT GAGACATAAG TACGAATTC TCTAATCTC TTTGCAGAAG CTTCATCTGC	4500
AGGTTCAACT AGTATGTTTT GTTTTCCCAT TTCAGTTATA CGCATATGAA TTTCTTCATC	4560
CAACAATGGA AAAATTTCAA GTTGTTTAGC AAAGTAATCA TGTATTTCTT GTAAAGGTGT	4620
ATCTAGAGGA AGATTACTGC TCCAAAACCTC gtTCACGATT TTCATGGCAC AACAATTCAA	4680
TTACAGTCAT GTGAATAGAA TTCCTTGGAG TTAAAGTAAA CTTATCGATA AATGGTAATT	4740
CTCTATAACG TGATTGAATA ATATCAACAA CTCCATCAA ATCTTGTTTA GTATAAAGAT	4800
TTGCTACAAC TGTATTCCCA GGGAAATGAT TAAATTCCCC ATTCTCGG	4848

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3763 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GTATAAGCA ACACCTTCTT GCTTGCCATA AGTTGTGAAA TGGGTAGAAT CGATATCTAC	60
AATGAGTTGG TTTAGCTGGT GAAACTGTAA AAAGAATTTCG ACCAATTCAA GGTGAGGCA	120
TCGCAAACTA TGGACTGTTT CCTCGTCAGT TCTGGAAAGA AAACGGGATA AGGTTGGCTG	180
TGAAGCAAGC TGCCCTCCTT CCAATAATTT TGGAAAGTAG GCATCAGCTG ACAATTCTTT	240
ACAAGCATAG TCCGTTCAT AACCTGTTAA CAGTTGAAAG AGGAACTGGA CAAGGATATC	300
TGAATCCGAA TAACGACAGT AGCGGCGTTG GTCATTTCGTT ACTAAATACT TAGAAATCCG	360
CTCTTTTACT TTCAACTGGG AAAAAAGTTC CTGAAAAAAG ATAAGACCAC CATACTGGGT	420
TAAATGACCT CCATCGAAAG ATAGTTGGTA AAAAGACTTG TTTTGGAAGT GATGATTGG	480
TAAACTGTTT ATGTGAGTTT CCTTCTTTT TGTGTTTTT TCTACACTTA TACCATAAAG	540
GGGAAACTCT TTTTGTCTA GTAAAAACA CCCATTGGGT GAAAAAGAA ACCATCCAGG	600

1136

ATCTAAGCTA	AGGCAAGGAT	TCTGGATGGT	TTTTAGATTT	GGGGTGAATA	ATTGGGGATT	660
TAGGAGAAAT	GATGGTATCT	TCCAAATCAA	AATCAACTTC	ACTCCATAGT	CTCAACTGAT	720
TGATTTTCCC	ATCTTGATAG	GTCACATCCT	TGTCAAGGAT	AAACTGAGTC	AACACCTCAT	780
GTTGACCTTG	ACACCTGATG	TCATCTACCA	AGAGCCAGAC	ATCCTCTACC	AACATGAGGA	840
TTTTTCTCCT	GTGAAGATAA	GGCAAATCAG	GTTCTGCTGA	CCAATAAGCC	CCCTCAATAT	900
AATGCACTCC	CTCCCTTTCT	TTATGGTGAC	AAAACAGGGA	GTGAGGATAG	TATTCATATT	960
CCCAGGATCC	CGTGATTCTT	TCCGGAGCTT	TCCCATCTAC	AATGCAGGTC	GAATGACTCC	1020
AAGCACTCTT	TAAGAGATAA	CGTTCATATA	TCTCCCGATA	AGAATAACGC	CCAGCATCTA	1080
TGAAAATAGG	TTGGCCTTGA	TACTGTAAGC	AAAACTATT	CTCGTCACTA	TGACTATGGG	1140
CACTTCCTAG	CGGACCATTT	TTGAAAAATA	GATAACGATG	TTCATCCTTA	ATGCAGACAT	1200
GTCCAGAGTC	TTCAAAGATC	ATGGACTTAG	GCTGCCAAGC	TCTCTTTTCA	AATTCCTGCA	1260
GTCGCTTGAC	CTTTTCTCGC	CCCAGGAACA	AGAGGCTAAG	CAAACTCACT	TTAACATCCA	1320
GACCGTTAAG	AAGGTCTTCC	TGGTTCAAAA	CCACAGCAGA	CAGGCTCAAA	ATTTCTGTCTG	1380
TTTCTGTAGA	ATCGCTATCA	CCAAAAGCCA	AAGTCCGTCC	ATCTAAGCCT	GTCATCATTT	1440
GAATATAGGT	CGCCATCTTT	TCCAGCAACT	CTTGGTAACT	ATCTTGCAAG	TCTGGAAGCA	1500
AGAGACACAA	ATCCAGCAAG	GCTTTATAAA	CCTCTACATG	ATAGAGAATC	GA CTGTTCAA	1560
ACTGGCTTCC	ATCTCCTAAA	ATCTGTGTCT	CAATTTGCTG	TTTCAACTCC	TCTGAAGCAA	1620
AATGGTAAGC	TTCTTCTAGA	TCCATCTTAT	CTGAAAAGAA	ATGATAGATA	GCAAGCATCG	1680
GAATTGTTTG	TAAATCCCC	CAGTTACTAA	GGGTGTACTT	GGCGCGATAG	TAGCTTTTCA	1740
TAAAGTCAAT	CTGCTTTTCT	AGACTGACCA	AAATTTTCTC	TAGTTCTTTC	TCCTCTAGCA	1800
AGTCAAATTT	CAAGAGGAGC	AAGAGTAGTT	TCAACCAAGT	AAAGGAACGA	ATACCCGTAT	1860
CCAAGTTCT	AGTCATCAAG	GATTGAGGAG	AAAATTCTCT	CACCTGTCTA	ATCCAATCAA	1920
ATAGAAAGAA	CTTGCACTTT	TGAATATAGT	CCTTATCTCC	TTCTACCAGA	TACCCATCA	1980
TAAACTGCAA	GAGATATTCT	TGTCGATTGA	GCATATAAGA	CCATTCTGGA	TCATCTTCAA	2040
ATACTTGATC	CCATACCATC	GGCTGGATTT	GATGGATTTT	TGAACAAGGC	TCCATATCCC	2100
AAGGACTATC	AAACATAAAA	CGATTGTCCA	TCAAGCGTTC	AAGGGAAC TC	TTGACTTTCT	2160
CATAGTCTTT	TGAACAGTGC	GACAAGATAT	AATCACGACA	TTGATTTCCA	TCGACTCTTT	2220
CAAAAAATTG	TCTTCTTTCT	TCTTTCATTA	TCTATTACCA	GAAAAAGAAC	TACTTAAAAA	2280
GCAGTTCTTT	TGTCTTTCCC	ATTACACTTT	CCTTTTCTAC	ATGGATGACC	ACACCTTTTG	2340
CAATCTGCAA	GGAGACCAAG	TCATCTTGGA	TAGAAATGAT	TTTTCCATGA	ATTCCAGACA	2400

1137

ATAACAACAC TTCATCACCA AATGTTAAAG AAGCTAAATA CTCTTGTCGT TGCTCCATCT	2460
GTTTGCGAAG CAACTTTTGC TGACGAATAG AATGAAAGCT TGACAGTAAA AGGGGACTCA	2520
CTGCCAAGAC AATCACTATT CCATAAAACA ATGTTGTATC CATTAAGCTA TAATCTTAAG	2580
CCAGCTTCCG ATAATTCCGA TGATAACTGT TAAAATAACG AGTTTATATG TTGTCCATTT	2640
CTTTTCTTTG ATCAAGTAGT AAATAAAAG TGTAAATAGG GCTGGTAGAA GAGCTGGAGC	2700
AACCTTATCA AGCATTCCTT GAATACTTAC GATACTTTGT TTAGCGTCTG CTTTAACTTC	2760
CCCTGCAGCA AAGGTAATCG GCACCATAAT CTTAACAGAT GTCGCTGCCA AACCAGCAAT	2820
TACGCTACAC CGATAATATT GGCAATACGA GAAATCGTTG CCATCTGTTT GCTTAGTTTA	2880
TCAATCACAG TTGTTCTTAG TTTGTATCCA TACAGACCAG TTGACAATTT AATCGCTGTT	2940
AAAATCGTAT TCATCGCAAG GAAGAACAAG ATTGGACCGA CAACCAAGCC TTCTTGAGCA	3000
AACGAAGCTG CGATGGTTGA GAACAATGGA GCTAAACAGA ATTGAGAAAG AGAATCCCCA	3060
ATACCTGCCA ATGGTCCCAT CAAGGCCATC TTGATGCTAC GTGTTTCTTT TGCCGGACGG	3120
CCATTTTCCA ACATTACAAG ATGCAAGCTG GTAATAAAAG GCAGGAAGTG TGGGTTGGTA	3180
TTATAGAATT CACAGTTTTC TTCCAAGGCT TGGTAGAAAC CTTCTTGATC CTCTCCATAG	3240
TGTTTTTTCA AAGCAGGATA CATCACATTG GCATATCCCA ACCCTTGATA GTTACTATAG	3300
TTAAATCCAT TTTGACAAAA GAATGCCCGC AAAGACGTTT TAAGATAATC ACGTTTGTGTT	3360
AATTTGTTAG ATCCAGTCAT CGTGTGCTTC CTCCTCTACC ACATGATCCG CTGTTTTTGG	3420
CTTGTTATAA AATTCAATCA AAGCAAAGAT AGTACCTACA ATTGCAATAC CAATTGTTGG	3480
GATGTTTAGA TAAGCTGCAC AAACATATCC CAACAAGACA AAGGGAATCA ACTCTTCTTT	3540
AGCCATCACT GACAAGATCA TCGCAAAACC GATAGCTGGG AGCATTTTAC CAGCAACTGT	3600
CAAACCTGTA AGTAATACCG GTGGAATGTA GTCTACGACT TTCAACAAGG TATCCATTGA	3660
AAGGGCACCA AGCAACCCAA GGTAAATCCA ATAAAGGCAA ACAACCAAAT TGTTCATTTT	3720
AGAGTGAAGT TAAATTTCTT CAAATTATGG TTTTCAAGT GCT	3763

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5053 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

1138

CAATCTCTGA GTATGTGCGG TCAATACTAw CAAAGGGAAT yCCTGACGTC AAGTAATGTT	60
CAATTGGmCT ATAGGTAATG GCAACCACTC CATCAACTTT ATTATGACGC AACATCTCCA	120
GATAGTCTTG CTCTCTATTT GTACCATTGA TAGAACATAA GAGTAATTTG TTATTTCTCT	180
TATAGACTTC ATTTTCCACA TGCATAGCAA ATTCTGAAAA GAAGGGATGC CAGATACTTG	240
GTACAATGAT TGCAATCGTT TCTGTTTCGAT TTTTTTTCAT TCCTCTAGCG TAGTAATCTG	300
GAATGTAATT CAAAGTTTTA ATCGCTTGTT CCACTTTTTT CAAAGTFACT TCTTTAATGC	360
CTTTTCTTTT ATTAATTACA CGTGAAACAG TTCCAACACT AACTCCTGCT TCTAAAGCAA	420
CATCTTTCAT GGTAATTGAT TTTCTTTGTT CTACCATATT ATCACCTCCT TTCAATATAT	480
AGTATCATGC AAATGCTTTT TAAGCAACTA TTTCTCAATC ATTTTGGCC AGATCATTTA	540
TCCCATCATG AATAAAATCA CTCCAATTAG CTTTGTAAAA TACTTCAATT TTCATGTGTA	600
AACATCTACA TAAACAGGA AAAGCCTTGG TTTTCATGGCT TTTTTCGTAT CTTCTATAAA	660
AAAAGCAAGA GTTTTAGATG GCTATAAATC TAGATGTACA TTTTGCTTAA ATGATTGAAG	720
GTCTTTTCTT AACAAAAACA CCCCCAAAAT TAGACTTTTT CTGTCTAACT TTTGAGGTAC	780
AGTTCAAACG CGAAATAGCG TTTTTTTGTT ATTTTGGTT ACTCATCTAA TCGAATAAAC	840
ATCATGGCAT TTAACAAGTA TATGAGTGAG ACCGTGTTTA TATTATTTGA ATAGATGAGT	900
CTCTTATTTT CAATAGGAGG AATAATAAAA TTAGAAATAA TGATATCATA AGGTGAATCT	960
TCTAAAGATT CCTTTGATAA TTCTAATTCA GTCCAACTT CCAGTTCAAA ATTATTGCTA	1020
CAATAATAAG AAAGTGCTC TGCAACGAAT TTTGCATGAT ACTGATCAAA ATTACTCATA	1080
ACTAAACCT TTAGTTTAGG CTGATTTTGT AGCAAATTAA TCACCAAATG TTTGGTATGA	1140
GTGATGAAGG TATAAGATAG ATGATTTACC ATCATTGAAC TAGAACAAAC CTCAAGAGTC	1200
TCTAAATAGT GAGAAAGCTC TTTTTTTATA TCTGAAACAA ATTTTGGAAA AATATTTTGA	1260
AAGTTCCTGA TTGTATCCC TTTTGTGATCA AATAAAATAA ACTCAGTAAA CAACTCTTGA	1320
CGATACAGAT GTGCGGTATT ATGCAGATGC CAAATCAGAT TATCCTTATT CTCCATTTCA	1380
ATCTGATACT TGA CTGAAAT CTGATCAATA AAATCACTCA ATAGATGGTA AGATTTTTC	1440
ACATAACTAT CCTTTTAC GCATTTTCATA AAGAGACTTT CATCTATGAA AAACATTTT	1500
TGAAAGTAAG ACACAAATAA TTGGCAAACA ACTTCTTCAT CTAAAGAGAT ATTGTATTCT	1560
GATTCAAAAC TCTGAGCAAC ACCTTCTATT CCTTCTGCCT GCATTAAAAA ATCCAACTT	1620
TGGTCGTAA AAGAATCTTT ATCTACTTCC ATAAAATGAC CAACTTTAT TCTATATAGG	1680
TTCTGTAATA GGAGCAACTT TAGCATTTCTA TGCGTTGACA AATTCATTGG AAAGCTTGTT	1740
TCCTTATAAA CCAATTCTAA CAATTGAGAT AGTGCTCTG ATGAAAAAT TTCAAATGGC	1800

1139

CATTCTAGGA AATAATATTT TTCTGAAAAA TATTGTGCAA AAAAGTAACG AATGTCTCTC	1860
TCATTTCCAA TGATTTGAAC AGGGGTCAGA CTAACCTCAA ATTGAAATG CCTTTTAATC	1920
ACTTTATTGA TTTGGCTAAT AATACGATAG AGCGAAGATG AACTGATATA AAATTCCTTA	1980
CAAATACTCT CAGCTTGACA ACCTTCATTA AAGAAGATGA ATTCTAAAAAT CGAAAAATGA	2040
GTTGAATGTT TAAAGAAATG ATGGTAAACC ATTTCAATAT CACTATCATC GGTATTAATA	2100
ATGCGTATAC CATTAGTAGA AGAATGAAAA ATCAAGTCAG GAAAAGCAGA TTTAACATGG	2160
GATAGATCAT CTTTGACTGC ACGTTCTGTA CAATTTAATA ACTCTGCTAG TTCAGAACGA	2220
TGAAACCAAC GTTTATGTTC AAATAATAAT TCTAATAATT CTAATTGCCT ATGACTTTTT	2280
TTAGATAATA AATCTCTCAT GAATATCTTT CTCTCTTTAT AAATTATCGG ATTAAACCTC	2340
TTGCAATTAT ACCACAAAGA ATAGGTATAG CATGATATAA CGACTTTTCC TAAAATCTTT	2400
TATTTTCGTAT AATAACACTA CGGAGACAAAT ATATAAACAA TTTTCTTATT TTACCGTCTA	2460
TTGAGGGCGT GAATACAGAA TCAAATTCOA GTCTAAAGAT TATATTTTTA ATTTTAAAAA	2520
TTATATAATA GCAACAATTA AAGAATTGTA TTTTTTAAAA TTATATAATA ATAACAATCG	2580
AAATAATTGA CTTTTCTATA TTAAAGTTAT ATAATAGTAA TAATCAAAGA AATTGATTTT	2640
TTGATATTAA AATAAAAAAG GAGGGTAGGC AGTGTGTGTA TCAATTATTG CTGGAGGTCT	2700
TATTGGTCTC TTGGCAGGTA AAATCACTAA AAAAGTAGTT CTATGGGAAT CATCGCAAAT	2760
GTATTCGCTG GTTTAGTCGG GGCATATGCA GGACAATCTC TTTTAGGTAG TTGGGGTCCA	2820
GCAATCGCTG GAATGGCTTT GCTCCCATCT ATTGTAGGTG CAGCGATTGT GATTACTGTA	2880
GTGTCACTCT TTACAGGTAG AAAGTAACT TTTCGCCAGT AAAGTTAGCA AACTATTTTT	2940
AAATCAATGA CGGGAAAAAT AGTTTAAATG TTAAATCGAA AGGATTGTAT ATGTCAAAG	3000
CAAAGAAAAAT ATGTTTCATT ATTTTCTGTA TTTTAATCTT GACAATTTTC CTTCTGTGTT	3060
TGATAGATTA TCATCAAGTT AGTGATCTAG GTATTCATCT ACTTAGCTGG AGACAGAACT	3120
CCGTAGTTGA ATTCTATCTT GCTAGATATG TCTTTTGGGG GACAGTGGTT CTATCAACTT	3180
TAGTTTTATT ATCCATTTTA GTTGTGATGT TTTATCCTAA ACGTTACTTG GAAATCCAAC	3240
TTGAACTAA AAACGATACA TTAAATTAAG AGAATTCGGC AATCGAAGGT TTTGTTAGAA	3300
GTTTGGTGAG TGATCATAGA TTGATCAAGA ACCCAACTGT TCATGTAAAT TTACGAAAAA	3360
ATAAATGTTT CGTTCATGTA GAAGGTAAAA TTCTTCCTTC AGACAACATC GCTGACAGAT	3420
GCCAAATAAT TCAAAATGAA ATAACATATG GATTGAAGCA GTTTTTTGGT ATTGAGCGTC	3480
AAGTAAACT TGAAGTTGCA GTAAAAAATT ACCAACCAAA ACCTCAAAAC AAAAAGACTG	3540

1140

TTAGTCGTGT GAAGTAAGGA AGTAAAAAAT GGAATGGCTT AAACAATATC GATATCCAAT	3600
TATCGCTGGT CTCATAGGCG TATTCTGGC TTGTTTGATT GTCTCCTTTG GCTTCTTCAA	3660
AAACAATATTT GTATTGATTT TAGGAGCACT GGGAGTTGCA GCTGGATTAT ATATCGAAAA	3720
AAACTATATA GATAAATAAA AAAATAAAAA TTACTAATTT AATTAAAGGA GTTTCATATG	3780
TCAAACGAAA AAAACACAAA CACTAACGTA GAAAAGAAAG ATGCTACTGT TGTAGCTCAC	3840
GAAATCAAAG GGGAACTTAC TTACGAAGAT AAAGTTATCC AAAAAATCAT TGGTCTTTCA	3900
CTAGAAAACG TTTCAGGTCT TTTGGGAATC GATGGTGGTT TCTTCTCAA TCTTAAAGAA	3960
AAAATCGTTA ACAGCGATGA CGTAACAAGT GGTGTTAACG TAGAAGTTGG TAAACACAA	4020
GTTGCAGTTG ACTTAAACGT TATTGTTGAG TACCAAAAA ATGTTCCAGC TTTATATTCA	4080
GAAATCAGAG AAATCGTATC TTCAGAAGTT GCTAAAATGA CTGACTTGGA AATTGTTGAA	4140
ATCAACGTAA ACGTTGTCGA CATCAAAACT AAAGAACAGC ATGAAGCAGA CTCAGTAAGC	4200
CTTCAAGATC GCGTATCTGA CGTTGCTGAA TCAACAGGAG AATTCACTTC AGAACAATTC	4260
GAAAAAGCTA AATCTGGTCT TGGATCTGGT TTCTCAACTG TTCAAGAAA AGTTAGCGAA	4320
GGTGTAGAAG CTGTTAAAGG TGCAGCAAAT GGTGTAGTAT CTCACGAAA CACTCGTGTA	4380
AACTAAGATA AAATAAATAT AACAGGAGAA ATTATCATGT CAGTAGAAGA AAAATTAAAT	4440
CAAGCTAAAG GTTCTATTAA AGAAGGTGTT GGGAAAGCCA TCGGTGATGA AAAATGGAA	4500
AAAGAAGGTG CAGCTGAAA AGTTGTTTCT AAAGTAAAAG AAGTTGCCGA AGACGCTAAA	4560
GACGCTGTAG AAGGTGCTGT AGAAGGTGTT AAAACATGT TGAGTGGCGA CGATAAATAA	4620
GGTTAAAAGT TACTTTATCT TTTTAGTAAT ATTAGTCAA AGAGTCTGAG TCAAGATGAT	4680
TCTCAGAAAA CAAAAGCTA GAGATTCCCA ATTGCGGAAC TCTAGCTTTT TAATTTTGCC	4740
TCTTTCTCTT ATTATATTTC AGCAGGTTGT TGGCCATGAG TACGAATCCC ATGTCAATTC	4800
TCACTTGACG CTTACCTCTC AGATGACATC TCTTATAACC CAAACAAACC TTTATCTGCC	4860
CAAAGACAGA TTTCATATCA ATCTTACGTT TAGCGAAAAT TTGTCTACCC TTGGAAGATA	4920
AAAGTGCCTG ATATTCTTTA GTTTTAAAC ACTGGTAACG TTCATTATA TACAGTCTCT	4980
TTTGAGGGGC TGATTCAGGT TCATAATCGC AGTCAACATT GATTTCAAGG CTGTTTGCTT	5040
TCTATCTCCC CGG	5053

(2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

AATTCTCTTT TTTCCAACAA AATGTATGAC CTGCACTTGA ATACTTCTCA TTGTTTGAC	60
ATTCATCTAC TTTCATATAA TCTTTTACAA AATCATAATA TGACATAACA CACTATCCCT	120
TTTAGACAAT ATTCCAATTA GCCTTATTAA TTCAAAATA TTGTATTAGT AATTATAACA	180
GATGTATAAT AGAAAAGCAA TGATAGATAT TATCAATTAA GCGAATTTAT ATCTAAAAGG	240
GATATTAAAG AAAGGAGATA TGCTTATGAA GATTTACAAA AAACATTG CTATGTCCA	300
AGATAAGAAA TATCTTGGGG TTTTGGCCAT AATTTTTTCT GCTATATCTG CTGCACTTAC	360
AGTATATGGA TATTATTAA TCTACAAAT TCTAGATAAG TTAATAATTA ATTCAAATTT	420
ATCCGGTGCA GAGAGTATAG CATTAATAATC TGTTATTACA CTAACAAGTG GAGCGATATT	480
TTATTTTGTC TCAGGAATGT TTTCACATAT CTTGGGATTC AGGCTTGAAA CAAATTTAAG	540
AAAAAGGGaA TCGATGGTCT GGAAAAAGCA AGTTTTAGGT TCTTTGACTT AAATCCATCT	600
GGTCAATAA GAAAGATTAT AGATGCAAT GCTGCACAAA CTCATCAGGT GGTAGCACAC	660
ATGATTTCCCG ATAGTTCTCA GGCAATAATC ACACCCGTAC TTGTACTTGC ACTTGGCTTT	720
ATAGTAAGTA TAAGAGTTGG CATAATTTTG CTGCTCTTA CTATAATTGG TGGCTTAATT	780
TTAGGGGCAA TGATGGGCGA GCAAGAATTT ATGAAGATAT ACCAAGAATC CCTATCTAAA	840
CTAAGTGCTG AAACGTGTA GTACGTGAGA GGAATGCAAG TTGTAAAAAT ATTTAAAGCA	900
AATGTAGAGT CTTTTAAAAG CTTTTATAAG GCGATAAAAG ATTACTCAA GTATGCTTAT	960
GATTATTCCC TATCTTGTA AAGGCCTTAT GTTTGTATC AATGGTTATT TTTTGGACTG	1020
ATTGCAATTT TAATTATTCC TATAGTTTAT TTTATGACTA GCTTAGCTAG CGCAAAGGTG	1080
ATTTTACTTG AGCTTATCAT GATTTTATTT TTATCAGGAG TTCTCTTTGT TTCATTCATG	1140
AGAATGATGT GACTCCATG TATATTTCTC AAGGAAATTA TGCAGTAGAT ACTTTAGAGG	1200
CGCTTTACGA AGATATGCAA AAAGACAAAT TAGTGCATGG TAATGTCAAT AATTTTAAAA	1260
ACTATAATAT AGAATTTGAG AATGTTAGCT TTGCTTATAA TGATAAAGCT GTCATTGAAA	1320
ATTTATCCTT TAATTTAGAA GAAGGAAAGT CCTACGCACT TGTCGGTTCA TCTGGATCAG	1380
GCAATCAAC AGTAGCAAA CTTATATCAG GTTTTACAA TGTTAATAAA GGAAGCATAA	1440
AGATAGGCGG GATAGCAATA AGTGAATATT CTGACGAAGC CTTAATTAAA GCCATTTCCCT	1500
TTGTTTTTCA AGATTCAAAA TTATTCAAGA AGAGCATTTA TGATAATGTA GCGTTAGCTA	1560
ATAAAGATGC GACGAAAGAT GACGTTATGA GAGCCTTAAA ATTAGCAGGA TGCGATTTAA	1620

1142						
TATTAGACAA	ATTCCCAGAA	AGAGAAAATA	CAATCATAGG	CTCAAAAGGT	GTTTATTTAT	1680
CCGGTGGAGA	AAAACAAAGA	ATTGCAATTG	CTAGAGCAAT	TTTAAAGGAT	TCCAAAATTA	1740
TTATTATGGA	TGAAGCATCA	GCATCTATTG	ACCCAGATAA	CGAGTTTGAA	TTGCAAAAAG	1800
CTTTTAAAAA	TCTTATGAAG	GATAAAACAG	TTATCATGAT	TGCACACAGG	CTATCTACAA	1860
TTAAAGACCT	TGATGAAATT	ATTGTCATGG	ATAGTGGAAA	AATTATAGAA	AGAGGGTCTG	1920
ACAAAGAATT	AATGTCAAAA	GATACAAGGT	ATAAGAGCCT	GCAAGAGATG	TTTAACAGTG	1980
CGAATGAATG	GAGGGTTTCA	AATGAAAGAG	TTTTATAAAA	AAAGATTTCG	TCTTACAGAT	2040
GGAGGAGCAA	GAAATTTAAG	TAAAGCAACA	CTGGCTTCAT	TTTTCGTTTA	TTGTATAAAC	2100
ATGCTTCCTG	CCATATTACT	TATGATTTTT	GCTCAGGAAG	TTTTGGAAAA	TATGGGCAAA	2160
AGCAATGGCT	TTTATATAGT	ATTCTCAGTT	TTGATTTTGA	TAGCAATGTA	TATTTTGCTT	2220
TCTATCGAAT	ACGATAAATT	ATATAACACA	ACCTATCAAG	AAAGTGCAGA	TTTAAGAATA	2280
AGGACAGCGG	AGAATTTATC	AAAATTACCT	CTATCTTACT	TTTCTAAACA	TGACATTTCC	2340
GACATTTTAC	AAACAATCAT	GGCTGATATT	GAAGGCATAG	AGCATGCAAT	GAGCCACTCA	2400
ATACCAAAGG	TGGGCGGCAT	GGTACTGTTT	TTCCCATTA	TATCTGTAAT	GATGCTAGCG	2460
GGCAATGTCA	AGATGGGTTT	AGCTGTAATT	ATTCCATCTA	TTTTAAGCTT	TATATTTATA	2520
CCTTTATCTA	AAAAATATCA	GGTTAATGGA	CAGAATAGAT	ATTATGATGT	CTTAAGAAAA	2580
AACTCAGAAA	GCTTTCAAGA	AAATATCGAA	ATGCAAATGG	AGATTAAAGC	ATATAATTTA	2640
TCGAAGGATA	TTAAAGATGA	CTTATATAAA	AAAATGGAAG	ATAGTGAGAA	AGTACACTTA	2700
AAGGCGGAAG	TAACTACAAT	TTTAACTTTG	TCTATATCTT	CAATATTTAG	CTTTATATCT	2760
CTTGCTGTTG	TGATATTTGT	CGGCGTAAAT	CTAATTATTA	ATAAAGAGAT	AAATTCCTCT	2820
TACCTTATAG	GATATTTACT	AGCTGCTATG	AAGATAACAG	ACTCTTTAGA	TGCATCTAAA	2880
GAGGGCTTGA	TGGAAATATT	TTATTTATCG	CCCAAATAG	AAAGATTAAA	AGAAATTCAA	2940
AATCAAGATT	TACAAGAAGG	CGATGACTAT	AGCTTAAAAA	AATTTGATAT	TGATCTAAAA	3000
GATGTTGAGT	TTGCCTACAA	TAAAGACGCA	AAAGTTTTAA	ATGGTGTAAG	TTTTAAAGCT	3060
AAGCAGGGAG	AGGTCACTGC	TTTGGTAGGT	GCAAGTGGCT	GCGGTAAAAC	AACTATCTTG	3120
AAACTTATAT	CAAGACTTTA	TGATTATGAC	AAGGGACAAA	TCTTAATCGA	TGGCAAAGAT	3180
ATAAAGGAAA	TATCAACAGA	ATCCCTTTTT	GATAAGGTGT	CTATTGTTTT	CCAAGATGTG	3240
GTTCTCTTTA	ATCAAAGCGT	TATGGAAAAAT	ATTAGAATCG	GTAAGCAAGA	TGCAAGTGAC	3300
GAAGAGGTTA	AAAGAGCAGC	AAAACCTGCA	AATTGCACAG	ATTTTATAGA	AAAAATGGAT	3360
AAAGGTTTCG	ATACAGTTAT	TGGTGAAAAC	GGAGCTGAGC	TATCAGGAGG	AGAAAGACAA	3420

1143

AGATTATCAA TAGCCAGAGC CTTCTTAAAA GATGCGCCGA TATTGATCTT AGATGAGATA	3480
ACAGCAAGCC TTGATGTTAA CAACGAGAAA AAGATTCAAG AGTCTTTAAA TAATTTAGTT	3540
AAAGATAAAA CTGTTGTAAT CATTTACAT AGAATGAAAT CCATAGAAAA TGCAGACAAG	3600
ATAGTAGTTC TTCAAAACGG AAGAGTAGAA AGCGAAGGTA AGCATGAAGA GCTTTTACAA	3660
AAATCAAAAA TTTACAAAA TTTAATAGAA AAGACAAAA TGGCAGAAGA ATTTATTTAT	3720
TAGGAGGACT ACAATGGATA ATAAAAATT AAAAGTAAAA GATTTAGTAA GCATCGGTGT	3780
TTTTGGCGTA ATTTATTTTG CCTTCATGTT TGGAGTTGGT ATGATGGGCT TGATTCCAAT	3840
ATTGTTCTTA ATATACCCGA CAGTATTAGC CATAGTTGCA GGAACGTGTG TTATGTTATT	3900
TATGGCTAAG GTTCAAAAGC CATGGGCACT ATTTATATTT GGTATGATAT CACCACTTGT	3960
GATGTTTGCA GCTGGTCATA CCTACGTAGT TGTGGTTTTC TCACTTATAG TAATGATAAT	4020
AGCAGAATTA ATTAGAAAGA TTGGTAATTA TAATTCATTT AAATACAATA TGCTTTCTTA	4080
TGCAATCTTC AGCACATgGA TATGTAGCTC TTTAATGCAA ATGCTTTTAG CAAAAGAAAA	4140
ATATATGGAG TGGTCTTTGA TGAATATGGG AAAAGATTAT GTTGATGTAT TAGAAAAGTT	4200
AATAACTTAT CCTCACATGG CTTTAGTAGC CTTAGGTGCT TTCTTAGGAG GAATTCCTGG	4260
AGCATATATA GGCAAGGCTC TATTGAAAA ACACTTTTC AATGGATTAT ATTGTGTGGG	4320
ATACTTTACT CCTTGCCTAA TTTTATGGTG CTATCTGAAT TAAACCCTAT AGTTAAGATG	4380
TTTTTGAGTA TACCTATTGT TATTAGAATG TTTATTTTAC CATTTATGGC AGCAAGCTTT	4440
ATGATAAAGA CCTCGGATGT AGGCGCAATA ATTTTCATCGA TGGATAAGCT TAAGATTTCA	4500
AAGAATGTAT CCATACCTAT TCGGTTATG TTTAGATTCT TCCCATCTTT TAAGGAGGAG	4560
AAGAAAAACA TCAAAATGGC TATGAGAGTA AGAGGGATAA ATTTTAAAA CCCAGTCAA	4620
TATCTTGAAT ATGTTTCTGT GCCACTACTC ATTATATCAT CTAATATATC AGATGACATT	4680
GCAAAAGCGG CAGAAACAAA GGCAATAGAA AATCCAATTG CCAAGACCAG ATACATTCGC	4740
GTAAAGATAC AGCTAATTGA TTTTGTTTAT GTTTTAGCGG TTGCTGGACT TATTGTGGGA	4800
GGCTTAATAT GGTTGAAATA AAAAAATTAA GTCTTGATTA TGGTGAAGAG CATATATTAG	4860
ATGATATATC ACTATCCATA GCCGAGGGAG AGTGCGTGCT ATTTACAGGA AAAAGTGGAA	4920
ATGGTAAGTC ATCTTTAATA AATTCAATCA ATGGACTAGC TGTAAGGTAT GATAACGCAA	4980
AGACAAAGGG CGAAATAATT ATTGATGGTA AGAATATAAA AAATTTGGAA CTTTATCAAA	5040
TCTCAATGCT TGTTTCAACT GTTTTCAAA ATCCTAAGAC ATATTTTTTT AATGTCAATA	5100
CGACATTAGA ATTATATTTT TATTTGGAAA ATATCGGTCT TGCAAGAGAA GAGATGGACA	5160

1144

GGCGTTTGAA GGATATACTT GAGATATTCC CGATAAAAAA TCTTTTGAAC AGAAATATAT	5220
TTAATCTATC CGGCGGTGAA AAACAAATTC TTTGCATTGC AGCTTCTTAT ATAGCAGGTA	5280
CAAAGATTAT AGTTATGGAT GAGCCTTCAT CGAATTTAGA TATTAAAAGC ATAAGTGTTT	5340
TGGCAAAGAT GCTAAAGATA TTAAAAGAGA AAGGCATAAG CATAATTGTT GCAGAGCATA	5400
GAATTTATTA TTTGATGGAC ATAGTTGACC GTGTATTTT AATAGATAAA GGAAAGCTTA	5460
AAAAAACTTA TACTAGAAGT GAATTTTAA AGCTAGATAA AAATGAATTA AATGCTTTAA	5520
GTTTAAGAGA TAAAGAATTA AGTAAATTAA AAGTTCCTTA TTTAAAAGAA GGTGGAGAGT	5580
ATCAGATAAA AAATCTTAGT TACAAATTTA CTGATGATGA GTGTTTAAGC TTAAAAGATA	5640
TTTCGTTCAA GCTTGGGAAA ATTTATGGCA TAATAGGATC CAACGGACGA GGAAAATCAA	5700
CGCTTTTAAG ATGTTTAATA GGTCTTGAGA AAAAATCAAA AGAAGAAATT TATTTTAAGG	5760
GAGAGAAGCT ATCTAAAAA GAAAGACTCA AAAACTCTTC ACTTGTTATG CAAGATGTAA	5820
ATCATCAATT ATTCACAGAT GAAGTATCA ACGAGCTTAG ATTAGGAGTA AAGAATTTTG	5880
ATGAAGAAAA GGCGAAAATC ATTTTAAACC CCAATTATTC ACCCCAAATC TAAAAACCAT	5940
CCAGAATCCT TGCCCTTAGCT TAGATCCTGG ATGGTTTCTT TTTTCACCCA ATGGGTGTTT	6000
TTTACTAGAC AAAAAAGAGT TTCCCCTTA TGGTATAAGT GTAGAAAAA ACACAAAAAG	6060
AAAGGAACT CACATGAACA GTTTACCAA TCATCACTTC CAAAACAAGT CTTTTTACCA	6120
ACTATCTTTC GATGGAGGTC ATTTAACCCA GTATGGTGGT CTTATCTTTT TTCAGGAACT	6180
TTTTTCCCAG TTGAAACTAA AAGAGCGGAT TTCTAAGTAT TTAGTAACGA ATGACCAACG	6240
CCGCTACTGT CGTTATTCGG ATTCAGATAT CCTTGTCAG TCCCTCTTTC AACTGTTAAC	6300
AGGTTATGGA ACGGACTATG CTTGTAAAGA ATTGTCAGCT GATGCCTACT TTCCAAAATT	6360
GTTGGAAGGA GGCAGCTTG TTCACAGCCA ACCTTATCCC GTTTTCTTTC CAGAACTGAC	6420
GAGGAAACAG TCCATAGTTT GCGATGCCTC AACCTTGAAT TGGTCGAATT CTTTTTACAT	6480
GTTCAACGAGC TG	6492

(2) INFORMATION FOR SEQ ID NO: 189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

AACTGAAGGT AAAGGCTTCG ACGCAGAACG TGACGCTGCC CAAGCTGCC TTGATGACCT	60
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1145

TAAGAAAGCT CAAGAAGACA ACAACTTGGA CGACATGAAA AAAAACTTG AAGCATTGAA	120
CGAAAAAGCT CAAGGACTTG CTGTTAAACT CTACGAACAA GCCGCAGCAG CGCAACAAGC	180
TCAAGAAGGA GCAGAAGGCG CACAAGCAAC AGGGAACGCA GGCGATGACG TCGTAGACGG	240
AGAGTTTACG GAAAAGTAAG ATGAGTGTAT TGGATGAAGA GTATCTAAAA AATACACGAA	300
AAGTTTATAA TGATTTTGT AATCAAGCTG ATAACATATAG AACATCAAAA GATTTTATTG	360
ATAATATTCC AATAGAATAT TTAGCTAGAT ATAGAGAATT ATATTAGCTG AACATGATAG	420
TTGTATCAAA AATGATGAAG CGGTAAGGAA TTTTGTACC TCAGTATTGT TGTCTGCATT	480
TGTATCGGCG ATGGTACCAG CTATGATATC ATTAGAAATA CAAACATATA AATTTGTAAT	540
ACCGTTCATA ATTGGTATGA TTTGGACAGT AGTTGTATTT CTTATGATCA ATTGGAATTA	600
TATAGGCAAA TACTAAGAAG AGACAAAAAT ATATAAATAT TTCTGTACTT ATAGGATATT	660
TAAAATCAAA ATAAAGTTAA TTTACTTATT TGCAGAGGTT GCAACCCAGC CTCTGTTTTT	720
CGATAAAAAG GGACGGAATC TCATTTGTTT GGGTTTGTGTC TCATCAATAG AAAGGAACAA	780
AGAGTGTTGC TAACTGAACA CGGGTTTCAG AATTTCTTAC TAAATATAAA AGAAAGGAAT	840
TGAACCCGAC CTAAATGGTG GTTCGATTCA GAACATCAAT AGAAAGGAAT AAGGGTGTTT	900
GTAACGAAC ACGGGCTATG GACTGTGCCA AAAAGATAGT TTTTCTAGG ACGTAAGCGT	960
CCGTCGTCAA AACTCCTAGA TGGCTGTGTC CGTTTGACGC CCTTTGTATC TTGAATTATG	1020
AACAATACTG AATTTTATGA TCGTCTGGGG GTATCCAAAA ACGCTTCGGC AGACGAAATC	1080
AAAAAGGCTT ATCGTAAGCT TTCCAAAAA TATCACCCAG ATATCAACAA GGAGCCTGGT	1140
GCTGAGGACA AGTACAAGGA AGTTCAAGAA GCCTATGAGA CTTTGAGTGA CGACCAAAAA	1200
CGTGCTGCCT ATGACCAGTA TGGTGCTGCA GGCGCCAATG GTGGTTTGG TGGAGCTGGT	1260
GGTTTCGGCG GTTTCAATGG GGCAGGTGGC TTCGGTGGTT TTGAGGATAT TTTCTCAAGT	1320
TTCTTCGGCG GAGGCGGTTT TTCGCGCAAT CCAAACGCTC CTCGCCAAGG AGATGATCTC	1380
CAGTATCGTG TCAATTGAC CTTTGAAGAA GCTATCTTCG GAACTGAGAA GGAAGTTAAG	1440
TATCATCGTG AAGCTGGCTG TCGTACATGT AATGGATCTG GTGCTAAGCC AGGGACAAGT	1500
CCAGTCACTT GTGGACGCTG TCATGGCGCT GGTGTCATTA ACGTCGATAC GCAGACTCCT	1560
CTTGATATGA TGCGTCGCA AGTAACCTGT GATGTCTGTC ACGGTCGAGG AAAAGAAATC	1620
AAATATCCAT GTACAACCTG TCATGGAACA GGTCAATGAGA AACAAGCTCA TAGCGTACAT	1680
GTGAAAATCC CTGCTGGTGT GGAAACAGGT CAACAAATTC GCCTCGCTGG TCAAGGTGAA	1740
GCAGGCTTTA ACGGTGGACC TTATGGTGAC TTGTATGTAG TAGTTTCTGT GGAAGCTAGC	1800

1146					
GACAAGTTTG	AACGTGAAGG	AACGACTATC	TTCTACAATC	TCAACCTCAA	CTTTGTCCAA 1860
GCGGCTCTTG	GTGATACAGT	AGATATTCCA	ACTGTTACAG	GTGATGTTGA	ATTGGTTATT 1920
CCAGAGGGAA	CTCAGACTGG	TAAGAAGTTC	CGCCTACGTA	GTAAGGGGGC	ACCGAGCCTT 1980
CGTGCGGGTG	CAGTTGGTGA	CCAATACGTT	ACTGTTAATG	TCGTAACACC	GACAGGCTTG 2040
AACGACCGCC	AAAAAGTAGC	CTTGAAAGAA	TTGCGGGCTG	CTGGTGACTT	GAAAGTAAAT 2100
CCAAAGAAAA	AAGGCTTCTT	TGACCATATT	AAAGATGCCT	TTGATGGAGA	ATAATACTCT 2160
TCGAAAATCT	CTTCAAACCA	CGTCAGCGTT	GCCTTGCCGT	ATATATGTGA	CTGACTTCGT 2220
CAGTCGTATC	TACAACCTCA	AAACAGTGTT	TTGAGCAGCC	CGTGGCTAGT	TTCCTAGTTT 2280
GCTTTTACT	TTATAGATTT	TTTAAGACTT	TCCTAAGTAA	TGACGGACGG	TAGTGACCTC 2340
CTTCGAAGTT	CCATACCTAA	ACTTTGAACC	TAAGTTTAA	AGTTTCCGGA	CAGCTGAAAC 2400
CAAGCTGTTT	CAGGTGTTTT	CATTACGGCA	GAAAGTCTTC	GATTTAGTTG	TGAAATGGTG 2460
AATGATACTC	TTCAAAAATT	TCTTCAAACC	ACGTCAGCGT	CGGCTTGTC	TGGGTATGGT 2520
TACTGACTTC	GTCAGTTCTA	TCCACAACCT	CAAAACAGTG	TTTGAGCTGA	CTTCGTCAGT 2580
TCTATCCACA	ACCTTAAAAC	GGTGTTTTGA	GCAGTCTGTG	CCTAGCTTTC	TAGTTTGCTT 2640
TTTGATTTTT	ATTGAGTATG	AATTACCTAA	ATTATGATGC	ATAGTTGATG	GGATATATAT 2700
AATAGATTGA	AATAGAATAT	GAACAAATTG	ATAAGAGGAT	TTTAAAGTAA	TCTCTAACAA 2760
TGCTTTAGAA	ACTATGGTGT	GCTATTCTAA	ATTCAATTCA	CTATAACTTG	TTTACGTTTT 2820
AAAAAAGAGC	CGTCGGGCTC	TTTTTACTTA	TCTTCAGTTC	CCTGCATTTT	TTTTATCACA 2880
GCTAGTCTAG	TCTGGATATC	CTTTTCCAAG	ACCTTAAACT	TGTAAGTCAA	GTCTTCTTGG 2940
TATTCCTTGA	TAAGTTCTTT	TTGCTGGTTA	ATGATTTGCA	GGCTGTTTTG	GATAATATCC 3000
ACATCGTCCT	TGATAGCTTG	AACGCGGTCA	GTGGTATTCA	AGACTTCATC	TGTGATGGTT 3060
TGGCGATTTT	TTGTAACCAG	ATAACTTCCG	GCTGCAGCTC	CTGCAAATAG	CAGTAGGTTG 3120
GATAATTTCA	TAGCAACTCC	TTAAGCGTTT	TTGATGGTTT	CAGCGACTTG	AGCAAGTTTG 3180
TCAAAGTCTG	GTTCTGGGGC	GATAAAATCA	ATCTTGAGGT	CATCGTCAGC	ACTGTAGCGA 3240
GGCACAAGGT	GAACGTGAGT	ATGAAAAACT	GTTTGACCAG	CGACTTCTTC	ACAGTTGGAA 3300
ATGATATTCA	TACCAGCAGC	CTTAGTGACT	TTCATGACTT	TTTGAGCTAC	TTTTGGTACT 3360
TGGGCAAAGA	GTTGGCTGGC	GCTCGTAGCA	TCCATCTCCA	AAAGATTGCG	ATAGTGTTCT 3420
TTTGGCACGA	CCAAGTGTG	TCCTAGTGTT	ACTTGAGAGA	TATCAAGAAA	GGCAAGGACC 3480
TGCTCATCTT	CATATACTTT	TGAAGCAGGA	ATTTCCCTTG	CGATGATTTT	ACAAAAATG 3540
CAATCTGACA	TAAATCTAC	CTCTACTGTA	CTGAATTTTG	ATATAATATA	GCTACATTAT 3600

1147

ACCAGATTTG GAGAAAATAT GTTAGAAATT AAAAACCTGA CAGGTGGCTA TGTTCATGTT	3660
CCTGTTTTGA AAGATGTGTC CTTTACTGTT GAAAGTGGGC AGTTGGTCGG TTTGATTGGT	3720
CTCAATGGTG CTGGGAAATC AACGACGATC AATGAGATTA TCGGTCTGTT GGCACCTTAT	3780
AGTGGCTCCA TCAATATCAA TGGCCTGACT CTGCAAGGAG ATGCGACTAG CTACCGCAAG	3840
CAGATTGGCT ACATTCTGA GACGCCTAGT CTGTATGAGG AATTGACCCT CAGAGAGCAT	3900
ATCGAAACGG TTGCTATGGC TTACGGTATT GAGCAAAAAG TGGCTTTCGA ACGAGTAGAG	3960
CCCTTGTTAA AAATGTTCCG TTTGGAACAG AAATTAGACT GGTTCCTGT TCATTTTTCA	4020
AAAGGGATGA AGCAGAAGGT CATGATTATC TGTGCTTTTG TGGTGGATCC AAGCTTTTTC	4080
ATCGTGGATG AGCCTTTCCT TGGTCTTGAT CCGCTGGCTA TTTCTGATTT GATTCAGCTT	4140
TTGGAAGTGG AGAAGCAAAA GGGCAAGTCT ATTCTCATGA GTACCCACGT GCTGGATTCC	4200
GCGGAGAAGA TGTGTGATGC CTTTGTCAIT CTTTACAAGG GAGAGGTGCG TTCCAAAGGC	4260
AATCTCCTGC AACTACGTGA AGCCTTTGAT ATGCTGAGG CTAGTTTGAA TGATATTTAC	4320
TTGGCTCTGA CCAAAGAGGA GGATCTATGA AAGACTTGTT TTTAAAGAGA AAGCAGGCCT	4380
TTCGTAAGGA GTGTCTTGGT TATCTGCGCT ATGTGCTCAA TGACCACTTT GTCTTGTTCC	4440
TGCTTGTCCT GTTGGGCTTT CTAGCCTACC AGTACAGTCA ACTCTTACAA CATTTTCCTG	4500
AAAATCATTG GCCTATCCTT TTGTTTGTAG GAATTACGTC TGTTTTACTT TTACTTTGGG	4560
GAGGAAGTGC CACCTATATG GAGGCTCCAG ACAAGCTCTT TCTCTTAGTT GGAGAAGAGG	4620
AAATTAAGCT CCATCTCAAG CGTCAAACTG GCATTTCCCT AGTCTTTTGG CTCTTTGTAC	4680
AGACCCCTTT CTTGCTGTTA TTTGCGCCTT TATTTTTAGC AATGGGTAT GGCTTGCCAG	4740
TTTTTCTGCT CTATGTGCTT TTATTGGGGG TAGGAAAATA TTTCCACTTT TGTCAAAAGG	4800
CCAGCAAAT TTTCACTGAA ACTGGACTGG ACTGGGACTA TGTTATTTCT CAAGAAAGCA	4860
AGCGTAAGCA AGTCTTGCTT CGTTTCTTTG CCCTCTTTAC GCAGGTCAAG GGAATTTCAA	4920
ACAGCGTTAA GCGTCGTGCC TATCTGGACT TTATTTTAAA GGCTGTTTCAAG AAGGTGCCTG	4980
GGAAGATTG GCAAAATCTC TATCTGCGTT CTATCTGCG AAATGGCGAC CTCTTTGCTC	5040
TCAGTCTTCG TCTTCTCTTG CTTTCTTTCG TGGCGCAGGT TTTTATCGAG CAAGCTTGGA	5100
TTGCGACAGC AGTGGTAGTT CTCTTTAACT ACCTCTTGCT CTTCCAGTTG CTGGCCCTCT	5160
ATCATGCCTT TGACTIONCAG TATTTGACCC AACTCTTTCC GCTGGACAAG GGGCAAAAGG	5220
AAAAAGGCTT ACAGGAGGTA GTTCGAGGAT TGACCAAGTT TGTTTTACTT GTGGAATTAG	5280
TTGTTGGGTT GATTACCTTC CAAGAAAAAC TAGCCCTTCT AGCCTTACTA GGAGCTGGTT	5340

1148

TGGTTTTACT	AGTCTTGAT	TTGCCTTATC	AGGTAAAACG	TCAGATGCAG	GACTAACATT	5400
GCTGATACGA	CACTAAAAAA	GAAGTTGAGT	TCAGTCTGTC	TCAACTTCTT	TTTGTTACT	5460
ACAGGATAAT	GGTTGGTCCG	TAGAGACTTA	TACTCTTCGA	AAATCTCTTC	AAACCACGTC	5520
AGCGTCGTCT	TACCGTACTC	AAGTACAGCT	TGCGGCTAGC	TTCTTAGTTT	GCTCTTTGAT	5580
TTTCATTGAG	TATTAACCTG	GTCTTGACTT	GGTCAAAGTG	GAAGCGGTCA	TAGGCCCCGC	5640
AAGCGGCGCG	AGTTGGAGCA	TCTGGATCAA	GAGCGCTGAG	TCCCATGAGA	AGACTGGAAG	5700
TCTGGTAAAA	TTTTTCTAGT	TCAATCAAGA	ATCGATTATC	CACTGTTTCA	GCCTTGGCTA	5760
GAAAACCAAG	AATAGAGTTT	AATTGCTCCT	GAAAGCGGAC	GTCGTCAGCG	CTTGCCTGTT	5820
TGCATGCTTG	GTAGGCTTTG	TTTAAGTCAG	TAATCAAAGT	ATGAGCTCTT	TTGATGGGGT	5880
CTGTATCTGT	CATGGGAATG	CCTCCTTTAA	TCTGGGTGCC	AGTCTTACTT	CTGGCAACTG	5940
TGTTTTGATA	CTGTTAGTTT	ATCACTTTTA	ATTCTTTTTT	TTTATTCAAA	TCTTTAATTG	6000
TCATTGAAAT	GTCTTGAATT	GCGCTGAGTG	AATTTTATGA	TAAAATAGTT	GTAAGCTCAT	6060
CATGATGTTG	TAGAAAATAA	TCCTTTTAGG	AGTTTTCAAA	GACTGTTTAG	GATTGGGTGT	6120
GCTTGGGCTA	GACCTTTTCT	GTTATTCTTT	TCTTAGGAGG	AGAATCCAAT	GAAATATATG	6180
ATTATTCAGA	CGCAGAAAAC	AGTCTATAAA	GTAAACATCG	ACGATATCTA	CTATATCCAA	6240
ACACATCCAA	CTAAAGCCCA	TACCGTACAG	ATTGTTACAG	AAGAAGCTAG	TTTTAATATG	6300
CTTCAAAATT	TAAGTAATCT	TGAGAACCAA	TGTGGGGAAA	CCTTGATGAG	ATGTCATCGA	6360
AATTGTTTGG	TTAATCTTGA	TAAATTAAAA	TCGATTGATT	TTCAAGAAAG	AATCCTTTTT	6420
CTCGGAGAAG	AAGGTCAATA	CGCTGTCAAG	TATGCCAGAC	GTCGCTATAG	AGAAATTCGT	6480
CAAAAATGGT	TGAAAGAGGG	AGAGTAAGAA	GATGAGAATA	TTTGTTTTAG	AGGATGATTT	6540
TTCCCAACAG	ACTAGAATTG	AAACGACGAT	TGAGAAACTT	TTGAAAGCAC	ATCATATCAT	6600
TCCTAGCTCT	TTTGAGGTAT	TTGGCAAGCC	GGACCAACTG	CTGGCTGAAG	TGCATGAGAA	6660
GGGGGCCCCAT	CAGCTATTCT	TTTTGGATAT	TGAGATTCTGA	AATGAAGAGA	TGAAGGGACT	6720
GGAAGTGGCT	AGAAAGATTC	GGGATCGGGA	TCCTTATGCC	CTGATTGTCT	TTGTGACGAC	6780
TCACTCGGAG	TTTATGCCCC	TGTCTTTTCG	CTACCAAGTG	TCTGCTTTGG	ACTACATTGA	6840
TAAGGCCTTG	TCAGCAGAGG	AGTTTGAATC	TCGGATCGAG	ACAGCCCTCC	TCTATGCCAA	6900
TAGTCAAGAT	AGTAAAAGTC	TGGCGGAAGA	TTGCTTTTAC	TTTAAATCAA	AATTTGCCCA	6960
ATTTCAGTAT	CCTTTTAAAG	AGGTTTACTA	TCTCGAAACG	TCGCCCAGAG	CCCATCGTGT	7020
TATTCTCTAT	ACCAAGACAG	ACAGGCTGGA	ATTTACAGCG	AGTTTAGAGG	AGGTTTTCAA	7080
GCAGGAGCCC	CGTCTCTTGC	AGTGCCACCG	CTCTTTTCTC	ATCAATCCTG	CAAATGTGGT	7140

1149

GCATTTGGAT AAGAAAGAAA AACTGCTTTT CTTT

7174

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

CCACCAGGGA AAATCATTGA AGTTGGTAGT CACCAAGAGT TAATGCAGGC GCAAAGTTTC	60
TACCATCATC TATTCAATAA ATAAGGAGAA TGTCATGAAT CCTAATCCTT TTAGAAGCGT	120
CGAGTTTAT CAGAGACGTT ACCATAACTA TGCACAGTG TTAATTATAC CTCTTTCATT	180
ACTATTTACT TTCATCTTGA TTTTCTCCCT TGTGTCACA AAAGAAATTA CTGTTACTTC	240
CCAAGGAGAA ATCGCCCCTA CAgTGTCATT GCCTCCATTC AGTCAACCAG TGATAATCCT	300
ATCCTAGCTA ATCATTTAGT GGCAAATCAA GTAGTTGAAA AAGGGGACTT ACTCATCAAA	360
TACTCTGAAA CAATGGAAGA AAGTCAGAAA ACTGCCTTAG CAACTCAATT ACAAAGACTT	420
GAGAAGCAAA AAGAAGGACT TGAATTTTG AAACAAAGCT TAGAAAAAGC GACTGATCTT	480
TTTTCTGGCG AGGATGAATT TGGCTACCAT AATACCTTA TGAATTTTAC TAAACAATCC	540
CATGATATTG AACTGGGTAT CACAAAGACT AACACCGAAG TTTCAAATCA AGCTAATCTT	600
TCCAATAGCA GTTCATCAGC TATTGAACAA GAAATTACAA AAGTTCAACA ACAAATTGGA	660
GAATATCAAG AGTTGAGAGA TGCTATCATA AATAACAGAG CACGCTTACC AACTGGCAAT	720
CCGCACCAGT CAATTTTGAA TCGTTATCTT GTAGCCTCAC AAGGACAAAC ACAAGGAACT	780
GCAGAGGAGC CATTTTTATC TCAAATTAAT CAAAGTATTG CAGGTCTTGA ATCATCTATC	840
GCAAGCCTCA AAATTCAGCA AGCTGGTATC GGAAGTGTAG CAACTTATGA TAACAGTTTA	900
GCAACCAAAA TTGAAGTACT CCGCACTCAG TTTTACAGA CAGCCTCACA GCAACAACCTA	960
ACTGTGGAGA ATCAATTAAC AGAATTAATA GTACAACTAG ATCAAGCCAC ACAGCGTTTG	1020
GAAAACAATA CCTTAACCTC CCCAAGTAAA GGTATCGTTC ATCTGAACAG CGAATTTGAA	1080
GGTAAAAATA GAATTCCAAC TGGTACAGAA ATTGCTCAAA TATTCCTGT CATCACAGAT	1140
ACAAGAGAAG TACTAATCAC TTACTACGTA TCTTCTGACT ATCTACCTCT ACTAGATAAA	1200
GGACAAACTG TAAGATTAAA ACTGGAGAAG ATTGGAAATC ACGGCACCAC CATCATCGGC	1260
CAACTTCAGA CAATTGATCA AACTCCTACC AGAACAGAGC AAGGAAATCT CTTTAAATTA	1320

1150

ACCGCTCTTG	CAAAACTATC	TAACGAGGAT	AGTAAACTCA	TCCAATATGG	CTTACAAGGT	1380
CGCGTCACTA	GTGTAAC TAC	AAAGAAAACA	TATTTTGATT	ATTTCAAAGA	TAAAATTTTA	1440
ACACATTCTG	ATTAATTTTC	AGATAACACT	CTATAACTAT	TTATTATCTT	ATCAAAAAGG	1500
AGAATCATAA	CATGGATAAG	AAACAAAACC	TAACTTCATT	TCAAGAACTA	ACAACTACCG	1560
AACTCAATCA	AATTACAGGT	GGAGGATTGT	GGGAAGATTT	ATTATATAAC	ATTAATAGAT	1620
ATGCTCATTA	CATCACATAA	GAAC TTCATC	ATCCAATACA	ACTATAAAAA	AATAAGACCG	1680
AGAAACAAGT	ACTCTCGGTC	TTATTTTTC A	TCATTCTGTA	TGTATCACAG	TAAGTACCTG	1740
ACGAAAGACT	TGATTTTGAC	AGGTGGTATT	TAGACTGGTA	TTAGGATGGC	TTTCCACAAT	1800
CTTCATGACG	GTATAGAGAC	CAACTCCTCT	CTCCTCCCCT	TTAGAACTGG	CTCCAAAGGA	1860
GAAGATTTC A	GAAATATCGA	TGCCCTCTTC	TTTGATGGAG	TTTTCGATGA	TAAAGGTCTC	1920
CTGTGCTCCA	TTTTTTAAAA	AGGCGATTGA	AACATGAGGT	TGACTAGCTT	CCACACTGGC	1980
TTCAATAGCA	TTGTCACAAA	GGATAGACAC	AATGGTTAGA	AAATCAAGTA	GACTCATCCC	2040
CTCGACCTGA	ATCTCCTCAG	GAAC TTCGAC	ATTAAAGACA	ATGTTCTTAT	CTCTGGCTTT	2100
TAAAAATTT C	CCTGCTAGAA	GACTTTTGAG	GGCTTTTATCA	CGAATATTTA	CCAATCTGCC	2160
CAGGTCATAT	TTATTGTTCT	GCAATTTCTG	ACTGGAATCC	TTTAAGACGG	AGCCATAGAC	2220
CTCTTTTATC	TGCTCCATAT	CCTCCTCTTC	AATGCCCAGA	CGTAAGCTAG	TCAAGAGGTT	2280
GGTATAATCA	TGACGAAAGC	TCCGTACTTC	CTTGTAAGC	TCCTCTATAT	GCCGACTATA	2340
GCGTTCCATA	TCTCTATAGC	GCAGGGCCTG	CTCTTGTTCC	AATCTCTCAT	AGAGTTTTTC	2400
CTTCAAAATAG	GTATCCAATT	TCTTGATAAC	CCCCATAAAA	AAGAGTAGGT	AAAAGACTAG	2460
GATGAGATGG	CGAACAGTCT	TTGATTGAAT	ACTTTGTTCA	TATTCAAAAA	AAGACAGACT	2520
TTCCATGACT	AGATAGTAGC	CACCCATTAT	CCAGTTAATC	TGAGTCAGGG	ACTTTTGAAA	2580
GGCTTTATCG	AGAATCTCCT	TTCTCAAGCT	AGTAAATCG	TAGTCCAACC	ATTTCAAAAA	2640
AGCTAGAGAA	ATGAAGAAAT	TGAAAATTAT	TATACATAAC	CCAGTAAATG	AGTAGCCATC	2700
ATATACTTGC	CCTTGTCCTA	AAAATGGAAG	CACAAAATAG	GAGACTCCTC	TATAAAAGAG	2760
ATTCACCAAT	ATCATTGGAA	AGAGACCATA	AAAGAAAAGG	AGTTTTTTAG	GAAGCCCTCT	2820
CAATAATAAG	AAAGATAAGC	CTATGCCGTA	CAAGGGTTCC	ATAAAATAAG	ATAGGTAAAC	2880
ATTTCTTACT	ATATAGCTAA	TCATCACAAA	AACAAAGGCC	AACAGTATCT	TCAAAAGAAA	2940
GGCCTTAAAA	ATCCTCTCGA	AAGTAAGATC	AATTCCATCC	ACCTTAAAGA	AGATGACAAT	3000
TTCTAGTCCA	TTAGTAACAA	GTGTATACAA	CAATATCCAA	GCAATGTTCA	TAAATTCTCC	3060
TAGCTCAGTG	TAATTTATTG	ATGGCCTCAG	ACACTTCCCT	GACCTTATAA	CGGGCGATTA	3120

1151

GACAACTTCC ACCATTGGGA GAGAAGAGCA GTTTTCTTT CTTATCCAAA TGCACCACAT 3180
 TTGCAGGATT GATGAGAAAA GAGCGGT 3207

(2) INFORMATION FOR SEQ ID NO: 191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

CTGAATCAAG TGTACTGCAC CAGTTCGTGC ATCAGGCATA ACAACATCTA CAGATATAAT 60
 ATTGTTTCT GAGTCCGCCT CATAAGTTAA AATCATAAAT TTTTCGATAT TCGAATTTTT 120
 AGTAGCTTGT TCAATTCTT GAATCATTTT ATCAGAACT AACTCCATCT GAATTGGAAA 180
 GGAATGACTA TTTTCATCAT TTTTGTAGGA AGAATGTTGA TTAAGATAAA GTGTATTCAT 240
 CTGAGCATAT TCAAATAAGT AGCCACTCTT ATTTTCTTGT ACCAAAGGAA ATTGGTTTGT 300
 AAGTCGCTTC TTACCCTTTA TAATTAACAA TACTTTCCCA TATTTTCTG TATTTGTTTC 360
 AAATTCTAAA TATCCCAAG TCTGCTCTGC TAATTGTAAT TTATACTCAA ACAAATCTGC 420
 TGATGCAAAAT GCAGTATCAA TATGATTAGG TCGCGTCCAT GCATAACCAT TCGACACTAT 480
 CATTGTCTCT CTTTTTCTA GACGTCATC TACATAATCT TTTTGCCTT TCATCAAAGT 540
 ATCTACAATT TTTTGTGCCT CAAGCGAATC AAAGAGATCC TGATTCAACA TAATCTTCC 600
 TCCTCCAAAT ACTTTTAAAT GAATTATACC ATTTCTTAA AGAAATTACT ACAATAATTA 660
 TCTTTTCTT AAAGTTCTGT GTCAGAGTAA TTTAGAAAAT TATATCTTCT ATAGTAAAAT 720
 CAATTAAAAA CTGAACAAAT TTATTGGGAA ATTCAAATCG CTTTCTGAAA ATATTTTAGG 780
 AACCGTAGTG TAATATTCCA GATTCAATTC ACTATAAAAC TGACCTTTCT CCTGCAAAAG 840
 AAAAAGGAAA GACTTCCTTT CGTGCCTTTC CTCTTACTTG CTAATTGTTT GATTATTTTT 900
 GGTAAGCTAC TGCTTGTCTG ATAAAATCCT GAATCGGCTC TCCTTGGTGG AGAGCTTTTA 960
 CTATTTTCGA ACCGACGATA ACACCATCTG ACACCGCATT GAAGCGTCC AGATCGGCTT 1020
 GACTAGATAC ACCAAAACCT GTCAAGACTG GGATGTCGGC CACTTGATGA AGTTGCGCCA 1080
 AGTGCTTGT CAAATCTGCA CGGTAATTGC CTGATTCCC TGTCCTCCA TTGATGGCAA 1140
 CGGCATAGAT GAATCCCTCC GCCCTTCAA TCAACTCTT CTGGCGCTCA ATTCCTGTGG 1200
 TCAAGCTTAC TAAAGGAATC AAGGCGATAT CTGTATTGTC CAAAAATGGT TCTACAAAGT 1260

1152

TGGCATGTTT	ATGAGGCAGG	TCTGGGATAA	TCAAGCCCTT	CACAGCTGTA	TCAGCCAGAT	1320
CTTTGACAAA	GTTCTCCACA	CCGTACTGAA	AGAGGGGGTT	GAAGTAGGTC	ATGATGACCA	1380
GTGGAATCTC	TGTTTCAATG	GTTTTC AAGG	TTTCAACTAA	AGCCTGGGTA	GAGGTCCCGT	1440
GGGCTAAACT	GCGCAAGCCA	GCTTCTTCGA	TAACAGGTCC	ATCTGCAACA	GGGTCTGAAA	1500
AGGGAATACC	CAC TTCAATT	GCAGAGACAC	CCAAATCTTC	TAAAAAGTGA	ATTGTTTCAG	1560
CAAGACCGTC	CAAACCTTTC	TCGTGGTCAC	CAGCCATGAT	ATAGGGAACA	AAAATTCCTT	1620
TTCCAGCTGC	TTTAATAGCA	TTTAATTTTT	CTGTAGTGT	CTTAGGCATG	AGCTTCTCCC	1680
TTCTTTGCTG	CATCTGCTTC	CAAGCGGTCC	TTGACTTGAA	CCACATCCTT	GTCCCCACGA	1740
CCTGATAGGC	AGACAATCAT	AGACTTTTCT	GGTCCAAGTT	CTTTGGCCAA	TTTCACCGCA	1800
AAGGCGATAG	CATGGCTAGA	TTCCAAGGCT	GGGATAATCC	CTTCCACACG	AGACAAGAGT	1860
TGGAATCCTT	CCAAGGCTTC	TTCGTCTGTC	ACAGGGACAT	AGCTGGCACG	TTTAATATCG	1920
TGGTAGTGAG	AATGCTCTGG	ACCGATACCA	GGATAGTCCA	AACCTGCTGA	GATAGAGAAG	1980
GCTTCAAGAA	TTTGACCATG	GGCATCTTGG	AGCACATCCA	TGAGGGAACC	GTGAAGGACA	2040
CCTGGACGAC	CCTTGGTCAA	GGTAGCTGCG	TGGTGTCTTG	TATCCACACC	AAGCCCTGCT	2100
GCTTCAGTTC	CATACATAGC	TACTGACTCA	TCTTCTACAA	AGGGATGGAA	GAGCCCGATA	2160
GCATTCGACC	CACCACCAAC	ACAGGCTACT	AGGGCATCTG	GCAGATCTCG	ACCTGTCAAG	2220
TCACGGTACT	GTTGTTTAGC	CTCTCGACCG	ATGACACTTT	GGAAGTCACG	AACGATTTCT	2280
GGAAATGGAT	GAGGCCCCAA	GGCAGAACCA	AGGATATAGT	GGGTATCGTC	GATATTAGCC	2340
ACCCATGAAC	GAAGGCTGCG	ATTGACCGCA	TCCTTGAGCA	CGCGCGAACC	ATCTGTTACA	2400
GCCTCGACCT	TGGCTCCCAA	AAGCTCCATG	CGGAAGACAT	TGAGGGCTTG	GCGTTTGACA	2460
TCTTCCTCAC	CCATGTAGAT	GGTACATTCC	ATGTTAAAGA	GGGCTGCAGC	AGTTGCAGTT	2520
GCCACACCGT	GCTGACCAGC	ACCCGTTTCT	GCGATAATTT	TCTTTTACC	CATGCCGTTG	2580
GCAAGCCAAA	CTTGTCCTAA	GGCATTGTTA	ATCTTGTTGG	CTCCTGTATG	GTTAAGGTCT	2640
TCCCGTTTGA	GATAAATCTT	GGCTCCGCCA	ATATGCTGGG	TCAAGTTTTT	TGCGTAATAA	2700
AGAGGAGTTT	CACGTCCTAC	GTA CTGGCGC	AAAAGCTGGT	TTAATTCCTC	TTGGAAACTT	2760
GGGTCTGCCT	GACTTTCACG	G TAGGCCTTC	TCCA ACTCCA	AAACTGCTGT	CATCAATGTT	2820
TCTGGGACAA	AACGTCGCC	GAATTTTCCG	TAAAATCCAT	CTTTATTTGG	TTCTTGATAT	2880
GCCATGCTTT	ACCTCTCTA	TAAATCTTCT	AATCTTTTCA	TGATCTTTTT	GTCCATCTGT	2940
CTCCACTCCG	CTCGATACAT	CTACTGCATA	GGGAGTAAAG	TGTTGAATTG	CTTTTACTAC	3000
ATTATCTTCA	TTAAGGCCAC	CTGCGATAAA	GAAGGGCTGT	GCTAGTCCAG	TCGTATCCAG	3060

1153

TTGACCCCAA	TCAAAGGGCT	GGCCACTTCC	TGCCACAGGG	GCATCAAAGA	G TAGATAATC	3120
TGCCTGAGAA	TTGGGGACAT	GCCCATTTCC	ATCTACCTGC	ACAGCCTGAA	TACTGGCACA	3180
AGGCAAATTC	TCAAATAAAT	CATCTGCCAC	CTGACCGTGA	ACTTGAACCA	AGTCCAAGCC	3240
AACTTTGTCA	ATCGCTTCCA	GCAGTTCTAC	CCGACTTGGT	GAAACAAATA	CTCCAACCTT	3300
TTTCACATCT	GCAGGAATAA	GCTTTGCCAA	CTCAGCTGCC	TCTTCTAAAG	TCACCTGTCT	3360
TTTACTAGGT	GCAAAGACAA	AACCGATATA	GTCGGCTCCT	GCTGAAACGG	CTGTTTCCAC	3420
CGCTTCTTTG	GTCGATAGTC	CACAAATTTT	AACCTTTGTC	AATCTGCAAC	TCCTTGATTC	3480
TCTGGGCCAC	ATTTTCTGCC	TGCATAAGAG	CTGTCCCTAC	CAAAATTCGG	TTAAAGTATG	3540
GGGCTAGTCG	TTCCGCATCC	TGCCCTGTGA	AAATGGCAGA	TTCAGAAATG	TAATAGCGAC	3600
CTTCCTCAAA	GTAAGGGGCT	AAATCTACAC	TGGTCTGCAA	GTCGACCTCA	AAGGTAGTCA	3660
AGTTGCGGTT	GTTGACCCCG	ATAATCTCAG	CACCAAGTCT	GTGGGCTACC	TCTAGTTCAG	3720
CTAGATTGTG	AGTCTCCACT	AAGACTTCCA	GACCAAGCTC	TGTCGCGTAG	TCATACAGTT	3780
CCTTGAGGCG	TTCTTCGGAC	AAGGCTGCCA	CAATGAGCAA	GATAACTGTC	GCACCTGCAT	3840
TGCGAGCGCG	GATGATTTGC	TTTTCATCGA	TGATAAAGTC	TTTGTGAGC	GTCGGAATCT	3900
CTACCTGACT	GGAAATTTCC	CGTAGATAAT	CCAAATGCCC	TTTAAAGAAA	ACCTCATCTG	3960
TCAACACCGA	AATCATCACT	GCTCCGTTTT	CTTCATAAGT	CTGGGCCTGT	TGCACAATAT	4020
CCACATCGAG	ATTGATATCT	CCCAAAC TAG	GGCTAGCTTT	CTTGACCTCA	GCGATTACCT	4080
GCAAGCGGTC	CTGATGATTC	TTCAAAAATT	CTGCCAAGCG	ATAGGTCTGG	CGCAGAGGCT	4140
GGATTTGCTC	CAGCTTCATC	TGCTCCACCT	CACGCGCCTT	CTGCTCTAAG	ATTCGTGCTA	4200
AAAATTCCTG	ACTCATTTTT	GGTACTCCTG	TAACAGTCTG	AGTTTTTCAA	GGGCCTTGCC	4260
TCTAGCAATC	ACTTGACGGG	CCAAGGCAAC	CCCTTCCTTG	ATGCTATCAA	TCTTACCATT	4320
AGCATAGAAA	CCAAGACCAG	CATTCAAGAC	TGTCGTTTCC	AAGAATGGAC	TTGCTTCGTT	4380
TTTCAGAACG	CTAAGCAAAA	TTTCTGCATT	TTCC TGAGCA	TTCCCACCAC	GAATATCTTC	4440
CATAGCATAG	CCTTCCATTC	CCAAATCCTC	TGGAGTAAAG	CTTGACAAGC	TGATTTCGCC	4500
ATTTTCAAGA	AGTGCAATCT	TGGTTGTTCC	GTTCAAGCCA	GCTTCATCCA	ACCCTTCTGG	4560
TCCAGCAACC	ACGATGGCAC	GTTTGCAGCC	CATATTTTTC	AAAACCTGAG	CTGTACTTTC	4620
TAGGAGTTCT	GGACGACTAA	TTCCAAGAAG	CTGTGTTTCT	AAAGCCATTG	GATGAATCAG	4680
TGGACCAGTC	AAGTTCATAA	TCGTTGGAAT	TCCCAATTCC	AAACGAGCTG	GCATGATGTA	4740
TTTCATAGCT	GGGTGCATAT	TTTTAGCGAA	GAGAAAGACG	ATTCCAGTTT	TATCAAAGAC	4800

1154

CTTACCTAGT TCAGCTGGTT TGAGGTCAAG ATTGATTCCC AAGGCTTCGA GGACATCTGC	4860
GGAACCAGAT TTAGAAGATA TCGAGCGGTT ACCGTGTTTG GCCATGTGAA TACCGCCACC	4920
AGCCAAGACA AAGGCTGCAG TTGTGGAAAT ATTAAAACGT AAAGACTTGT CCCACCTGT	4980
ACCACAGTTG TCCATGGCAT CATGAATCTC AGTTGGAATA TGCTGGGCAT GTCCTCTCAT	5040
GACTTGGGCA ATGGCTGTGC GTTCTTCAGG TGTTCCTCCC TTCATCTTAA GAGCTAAGAG	5100
GAGAGAAGCA ATCTGCGCTT CAGTTACACG CCCAGTTACG ATACGCTCAA TGACATCCGT	5160
CATTTCCACA CCTGATAAAT TTTCAAATTT TGCTAGTTTT TCAATAATCT CTTTCATCCT	5220
AGTTTCCTCA CTTTACAACC TCCTCGATAA AATTCCGAAT AGAAGACAAG CCGTCTGGCG	5280
TTCCAATGCT CTCTGGATGG TACTGGAAGC CATAAATCGG TAGGTTTTTA TGTGAATCC	5340
CCATGATGGC TTGGTCATCA GTCGAACGAG CTGTCACTTC AAAGTCTTCT GGCATTTCTT	5400
CAATCAAAAT ACTGTGATAA CGCATGACCG CACGGCCATC CTCAATACCT TGATACAAAA	5460
CAGATGGCGC TTCAAAGTTG ATATTGCTCT GTTTCCTCATG CATGACTTTT GGAGCCAAAC	5520
CTAGCTTACC ACCAAAGACT TCTGCAATGG CTTGGTGGCC CAAACAAATC CCAAGAATCG	5580
GCTTCTTGCC TGCAAAATCA CGAATCATGT CTTCCATCTT TCCAGCATCA ACTGGCCAAC	5640
CAGGACCAGG AGAAAAGACC AGACCATCTG CTTTTTCAGC TTCTTCATAC AGCTTGGAAT	5700
CATCATTTCT CAGAACCTGA ACTTCTGCAA AATTCCCAAT GTATTGGGCC AAGTTATAGG	5760
TAAAAGAATC ATAGTTGTCA ATCAATAAAA TCATGGTCTT AGTTCTCCAA TTCTAGTCAT	5820
AGATTTTGCT TTGTTAATGG TTTCTTGGA TTCGTTTTGG GCGATAGAGT CGTAGACAAT	5880
CCCTGCCCA GCCTGCACAT AGGCTCTTGT ATTTTTGAGA ATCATGGTTC GGATGGCGAT	5940
GGCCAAATCC ATATCACCCG TCGCAGACAA GTAGCCGATT GCCCCAGCGT ATACTCCCCG	6000
TTTTTCCGTT TCCAGTTCAT AGATACGTCT CATCGCTCGA ATCTTTGGTG CTCCAGAAAC	6060
GGTTCACGA GGAAGCGTTG CTTTCAAGGC ATCCATGGCA GTGAGTTCTG GAAGCAAACG	6120
CCCCTTGACT ACGCTGGTCA AATGCATGAC GTAGCGGAAG AGCTCCACTT CCATATACTT	6180
AGTGACTTGG ACACTGGTCG TTTCAGAGAT GCGGCCAATA TCGTTACGCC CCAAGTCTAC	6240
CAACATTCTGA TGTCTGCTG TTTCTTCTC ATCAGAGAGG AGGTCAGTCG CCAAGGCCTT	6300
GTCTTCTTCA TCCGTAGCCC CTCTTGGTCG CGTCCCTGCA ATCGGATTGG TTGTCACGAT	6360
GCCATTTTGT ACAGAAACCA AACTTTCTGG ACTAGCTCCG ATGATTTGAT AATCCCCAAA	6420
ATCATAGAAA TAAAGGTAAT TAGAAGGATT AGTCACGCGG AGATTTCTGT AGAAGTCAAA	6480
TGGATTTCCA GTAACCTCTG CTGAAAAACG CTGGCTGAGT ACACATTGGA ACATATCTCC	6540
GTTACGAATC AAGTCACGAG CTGTTTCTAC CATTCCCTCA AACTTATGTG GAGCGATATG	6600

1155

CGGTTTGAAG TCTAACGGAG ATAGATCCAA ATCTTCAAAT TCATTTGGAG CAGGAATGCG	6660
TAATTCCTCA AGCACTTGGT TCAAGGATTT TTCCAAGGCC TCTTGACTGC GCTCACTATA	6720
AAGTGCAATCC TCTATGACAT GTATCTTCTC CTCTTGTGG TCAAAGACCA TATAGCTCTC	6780
ATAGACAAAG AAATGCATGT CTGGCGTCCC AATTGTATCC TCAGGGATT GACCAATTTC	6840
TTCATAAAGC GAAATCATAT CGTAACCCAC AAAACCAATG GCTCCACCAC CAAAAGGTAG	6900
CTCTGAGTGG TGCTGACTCT TATGAATCAC TTCATAAAGG AAATCCAAGG GATCCCGATC	6960
AATCACTTGA CCATTTTGAT AGAGAACCC ATTTTCAAAC TTAATCTCAA AAAGTGGATT	7020
ATAGGCTAGG ATAGAAAAAC GAGCTGTTC CTGTCTCTC GGAATACTCT CTAATAAAC	7080
CTTATGTTGC CCCTTTAAGC GCATATAAGC CAAGATTGGT GATAAGACAT CTCCATGAAT	7140
GATTCGTCC ATTGTAATTT CCCTTTCAGT TCTACTCTA GTCCGTGGTG ACTGTATGAA	7200
AAATCCCCAC GCAATAAAC TTGCGTGAGG ACGAAATCG CGGTGCCACC TCAATTATAG	7260
GATTTCTCCT ATCTCTCATT CCTGTCTCAG ATATCTCTG TAACAGGCTG TCGGATAAAG	7320
GGCACTCCCT TGAGAATGAT GTTTTCTTCT CTCGTTTCAG ATGAACCAA CTTTACAGCT	7380
TTCTCTGCTT GTTTTCAGCA ACCACAAGCT CTCTGTGAGA GAAAGAACTG TAATTTTCC	7440
ATCTATTATT TTTTAGCTTC TAGTAGTCTG CAATCGCAGC TAGGTCCTTG CCTCCACGAC	7500
CAGAGACATT GATGAAGAGA TGTTCATCTC GGTACACCTT TATACTCTC GAAATCTCT	7560
TCAAACCGCG TCAACGTCGC CTGCGCTAG GTATGGTTAC TGACTTCGTC AGTTCTATCT	7620
GCAACCTCAA AACAGTGTTC TGAGCTGACT TCGTCAGTTC TATCCACAAC CTCAAACAG	7680
TGTTTTGAGC TGACTTCGTC AGTTCATCC ACAACCTCAA AACAGTGTTC TGAGCTGACT	7740
TCGTCAGTTC TATCCACAAC CTCAAAACAG TGTTTTGAGC AGCCTGCGGC TAGTTCCCTA	7800
GTTTGCTCTT TGATTTTCAT TGAGTATTAC TAGCTTTTTT CGTATTAGTC CAGCCTTTTT	7860
GTTTGCTTTT AGTAGTAGGC ATGGAGCTGT AGATAGAACT CAAGTTCATC AAAGCGACTT	7920
AAGGCCCTAA TAAAGATAA ACCAAACGAC GGATAGAAAA AAGCCCACAC ACAGAATATA	7980
CTTCCGTGTG AGGGCGTTGG TAACGCGGTG CCACCTCAAT TATAAAGGGA CTATCCCTTT	8040
ACATCTCTGC CTGTTTAAAC AACAAGCTGC ACTGTAAGGT GTGCGCACCG AATTTTCATT	8100
GTTTCAAATT CATTTTCAAA ATCAGCCAC TTTCACTACT TCCAACCACC TATTCACAAT	8160
CACCACAGGC TCCCTGAAGA TCAAAAATAG TTACTTTTCT GATTGTGTA ACTTATTTTA	8220
ATACTTTGTT TTTTCTTGT CAAGACTTTT TTACGATTTT TTTGAAAATA TCATTCGAAT	8280
ATGACCATGT CTTCTTAGA TCGAACATGA ACATGTCCCA CTTCTTAGAA ATTGGATCCA	8340

1156

ACTCAATAGA AACTGAATGG AGGCTAAACA GAACTTATTT TAGAACACTC CATCTTTTCC	8400
ACTAGGATTT TCAAGAATTA AACAACTACTA GAAACTCTGT CTCCTAACAA ATTTAGGAGA	8460
AACTTCAACA GATGTGACAC TTTCCCTTTT AATAATTGCT AAAACACCTT CTATCATTTT	8520
TTTAGCCAAT TTAACATAAT TGGGAGCAAT TGTAGACAAA GCTGGAGTAT AATACTGAGA	8580
AATAGGAATA TTATCAAATC CAATGATAGA AATATCATCT GGAATAAGAA TTCCTTTCTC	8640
ATAGCACGCA CGAATCAAGC CCTGAACCTT TTCATCTCCT GAAACAAAAA TAATGTCCGG	8700
ATAATTTTGG GTAGTCAAGT GCTGCATTGC ATAAGAATAA ACTGAATCAA TTGTAGATAA	8760
GCCATAAATG ACTTTTAAAT CCATAAAGTA ATTTTATCA TTCAGAAAAG AACGCACACC	8820
TCTTTCACGA TCCTTATTAA CATGGGATTC TCCTCCCATAGCAACCACA TATTTTAA	8880
TTTTTCTTCA GTTACAGCTT TCATCATATC ATAAGTAGCT TGAAAATTAT TATTAGATAC	8940
ATAGACTACT CCAGACGTTT GAGATTCACC GAAAAACAAGA AAAGGCATAT GGTTCCTCTT	9000
TAAATACTGA ATTCTGATAT CATCTACACT TTCATAAAAA ACAATAACAC CATCTACTAG	9060
GCTACCTGTG CTTGATATAA TTGAATTACT AATTGTATCC TCCTCTCCAA AGTACTCAAC	9120
TATAGCATTACACCAAATTTTACACGT CCGTAACACT TTATCTAACA GCGTATGAAA	9180
CCAAATTAAA GGAAGAGT CGATTTTTT TACAGAAATC AATATATTTA TAGCTTCTTT	9240
TTTAGTTAAA TTTTGTGCAT ACGCATTTGG AATATACGAC AATTCCTCTA TAACTTTGTG	9300
AATCGCTTGA TAAGTTTCTT CTTTAACATT TACTCCACCA TTAATAACTC GTGAACTGT	9360
TTTTGGAGAA AAACCTGATA AACGTGCAAT ATCATAAATA GTTACCTTTT TCCCATTAT	9420
ATTTTTCATT TCAGTCCTCC ATTACGAACA TTCTAATATT ACTATACAAT ATTTAATTTT	9480
TTTTAACAAG AGAATTTAGT AAATTATTTA AGATCCACAA ATTCACAAAA TTAATTTTAC	9540
AAATATTCTT CCCCTTCAAA AAAGTTTAAA TTGCATTTCA CACCTTTATT TTTAAGAATG	9600
TTTCCAACCTT CACGACAAAT AAATTCATAT GAGAAAAAAC TGCCATAAAA TTGTAGATTA	9660
ACTTTTTCAG TAAAATGTGT AGGATTTATA AAAACATATA ATAGCCTGTC AATGTAACAT	9720
TTTAACATAG AGTTAATTTT TTCTTTAAAG ATAACATTTG TTATCAACTC ATCAGGAGGT	9780
AAATGAAAGG CAAACACCAT TTCACAAATA TCATAAAAAG AAATAAATTT GTATACTTGT	9840
ATCAAACAAT TATTATCAAA ATATTCTATT TTACCTAAAT CAAAATTGAT TTTATAATCT	9900
TTCATAAAAA CCTCTGAGCA AAAATCTACT CAAAAATTAG ATGATTAAAA CATCTAAAAA	9960
GCAAAAGGAC AAAAACATCT GTCCCTTTGT TTAATAAATT TCAGCTAATT TCTTCGACAT	10020
AAATAACACC TACAATATTA GCAATTTCTT CCATCAGTCG AAGATGTTCA AATCTACCTG	10080
ATAATTCCAG AGTAATAAAT GACGCTATTT TTTTGTCCGG AACATCAAAG TATTCAATTC	10140

1157

TGTCAGAATT AACATCTCCA AACGCTGTTT TTGAATCGGT CATTCTGATA CCATTTTCTG	10200
CACAATAAAC CAATACACGA TTATAGGCTT CTGTAGATTT AACCACTATA TACAATTCAA	10260
TCATTTTAGA ACGATTTTGC AGATATTTTT TTAGTGTTG GAACATGGAT ATCACACCCC	10320
AAACAGAAAT GGCTACTAAA AGAGCTCCCT CATAAGG	10357

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6867 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

CGGGACATTC TCAATCTTCT GTCTTTTGT TTTCTCTTCT TTCTATGATA CAATGGAAAA	60
AATAAATTC AAGGAGTTT TTTTATGACT TATCCAAATC TCTTGGACCG CTTCTTAACC	120
TATGTTAAGG TCAACACGCG CTCTGATGAA CACTCTACTA CTACTCCAAG TACACAGAGT	180
CAGGTTGACT TCGCAACAAA TGTCCTAATT CCTGAAATGA AACGTGTTGG ACTGCAAAAT	240
GTTTACTATC TACCGAATGG TTTTGCTATT GGAACCTTGC CAGCCAACGA TCCGTCTTTA	300
ACACGTAAGA TTGGTTTTAT ATCGCACATG GATACTGCTG ATTTTAATGC TGAAGGAGTC	360
AATCCACAGG TAATTGAAAA CTACGATGGT GGTGTGATTG AACTAGGGAA TTCTGGTTTC	420
AAACTCGATC CAGCTGACTT CAAGAGTCTT GAAAAATATC CAGGACAAAC GTCATCACA	480
ACAGATGGAA CAACCTTGCT AGGTGCTGAT GACAAGTCAG GAATTGCTGA AATTATGACA	540
GCCATTGAAT ATCTAACTGC TCATCCTGAA ATTAAGCACT GTGAGATTCTG TGTGGTTTTT	600
GGTCCAGATG AAGAAATCGG TGTGGTGCC AATAAATTTG ATGCAGAAGA TTTTGATGTG	660
GATTTTGCCT ACACTGTGTA TGGTGGTCCA CTAGGTGAAC TTCAGTACGA GACTTTCTCA	720
GCCGCTGGTG CTGAATTGCA TTTCCAAGGT CGTAATGTCC ACCCTGGTAC TGCCAAAGGG	780
CAGATGGTCA ATGCCCTTCA GCTAGCAATT GATTTTCATA ATCAACTTCC AGAAAATGAC	840
CGACCTGAGT TAACTGAAGG TTACCAAGGT TTTTACCATC TAATGGATGT GACAGGTAGT	900
GTTGAGGAGG CGCGTGCAAG CTACATCATT CGTGATTTTG AAAAAGATGC CTTTGAAGCG	960
CGTAAAGCAT CCATGCAATC TATCGCTGAT AAGATGAATG AAGAACTTGG GAGCGACCGT	1020
GTCACCTCTCA ACTTGACAGA CCAGTACTAC AATATGAAAG AAGTCATTGA AAAAGATATG	1080
ACTCCAATTA CCATTGCTAA AGCCGTTATG GAAGATCTAG GTATCACGCC TATTATCGAA	1140

1158

CCAATCCGGG GTGGAACAGA CGGCTCTAAG ATTTCCCTTTA TGGGAATCCC AACTCCGAAT	1200
ATCTTTGCAG GTGGCGAAAA TATGCACGGA CGTTTGAAT ACGTTAGCCT TCAGACTATG	1260
GAACGTGCAG TTGATACCAT CATTGGCATC GTAGCTTATA AAGGCTAAAA AGACGAGGTA	1320
GCTCAGCTAC TTCGCCTTTC TTTTATTCT ACTGGTTTTT CTTGATTTC AGTAGTTGTA	1380
GAAGATTCTG TTGTTTCATT TTCTGAAGTT GATTGAGCAG GTTTAGAATC TCTTGTATTG	1440
CTTGGTTTTGT TTTTCGTCGCT AGCAGTTTCA ATGTTAGATT CTGCAGTTGC GTTTGGTTGG	1500
TTCTCAGCAC TGGTGTTATC ACCATTTGCT TCAGCATTTT TTGCTGGACT TGTTTCTTCA	1560
CTTGCCTAG CTTTTGACTG GATTTGATGA TTCAAACTA GAATAGCTTT TGTCGATTCA	1620
AGTAAAGCTG TTTTGTCTTT ACTCTTAGCA GAAAGTTGAT CTAATAATGC ATCCACCTTA	1680
TCAAAGTCCG CATCAGATCC ATTATTACTT TCTAAATAAG AGTGAAGCGA CATGAGAATA	1740
TCGTAGAGTT TTTGATAGAG TACAAGTGTC TGAGGATCTT GCTCAGCATT TTCCTTTTCT	1800
TGTTGAAGGG CGCTAGCGAT ACGAGTCAAG ACATCTTTTA CCTGACTGTT TACTTCATCC	1860
AAGTCTGCAT CAGCCTTGTT TGTGGCAGCT TTTAGATTTT CTACTTCTTC TGCCAAGGAT	1920
TGTCTGATTC CTTCTTCATG GATTTGTTCC AAGAGTTGAT TTGCCTTGCT CAAAAGACTT	1980
TCTACTTCTT CCTTGCTATC TGTCGCAGAT TATTGGTTGC TATCTACCAT GTACTCCTAA	2040
AACAGGAGAG TTATAATCCA AGATTACAAG GCCTTACAGA AATAAGAAAT CCAGATAAGA	2100
CAATGTTTCGT CCAAGACGCT ATTTCGCTTCG CACAGCAGCA CGGATTCAAT ATGCTTTAAT	2160
TTTAAAGTTT AGGTGTCAAG ACCTCTTTTT AGTGTGCCCA AAATTTAGAG AAGTAATCAA	2220
TCAACTAACT TTTATTTTTT TCAAACCTTC AGTAACTGA CCTAAAGCTA ACTCAATCTG	2280
TCTTTGTAGA TGCTTCTGCT ATCAGCTAGA AGTTGATCTA CTTTGGCCAA GACTGCCTTC	2340
TCATCAAAAG TTCCAGGTTG ATAGTTGGAT TGCAGGGATG GAATCTTGTT TTTCAAAGCC	2400
GCTTCATATC CCTTAGTTTG AACCTTGATG TAGTGATTGT GGTCGCCATG AGGAATCACA	2460
AAACCTTCTG AATCTTCACT TATAATTCTG TTGGCATCAA AACCATGACC ATCTTCTTCC	2520
TCATGATGGA CATGTAGTGA CGGATTACTT AATACAGAAC TAGAAGAACT TCCTACCTCT	2580
TCCGTGTTAG AGTGTGATGG GGGATTGTTA AGAGATGACT TAGGAATATA GTGATAGTGA	2640
TCCCCATGTC TTACTATATA AGCATCACCT GTATCTCTGA CAATATCATT AGGGTTAAAG	2700
ACATATGTGG CTGCTAATTC ACCTGCCGAC AAGTCACTCT CAGGAATGAA ATGATAGTGA	2760
CCACCATGTG GTACTATAGT AGATTGAAAT AGAATATGAG CAAATTGATA AGGGGATTTT	2820
AAAGTAATTT CTAACAATGA TTTAGAACT ATGATGTGCT ATTCTAAAT CAACTCACTA	2880
TATATAACCA TCATCGGTAG TATAACGTCC CTGTAATTTT GCTACAGATA CTTCTGCACT	2940

1159

AGCTCCTTTA TCGTCTTTAC CATGTTCTTG TTTTGGCGA TTGATTTTCAT CTTTGTTCG	3000
TACATTTTCT GCATGAGCTT GATCTTTAAG GTAAACATAA TACTTTCCAT CTACCTTAAT	3060
AATATATCCT CCCTTAACCT AACTGACGAT ATCTTGATCT TTCGGCTGAT AGTTGGGGGC	3120
TTTCATTAAT AGCTCTTCAC TAAAGAGCGC ATCAAAAGGA ACTTTACCAT TATAGTAGTG	3180
ATAATGATCG CCATGAGAAG TTACATAACC TTGATCTGTA ATCTTAATAA CAATTTGTTT	3240
TGCTTGAATT CCTTCTTTT GACTAACCTA GTCTGGAGTC AAATTTTCAG TCTTCTTAGT	3300
GTCTTTATTA CTGTTTACAT ATGAAACACG ATTTTATCT GTATTGGCCT GTTAGCTATG	3360
TTGGTTCAGA GCATAACAC ACAGACTTAA GGAAAGGATA ACAACAGATC CAGCTGCTAT	3420
ATATTTCTTT TTAAATTTCA TAATTACCTC ATTTCTATAA TTATTTATAT GATGTCTTCA	3480
TTATTAAATG ATTAATAAAA TTAATTAACC AATTAATTAA CTAGTAAATA TTCCACCTCT	3540
TTTTAAGTTG TATGTCAAGA AATTTTATAT ATTAATAATA AAATGAAATT CTCCCAAAGT	3600
CAGAGTTTAA TTTCTAACTT TTGAGAGAAC TTCATTTTGT ATTCAGACTT TTTCTACTGC	3660
TATTCCTTAC GCTATGAGAT CAGATAAATT CTTTTTATC ACTTCTCCAC TTGGCAATCT	3720
TAATTCAATC GTTCCATCCA TATTGAATAT AACACTATCT AAGCCTAATC CGTAACTAGC	3780
TGTAAATTTT TCTAATTTT CTGTACAGG ATCTACTGCT GGAGCTTCCT CTAATGCTGG	3840
ATCTAACATA GGGTCACTCC CCACATTCCC TTCTGGATTC AACATTCCAT TATCCGTGA	3900
GTTTTCTGGT TTTACAGGTT TTTCGTTTGG TGCCTCTGGT AAAGAATCTG CTGGTTTATT	3960
TTCTGTGGT TGGTCTCAA CTGTCCAGT AGATACTTT CCATTTTCAG ATGGTTTATT	4020
TTCAACATTT CCTTGAGGTG CTCTCCTGT AAAATCTGCC ATATTCTTT TAATGACTTC	4080
TCCCGATGGT AAATATAATT CAATTGTTC GTCCATATTA AACAAGACAT TTTCTAGCTT	4140
CATCCATAA CTTTCAGCAA ATTTTGCTAC TTTTCTTGT ACAGGATCCA CTGTAGGAAC	4200
TTCTTCTAAC GTTGAATTAC TAGTACTATT CCCAGTTTCA GAAAGTTTTT CTTTTTCTAC	4260
CTTCTCACTA GTCTTTGGTT CTCTACCTT TTCATCAAGT TTAAAGTTTT CTGTGCTTT	4320
ATTCCTTTTA AATTGTGGTA GAATACTTGG TTTATCAGTT TGATTTTCTT TTTCCAAGAT	4380
AGGTACTTCC ACAATATAAG TCGATTGATT GTCCAAATAA GCATTTGCCA TGAAGGTAC	4440
AGGAATTTTA TTTCCGGCCG TTCTGGTTGT TCCTTGGTTT AATTTTCGAA TCGGTAATTT	4500
GATTTACCA ACTTTATAGT TATTTCTAA ATAAGCATTT CCATGAAATT CATCAAACAC	4560
TCTGACTAAA GCATCAGTTC CTTTAGGCAC TGCAAATTGA GGGTTCACCT TAAATAAGT	4620
ATCCCCTGCA TGGAAAGGAT AGAAAATCGT TTGACTGGCC ATTTTGTAAG CTAAAGAGGT	4680

1160

TGGAAGTGT	AATGTACCAT	CATAACTTAC	TTCTGGATAA	TCTTTTGAAG	CGATAGTATA	4740
CTTAAATGTT	TGTCCTGGTA	AATAAGGTTG	ATCTAATTCA	AAGTTTGCAA	TATTCCCTAC	4800
TCCTTCTCCA	AATACTTTAC	CAGATACTTT	CTCCAATACT	TTTCCATCTG	GTGTTATTAA	4860
TTTTACTAGC	ATATTGATAC	CTAATTTTTT	CTCCAATTCA	GGCGGAAAAC	TAAAAGAAAC	4920
GCGTTTTTGA	CCATTGGCTA	GAGTAAAGTT	TTGATTATTA	AACGTACTAT	TTTTTAACAA	4980
ATTAACAACA	TCGTTAATT	CTTCTCCAGT	ATAAACTTTA	TTCCCTTCTT	TTTTAGCAAC	5040
TCCTTCTTCG	GGTTTAAACA	GTTTCATAGT	ACTGTGAGAA	TGACCAATTC	CAACCGGTTT	5100
ATGTTTCATCA	ATCGGATCTG	CATGATGGTG	ATCTCCATGC	GGATAAATAA	TCGCATTTTT	5160
TTCTTTATT	ACGACAATAC	TTTCACGTTT	GACACCATA	TGTTTCATAA	TGCCAGCAAT	5220
TTTTTCTTCG	ATTTTATTAT	CTAAATCTTT	CATTCTTTTG	GCATTACTTG	GATAATCCTG	5280
TTCATGAGAT	GACAAAGAAT	CTAATCCATT	ATGACTAGTT	TTAACTTCCT	CTAAATGTTT	5340
TTGCGCAsCT	TAATTTGCTC	TTCTGTCAAG	TCCTTCTTGA	AGAAATAATG	ATTGTGGTCT	5400
CCGTGACTCA	TGACAAAACC	TGATTTCATCT	TCAGCGATAA	TACGATTAGC	ATCAAATCCG	5460
TATCCATCTT	CTTCATGTTT	CTCATGTGAA	GTTCTCGGAT	TGATTGGAAG	AGATGGAGAA	5520
GGTGTGCTA	GACTATTGTT	TGGAAGAGTC	GGTTGCCCAA	TTTGATTGTA	TTTTGGAATG	5580
TAATGGAAAT	GATCACCATG	TCTTACAATA	TAAGCTGTAG	CCGTTTCTTC	AACGATATCT	5640
TTTGGAATTAA	AAATATAACC	ATCAGATGCT	GAAGAGAGCT	CCTTACTTGT	CGTTAAAGAA	5700
GAAGGATTGC	TTGAAAGACT	GCCTAGACTA	GACACTACTT	CATTAGGTTT	TGCATTTGTA	5760
GAAACTGTAG	AACCAGTTCC	ACTGATAGGC	ACCATTCTGG	CAATCTTTTC	TTCTAAGGCA	5820
GAAAGCTTGC	TGTAAGGAAT	AAAGTGGTAA	TGGTCGCCAT	GCGGAATCGC	AACTCCATTT	5880
GGGTACGAC	TGATAATCTT	AGCAGGGTCA	AAGACCAGGC	CATCTGATTC	ACTGTAACGT	5940
TGGGCGCTAG	GTGAATCATA	GAGTTCCTTC	AAAAGACTCT	GGAGATTTTC	AGATTTATTT	6000
GCTGGCTTGC	TAGTTGATCC	TTTTGCTACA	GATTGCGTGT	TATTGTCACT	AGCTGTTGAA	6060
GAATAGCTTA	ACTGACTCGG	TTGCATATTT	TTTCCAGCCA	GATGTGCTTT	AGCTGCTGCT	6120
AATTCACTAG	CAGATAAATC	GCTTTTGGA	ATGTAGTGAT	AGTGACCTCC	ATGAGGAACG	6180
ATATAAGCAT	TACCCGTATC	TTCGATAATA	TCAGCTGGAT	TAAAGACATA	ACCATCATTT	6240
GTCGTATATC	GTCCCTGAGA	CCTTGCTACA	GCAACATTAG	AGTTAACCTT	CTCATTATCT	6300
TTGACATGTT	CTTGTTTTTG	ACGATTGATT	TCATCTTTAG	TTCGAACATT	ATCAGCATGA	6360
GCTGCATCTT	TCAGGTAGAC	ATAATATTTT	CCATCGACCT	TGATGATATA	ACCACCCTTG	6420
ACTTCATTGA	CAATATCAGC	GTCTTTAAGT	TGATAGTTTG	GATCCTTCAT	CAAGAGTTCT	6480

1161

TCACTAAAGA GGGCATCATA AGGAACTTTC CCATTATAGT AATGATAGTG GTCACCGTGT	6540
GACGTTACAT AGCCCTGATC TGTAATTTTG ATTACAATTT GCTCAGCCTG AATTCCTTCT	6600
TTCTGGCTAA CCTGGTCTGG TGTCAAGTTT TCACTTTTCT GACTTGACTG GCTGCCATCC	6660
ACATAAGAGA CACGATTATT GTCCTTATTT TCCTGCGAAC GATGCTGGTT TAGTGCATAG	6720
GCACATAGAC TCAAGGATAC GATAACAGCT GATCCAGCTG CTATATATTT TTTACTAAAT	6780
TTCATAAATC CCTCATTTCA ATAAATGATG AAGTTTTTTC TCAACTTCTT TTACTTTATT	6840
AAATAGTTTT CTAAACCCGG GGTACC	6867

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

CGTTCTAAAA ATGCAGTACG TTTGATTGAG AAATCAGTTA AAGGTATGCT TCCACACAAT	60
ACACTTGGAC GCGCTCAAGG TATGAAGTTG AAAGTATTTG TTGGAGCTGA GCACACTCAC	120
GCTGCACAAC AACCAGAAGT TCTTGACATT TCAGGACTTA TCTAAGGAAA GGAACAATAA	180
AGTATGTCAC AAGCACAATA TGCAGGTACT GGACGTCGTA AAAACGCTGT TGCACGCGTT	240
GCGCTTGTTT CAGGAAGTGG TAAAATCACT GTTAACAAAA AAGATGTTGA AGAGTACATC	300
CCACACGCTG ACCTTCGTCT TGTCATCAAC CAACCATTCG CAGTTACTTC AACTGTAGGT	360
TCATACGACG TTTTCGTTAA CGTTATAGGT GGTGGATACG CTGGTCAATC AGGAGCTATC	420
CGTCACGGTA TCGCTCGTGC CCTTCTTCAA GTAGACCCAG ACTTCCGCGA TTCATTGAAA	480
CGCGCAGGAC TTCTTACACG TGAATCACGT AAAGTTGAAC GTAAGAAACC AGGTCTTAAG	540
AAAGCTCGTA AAGCATCACA ATTTAGTAAA CGTTAATTCG AAAGAATTAC TATACTTATA	600
CAGAGCACCT TTCGGGGTGT TCTTTTTTTA TACTTTCTTA CTAAATTGGT GCAATTGACA	660
CAGTTGTTGC GACTTTAGTC GCTTACAAAT GTGGCTGCAA CCTGACATGG TCAGTTGCCT	720
CAAAACGTTA ATCAATACGA TTATATCAAC GTTTCAAAGC ACTCAAGGGT TTACCCTATG	780
GGTGCTTTTT TCTATACTTT CTAAAAAGT TTACCCTAAA ATTTGCCCTA AAATTACCCT	840
ACTTATTTTT AAGATGTTGG TAGGCAACTT GTCCAGCAGA TAATGGAAC ATGTTTGAAG	900
TATTAACATA AGTCTTAGTT GTAACGGTAT CGCTATGAGT TAATGCTTCA GAAATGGCTT	960

1162

CTAAGCTCAT TCCTGCTTTT TTAGCAAGTG TCGCTCCTG 999

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

AATATTATCA CTGTTCTTGA AGGCAGAACA CAAGCTGTCA TCCGAAATCA CTTTCTTCGC	60
TACGATAGAG CCGTTCGTTG TCAAGTGAAA ATCATTACGA TGGATATGTT TAGTCCTTAC	120
TATGACTTGG CTAACAGCT TTTTCCGTGT GCTAAATCG TTCTAGATCG TTTCCATATT	180
ATCCAACATC TCAGCCGTGC CATGAGTCGT TTTCGTGTTC AAATTATGAA TCAGTTTGAA	240
CGAAAATCTC ATGAATACAA GGCTATCAAG CGTACTGGA AACTCATCCA ACAGGATAGT	300
CGTAAACTCA GCGATAACG TTTTATCGC CCTACTTTC GCATGCACTT AACAAATAAA	360
GAAATTCCTG ACAAGATTTT AAGCTATTCA GAAGACTTGA AACACCACTA TCAGATCTAT	420
CAACTCTTAC TTTTCACTT TCAGAACAAA GACCTGAGA AATTTTTCGG ACTCATTGAG	480
GACAATCTGA AGCAGGTTC TCCTCTTTT CAGACTGTCT TTAACCTT TCTAAAGAAC	540
AAAGAGAAAA TCGTCAACGC CCTTCAACTA CCCTATTCAA ACGCCAAATT GGAAGCGACC	600
AATAATCTCA TCAAACCTAT CAAACGCAAT GCCTTTGGTT TTCGAACTT TGAAACTTC	660
AAAAAACGGA TTTTATCGC TCTGAACATC AAAAAAGAAA GGACGAAATT TGTCCTTTCT	720
CAAGCTTAGC TTTTCTTCAA CCCACTACAG TTGACAAAGA GCCTATTTTC GCTGATTCTC	780
CACTACATTT GACTGGATTC TAATTTTTTA GAGAAATACA AAAGAGCTAG CTTTAGCTAG	840
CTCTTTTCCT ATGCGGAGAG AGGGACTTGA ACCCTCACGA CCTAAAGCGG TCACAGGATC	900
CTTAGTCCTG CGCGTCTGCC AATTCCGCCA TCCCCTCGTC GATTACTTTA CTAGTATATC	960
AACTTTTGGG ATGCTTGTC ACACTTTTTT TCAAATTTTT TCATTTTCAC CAACCAGGTT	1020
ACTCAAAAAG TTCATTAGA TTTTCATCTA CTAACCTAGC TCCGAGTGTA TTTTGAAT	1080
GACCTAGGGC AAATTGATGA TTTTCAGGCC AGATGGAAGC AACAGCTGGT TTAACAATCT	1140
CGATGTCATA TCCTAGATTA TAGGCATCTA TAGCTGTATG TAGGACACAG ATATCCGTCA	1200
AGACACCTGT TAAGATAACG GTAGACACTC TACGCTCTCT CAAACGAATA TCTAGGTCAG	1260
TCCCTGAAAA AGCTGAGTAA TGGCGTTTAT CCATCCAAAA GACACGACTG TCTGAACCAT	1320
GCTCTTGATA AAAGATCCCC AAATCTCCAT ATAAATCCG TCCACTCGTC CCAATCAGAT	1380

1163

TATGAGGAGG AAATAACTTA CTTTCCGGAT GGAAACAATC GTTTTCTTCA TGAGCATCAA	1440
TAGTAAAGAA GATATAATCT CCTCGTTCAA AAGCTAATCG AGTTACCTTG CTGATGGCAT	1500
CCGAAATCGC CTGAGCTGGA GCACCTGCTG TTAGTTTCCC ACTATCAGCA ACAAATCTT	1560
CTGTATAATC AATCGAAATT AAAGCCTTTG TCATTAGTAA TCTCTTTTCT TCACTTCTTC	1620
AAAAATATCT GAAATCAAGA CCTTAAGATA GGTTCCCTTC ATTCCAAGTG AGCGACTTTC	1680
AATAATCCCC GCAGACTCAA GTTTACGAAG AGCATTGACA ATCACAGAGC GAGTGATTCC	1740
GATACGATCT GCAATCACTG ACGCAGTCAA CTTCCCTTCA TTTCCATTTA ATTCCCCTAA	1800
AATTGCTGAA ACAGCACGGA GTTCGGAGTA AGAAAGGGTA TTGACCGCCA TGGTGACAGC	1860
AGTACGACGA CGAATATTTT TCTCATCTTC TTCACGTTGG AAGTTAAGAA GCTGAATCCC	1920
AACAACGGTA CTGGCAATCT CAACAAGAAC CAAGTCTTCA TCTTCGAATT TTTTATCATT	1980
ACGCCAAATA ATCAAAGAAC CAAGGCGAAT CCCCATAACA TGAATCGGTG CAATAGTCGT	2040
CAAGCCATCT GGAATATCAT CTCTACTCTC AATAGGGAAA ATACTCATAT CATGCTCAAC	2100
AGGCAAGTTT GCTTCTGTTT CGTAAATCAT ATTAGCCCCT TGAACGTAGT CATCTGGGAA	2160
AATCTTAGTT TGGAAGAATT GCTtACGCGA TCTGTATTG TTTTATAACG CATAAAATAG	2220
CCAAGCAGAC GTCCCTTACT ATTGATAATG CAGGCATTGC AATGAATAAT ATCCGCTAAC	2280
TGACGCGTAA TAGCGTTGTA AGGGAGCTCA TCTCG	2315

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

CGATTTCTTC CATTTCTTCA AATAAGAATA CTTTCATCTGA CATATGTGTT ACCTTCTTCA	60
TCAAAAATTA TTTTGTAATC GATTACATTG CAGATCGTAA CATAAAGAAA AACAGATGTC	120
AAATATTAAA CGTAAAAACA TGGTCACTAA AGAACTATAA GAGAAAAGGT AAACCTAGCG	180
ACGCGATGAA CGCTGGGTCG TTTGGTTTCG ATTGCTCTCT TCCTCTTGTT TTTTCTGTTC	240
TTCTTCTTGT TTTTCTCAG CTCCTTGGC CTCTTGTGTT GCTTTTTCCT CAGCTTCCAT	300
AATTAATTTA TCCGCCACAG TGTAGCTGTA GATTCCAGCT TCCATGTCGA CCACACTCGG	360
TTCTGACAAAT TGAGGCTTAA TCTTACTGTA ATATGGCAGT TTCTTACTCA TTTCAGATAG	420

1164

AGGAACCAAG	ACTTCGTCCG	AATCATTCAT	GGTCAATCGA	ATTAAATCGG	ATGTCACCTT	480
GCTTGGGGCT	AATTCCACCT	TTTGGATAGC	CGCCTTGAGT	TCTGGGCTAA	TTTGAGCAAG	540
TTCTGAGACA	AAAACCTTGA	TTTGTTCAC	ATCATTAAG	AGAACTGATA	AATAAGTTTC	600
TGGTAAACTG	TTCAGACTCA	CAGAACTAGT	CTCAAGCTGA	CCACTGGAAA	GAATAGGATA	660
ATGATTTTCA	CCAGAAATAT	AGTAGGCCAC	AATATCATAT	TCCTTGACCT	TAATAGTGAA	720
CTTAGTTGGA	AATTGATAGA	CAAGTTGAGC	TGATTCAACC	CAATAGTTAG	ACTTAATCTG	780
CTTTTCATAT	TTTGCCTTGT	CTAGCAGAAG	GTTAATCGTA	TAATCCGAAT	CCTGAATGCC	840
TGAAGCCTGT	CGAATATCAT	CAGCTGTAGT	TTGCACCGTT	CCCTCAACAC	GAATATCTTT	900
CATGGTCGCA	TAAGGACTGA	GCAAGTAGGC	AGAGACAAAC	AATAGAAGCA	GACTTGAAAA	960
TAAAATCGTG	AAGGCTCGCA	AGATATGGAT	ACCAGGAATC	TTTGCTTTGG	CTGGTTTTTC	1020
CTTTGTAGCC	TTTTTAGCAA	GCTTTTTATC	CTGTTCTCCT	TTCTCTTTAG	ACTCTGGTTC	1080
TTCTTTCTCT	TCTTTCTCTT	TGTCAGCCTC	TGAGGATGCT	ACTTTTTCTT	CAGACTCTTC	1140
CTTAGCTGAT	TCTGAATCTT	CCTGGTCTGT	TTCACCTCTC	TGGTCCTGTT	TATCCTCTGA	1200
CTTCTCAGAT	TCTTCTCCCA	TTGAGCTTGT	TCTTCTCCTT	TCCTTCTCCT	CAGCTAGAGC	1260
CGCCTCTTCT	TCAGCCTTCT	TTTTTAGATA	TTCTTGGTTT	CGTTTCTGCC	ATTCTGATAA	1320
CTCTTTCAAT	TCTTCGAGGG	TTTCTTTGTC	CTCATTTTTT	TTATCTTTTG	ACATTTACTT	1380
TCCTTATGAT	AAATCTTTTT	TCAACAATTG	ATAAAATCT	GCTAGAGATT	TCAATTCCTT	1440
AGAAGCTTTC	ATCTTAGCTT	GGTAATCTTC	CTTGTGACTT	AGTAAGTGAG	AAAGCTTCTC	1500
TTCCAAACTA	TCCAAGGTCA	AATCGCTTTC	TTGAAGGTCT	TCTGCATAGC	CTTCTTAAC	1560
AAAGTAAGCT	GCATTTTCAA	TCTGGTCACC	ACGACTAGCT	TCACGACCAA	GCGGCACAAT	1620
GACATGCAAT	TTTGCTATCG	CCAAGAGCTC	AAAAATCGTA	TTGGCACCAC	CTCGTGTCAC	1680
AACAATATCA	GCCAATTCCA	TCAAGGGTTG	ATAGAGATCG	GTCACATAGT	CAACACGAAA	1740
AAGATTTTGC	CTCAACTCAT	TCAGACTAGA	ATCTCCAGTT	AGATTGATAA	TATTGTAGCG	1800
CTCTGTTAGT	TCTTCTTAT	GGTCTGTCAC	CAATTGGTTA	AAGACACGAG	CGCCTGCAGA	1860
ACCGCCAACA	AACAATACAG	TTGGCAATTT	GGGATTAAAG	TGGGTTTGAA	TATCCACCAA	1920
TTCATCTGGT	TCTGGAGTGT	TTTTGTCCGA	AACCTTGGTC	ACCGCTCCCA	CATGCTCAAC	1980
CTTAGCCAAA	CTCGAAGCTT	GTTCAAAGGT	TGAATACATC	TTAGTCGCAA	ATTTATAGGC	2040
GATTTTATTG	GCCAAGCCCA	TAGACAGGTC	AGATTCTGTA	ATAAAGACAG	GCACTCCTGA	2100
CACACGCGCA	GCGATAACAG	GCGGTACTGA	GACAAAGCCC	CCCTTTGAAA	AAAGGGTCTG	2160
TGGACGCAGT	CGCAACATGA	TAAAGAGCGA	TTGGACAATT	CCCCAACCAA	CTTTGAAGAC	2220

1165

GTCCAGCATA	TTTTGCCAAG	AGAAATAGCG	ACGCAATTTT	CCAGTCGCAA	TAGAATGGAA	2280
GGTGACATCC	AAACCTGACT	TAAGGATTTT	TTGGTGTTCG	ATACCACACT	TGTCCCCGAT	2340
ATAGTGGA	TCCCAACCAT	CTTCGATGAA	CTTGGGCATT	AACAAAAGAT	TGAGGGTAAC	2400
GTGTCCAACC	GTCCCCCAC	CTGTAAAGAC	AATTTTTTTC	ATATTATTCT	TTTAACTCCG	2460
CTACTGTGTC	GATAAAGAGG	TCGCCACGTA	CTTCAAAGTT	AGCATACATA	TCCCAGCTAG	2520
CATTGGCAGG	ACTAAGAAGA	ACCACATCTC	CTTGAGTCGC	AAGCTCATAG	GCCTTGCGGG	2580
TCGCATCTGC	AATATCTGTC	GCCTCCACAT	AAGCGACACC	AGCCTTGTCT	GCTGCCCGTT	2640
TGACACGTTT	TGCAGATTGA	CCCAGGATGA	CCATCTTCTT	GAGTCCAGTA	ATGTCTGGCA	2700
CCAATTCGTC	AAACTCATTG	CCACGGTCCA	AACCACCTGC	AATCAAGACG	ACCTTGCTGT	2760
TGTCAAATCC	TGACAAGGCT	TTTTGAGTAG	CCAAGATATT	AGTTGATTTA	CTGTCGTTAT	2820
AGAATTTAAC	ACCCTTGATG	TCATCCACAA	ACTGGAGACG	GTGTTTGACA	CCACCGAAGG	2880
CTGAAAGAGT	TTCCTTGATG	GTTTGATTGT	CCACATCACG	AAGCTTGGCT	ACAGCAATAG	2940
TCGCAAGGGC	ATTTTCCACA	TTGTGGCTAC	CTGGAACACC	GATTTTCATTC	GCTGCCATGA	3000
CTACTTCACC	ACGGAAGTAG	AGTTGACCAT	CTTCCAGATA	AGCTCCATCA	ACCTTTTCAA	3060
GTGTTGAAAA	TGGTACAACA	GTGGCTTCTG	TCTTGGAAGT	CAAGTCTTTT	GCCAAGTCTT	3120
GATTAAAGTT	CAAGACAAGG	AAATCAGCTG	CTGTCTCTT	GTTCTGGATA	TTCCACTTGG	3180
CTGCTACATA	TTCCGAAAAT	GACCCATGGT	AGTCGATATG	AGTTGGCATG	AGGTTGGTAA	3240
TAACCGCAAT	CTCTGGATGG	AATCTTTGAA	CACCCATGAG	TTGGAAAGAA	GAAAGTTCCA	3300
TAACAAGCGT	GTCCTTATCT	GATGCTATTT	GAGCAACCTG	ACTAGCTGGA	TAGCCGATAT	3360
TCCCTGATAA	AAGACCATGT	TGGCCAGCAG	CAGTCAAAAC	TTCCCCAATC	ATAGTCGTTG	3420
TGGTTGTCTT	ACCGTTTCGAT	CCTGTGATAC	CAATAATCGG	TGCTTCTGAA	ATCAAATAAG	3480
CCAATTCAC	CTCAGTCAAG	ACTGGAATTC	CCTTGGCCAA	AGCCTTTTCA	ATCATGGGAT	3540
TGTTGTAGGG	GATACCTGGA	TTTTTCACCA	TAAGGGCAAA	CTCTTCATCC	AAGAGTTCCA	3600
AAGGATGGCC	ACCTGTAATG	ACCTTGATCC	CTTCTTCCAG	CAAACCTTGG	GCAGCTGGAT	3660
TGTCCTCGAA	AGGTTTCCCA	TCATTTACTG	TCACAATGGC	ACCTAGCTTG	TCCAACAAAC	3720
GAGCTGCAGA	TTCAACAGAC	TTGGCCAAAC	CTAAACAAG	GACTTTCTTA	TTTTTAAATT	3780
GATCTATTAC	TTTCATGTCT	CGAACTCCAT	TTCTACTCCT	ACTATTTTAC	CATTTTATG	3840
GAAATAAAAA	AGCCACAAAG	TGTGTTTGTG	ACTCTTCTT	CTAACTGAAT	CTTACCATAT	3900
CATCTATGTG	ATAAATCGGT	AACTCGAATG	ACCTGATCCA	CTTGCTCCCA	AATCAGAGGA	3960

1166

TTATGGGTCG CAATAATAAT GGTCCGATTC GGATTTTTTA AAGATTCTAG GATGGAAAGT	4020
AATTCCTCAG AGTTTTTGGG GTCTAAGGAA GCGGTTGGTT CATCTGCGAG GATCAAAGGT	4080
GGATCCTTTA AAATTATCTT CGCTAGTGCA ACACGTTGTG CTTCTCCTCC TGATAACTCA	4140
AATATAGGTT GCTTCAAATC CAAATAAGAG AGGTTTACAC GGTTTAGAGC TTGTTTCATC	4200
AAAGAGATTT TCTCTTTTTC CTTCAACTTT TTACCAACTA AACCCAGATT GAGATTCTCT	4260
TTGACGGTTT GGCTTTCAAT TAAGCCAAAA TCTTGAAATA AGTATCCTAA GTAATCTCTA	4320
AAGAAAACAG AAGGCTTGAT GTCCTTAAGA GAAGTGCCAT CATAGATGAT TTGCCCTTTG	4380
TCATATGGCT CCAATCGTCC AATCATATTC AAGAGTGTG TCTTACCACA GCCACTTGTA	4440
CCGATTAAGG CATAAATTTT CCCACCTTCA AAATGAAGAT TCATATCTGA AAATAGCTGA	4500
CGGCTTCCAA ATTTTTTAGA TATATCTTTT AGTTCAATCA TCCTATTTTC CTTTCATAAT	4560
TGTCATAGAA ACACGAGATT CTTTCTGCGC TTGACGGTAA AGCGTCAAAA CTGCACTAGC	4620
TAGAAAGACC AATAAAGTGA GCAAGCCAAT CACCAAGTCT CGACTGCTTA AAATAAAGAG	4680
ACTAGACCA AATACAAAAC TAGCAAATTG GCTAACCATTA TACTGAGCAT GTGTTTCAAA	4740
AAATCGTAAA CCTGAAATTC GTTTAATCAA GATATCTCGG CGGAATTGCT CGAAATATAG	4800
AAGATTGACA GAATAAAGA GTAACAAGGA ACTGGCTATT CCAACAATAG CTCCTAAGAT	4860
TAAAGTTGCT GTTTCAGTTT GAACTTCATT ATAACGAGTT AGATAAACAC TTCTTCCTTC	4920
TTTAAGATAG GATACTTGCT CATAAATTCC AGCTTCTTTC AAGAGTTCTA GCCCACTCTC	4980
ATATCCTTTG ATAAAGAGTT GTTTTCCAGC ATTGATAGAC CAACTAGATA AGGATATAAA	5040
ACTATCACCT GTAGAAGTCG GCGTGAATAC CACTAAAATC GGATCAGTCA AATACTGAGT	5100
AGATACGGGA TTCTCACCGT TATTATAAAC AAACCGCTTT TCTCCCATTG AAAGATAACT	5160
AACGTGCGCT TTCATCTCAT AATCCAAAGG AGCACTTGCC TCCTCACCAG ATTTTCCATA	5220
ATAACTCAAT CTTTCTTCAA AAACCTTCTT AAGTTCTGCT TCTCGAGAGC GCAAATGTTT	5280
TGGGAGCAAG AGGATAAACT CACCTTTTTG GAGATGGGCT AACTTCTGTT TGGTCTCAGC	5340
ATCTACCACG ACCTTTTCCT TGTCCAAATA ACTGGGACTA ACATAGAGCG TATTAGCATC	5400
TGAACTATAG GTATCCAGTG TCTCTCCCTG TTCATTTTTT CCTTGTGGAT TGGCAAAATG	5460
GAGCAGATTA TCCTTTACAT AAAGAGCTTG TTCTTCTTCG ATTGCTTCCT TGGCAAAGGC	5520
ATACCACTTG CTCTGATTTT CTGTATCTTT TCCTCTATCA CCTAAGCCAA AGGAAATCTG	5580
GTAATAGTCT GCTCTGTCCT GCCATGCTTG TTTTGAAATT TCAAGTTCTT TCAATCGTTG	5640
GTAAGACGTC AAACCTGTCT TAACAGCGTA GCCTACTGTA AAAACAGCTA CTAAGTACA	5700
CAATAGGGTT AAAGCCATCA AGCGTTTAAG GGGTAATCTT CCCTTAATAA CGGGAACATA	5760

1167

TGCTTTGTAA CTCAAACCTCA TTAGGTAAAG GAGCATTAGT AAAATTGAAA TCGCCAATAA	5820
AAACAACAGA TAGAAACTAA TCCCAAAACC ATAGGTGGCT AACAAGATAG GATAAAACAA	5880
ACCTTGACTA AAAAGAACGA CTCCCCACC TAGGAAGGAA AGGAGGGCTG ATAGAAGGAG	5940
CCATTTGATA TCAGTAGATA AAGAATGCCC CATGATGGAT AAGAGAGTCT GACCAGAAAA	6000
GAGTTTATA CCTGCTGCTC TCATTTCCCTT AATCCGAGTG ATAATCACTA AAGCAAAGAA	6060
AGATAAGCCA AATATTGCTA AACTAATTAA AATAAGGGGA TTTAGTAATA TTCGAAAAGC	6120
AAGAAAATAG GCGGTATCT TTCGGTCAGC ACTTGCTTTA TAACCCAAAT CTCCTAATTT	6180
ATCGGCAAGC TTTTCTTTTCG TCAAGGAGCC TGACAAAAGG AGATAACTAT TTAGCGGAnT	6240
AtACGTTTAC GACTTTCTTG GCTAGCTTCT TGGAATTCCT TTGGTAAAGT TCCCTGACCA	6300
TAAGTTGCAT AAGTAAAGTG AGTCGTCCA TCCTTACTCG GCTCTACAAT TCTTCTAGCT	6360
ATTAACTCT GTTCTGAGTT TGCAAAATTC TCCAATTCCT GTTCAAATAC CTCACGCGTC	6420
GGTTCCTGAG TATCTTTTTT GACACGAAGT AAAGAAACGG AATCATAGCT TGCATATAAA	6480
TATTGTGGCG CACGTAAGAC AATAATCCAA GCAAGGAAGA AGCTGAGAAA AAAAGTTGAT	6540
AATAATATGA ATAGTTTCTT CATAGTAGAC TCCTTGTAAG CAAAATTCCC CCTGTAATTT	6600
CTTACAAGGG GAACGATTTA AATCAATGAA CGATTAGTCA TAATCACAGT AAAATGCTAC	6660
TTGTTCTCCC CATTTAGTCC AAATCCATGC AGG	6693

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1847 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

CCGGTCTATG TACCCACTAC TTTGGGACAA TATGGGGATC AGCTACCCAA AACTAATCGA	60
GCGTTTGGTT GACCTTGCCA AGGAAAGTTT TGACAAGCGC GACGATTGA TATAAAATGA	120
AAGAGAGGGT AGAAGCCAGA ACCATCACTG CACGGTGACT AGAGTCTCG GACTTCAGCC	180
CTTTTAAAG GAGTAGAAAT GAAATTAACA ATCCATGAAA TTGCCCAAGT TGTGAGGCC	240
AAAAATGATA TCAGTATCTT TGAGGACACC CAGTTAGAAA AAGCTGAGTT TGATAGTCGT	300
TTGATTGGAA CTGGAGATTT ATTTGTGCCA CTTAAAGGTG CGCGTGATGG CCATGACTTT	360
ATTGAAACAG CCTTTGAAAA TGGTGCAGCA GTAACCTTGT CTGAGAAAGA GGTCTCAAAT	420

1168

CATCCTTACA TTCTAGTAGA TGATGTTTTC ACAGCCTTTC AATCCTTAGC ATCCTACTAT	480
CTTGAAAAAA CGACTGTTGA TGTCTTTGCT GTTACAGGTT CAAATGGCAA GACAACGACT	540
AAGGATATGT TGGCGCATTT ACTGTCAACA AGATACAAGA CCTACAAAAC ACAAGGCAAT	600
TACAATAATG AGATTGGCCT TCCTTACACA GTTCTTCATA TGCCTGAAGG AACAGAAAAG	660
TTGGTTTGG AGATGGGACA GGATCACTTG GCGATATTC ATCTCTTGTG TGAATTGGCT	720
CGTCCAAAAA CAGCCATCGT GACCTTGGTT GGAGAAGCCC ATTTGGCCTT TTTCAAAGAC	780
CGTTCAGAGA TTGCTAAGGG AAAAATGCAA ATTGCAGACG GAATGGCTTC AGGTTCCCTG	840
CTTTTAGCGC CGGCTGACCC TATCGTAGAG GACTATTTGC CAACTGATAA AAAGGTGGTT	900
CGTTTTGGGC AAGGGGCAGA GCTGGAAATT ACTGACTTGG TTGAGCGCAA AGATAGTCTG	960
ACCTTCAAGG CCAATTTCTT AGAGCAAGCC CTTGATTTCG CAGTAACTGG CAAGTACAAT	1020
GCGACAAATG CTATGATTGC ATCCTATGTT GCCTTGCAAG AAGGAGTTTC AGAGGAGCAA	1080
ATTTCGTTGG CCTTCCAAGA TCTTGAATTG ACGCGTAACC GTACCGAGTG GAAGAAAGCA	1140
GCCAATGGAG CAGATATCCT GTCAGATGTT TACAATGCCA ATCCAACGTC TATGAAACTG	1200
ATTTTAGAGA CTTTCTCTGC CATTCCAGCC AATGAAGGTG GCAAGAAAAT TGCAGTGTG	1260
GCGGATATGA AGGAGCTTGG TGACCAGTCT GTTCAACTTC ATAATCAGAT GATTTTGAGC	1320
CTTCTCCAG ATGTGCTTGA TACCGTGATT TTCTATGGAG AAAATATTGC TGAATTAGCC	1380
CAATTGGCCA GTCAAATGTT CCCAATCGGC CACGTTTACT ACTTCAAGAA AACAGAAGAC	1440
CAGGATCAAT TTGAAGACCT AGTCAAGCAG GTCAAGGAAA GCCTTGAGC CCATGACCAA	1500
ATCCTGCTCA AAGGCTCTAA CTCTATGAAT CTAGCCAAGT TGGTAGAAAG TTTAGAAAAT	1560
GAAGACAAGT GATTTTGTC AGTATTTGCA AAGAATGATT GCCATTACAG ATACTGGCTT	1620
AACCTTTACA AAAGATCCGT TTGACCGTGA GCGCTACGAA GACTTGCGAA GTCTGTTATC	1680
TGAAATGTTG AATCAAGCAT CAGACCTTGA TTCCGAAGAA GTGGCAGAAG TCTTGAAGCC	1740
AACCTTCTGCT TATGCGACTC CGTTAATGGA CGTCCGTGCT TGGATTGTTG AGGATGAGAA	1800
GATTTGTCTG GTTAGGGGAC AAGGAGAGGA TAGTTGGGCT TTGCCGG	1847

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1062 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

1169

CAAGCGAAAA CATTTTTAT TCCAAATAAA CAGAGCATT TAGGAGAACA AGAGATTTTG	60
AATGCCAAGT CGATCTTGGC CTTGCTAGAC GGTTTGGAGT CACATAGCTA TGATGTAGTC	120
TATCTCCGTC AGCCTCTTAA TCGTCTCGAA TATATCGAGT GTGCGATAGT GGGGCAATCA	180
CAATTTCTCT TTAAGGTCAG TTATGCTGAT GGTCAAAGG CTTACCGTGT CGATCTTCCT	240
GACCTACTAA CAAAGACAGA CTGGCAGATT ATCAAGTCAT TTTTAGATGC TTTGCTTGCT	300
TATACAGGGA CTGATATTGA AGGGCTAGAT GGTTTTGATT TTGAAGCTTA TTTCCAAGCA	360
AGTATTCAAG CCTATCTAGC AGACCCTGTA GCTCGTTTGA CGATTTGCCA AGGAATTTTT	420
AATCCTATTT TCTTTAGTCG TGAGAACTTG AAAAGCTTTT TAGAGGCAGA TGGCTTGGCT	480
CAGTTTGAAG CGCGTGTGCG TGGCGTTCAA GAGACAGATG CCTACTTTGC GAGACTTTCC	540
TTCTATCAGG ATGGAGAAG AAAAGTGCAT GCGTTTACC ATCTAGCTCA AGGAGTCAAG	600
ACAGTTTTAC CGAGAGAACC GTTTGTTTCT GCAGCCTATA TTGAGCAATT GGTGGATAAG	660
GAAGTCCAGT GGGAGATTGA CTTGGTTCAA ATCACAGGAG ATGGCTCTAA ACCAGAAGAC	720
TATGAAGCCA TTGCTCGCTT GGACTATGCA AAATCTTAG AGGTATTACC CCCATCTTTT	780
TACCACCAAC TAGACGCCAA TCAAATAGAA GTGCAACCCA TATTAGACAA AGATTTTAAA	840
ACATTAGCAC AAGAAAAGTA AAGCAGAAGC AGGTCAATCG ACTTGCTTTT TTGACATAGA	900
AAAAATCCTG CCAAGaTGAC AGGATTGCTA CTCAATGAAA ATCAAAGAGC AAACTAGGAA	960
GCTAGCCGCA GCTGTACTTG AGTACGGTAA GGCGAAGCTG ACGTGGTTTG AATTTGATTT	1020
TTGAAGAGTA TGAAGTTTAA AGAAAAGCCA AGATACGAAG AT	1062

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6846 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

TATCTACAAC CTCAAAAACA TGTTTTGawG gCTCGTCAGT cTATCTACAA CCTCAAAAAC	60
ATGTTTTgAa kGctcGTCAG tTCTATCTAC AACCTCAAAA ACATGTTTTG AcaGcCtCgT	120
CAGTTCTATC TACAACCTCA AAAACATGTT TTGAGCTGAC TTCGTTAGTT TCATCTACAA	180
CCTCAAAAAC ATGTTTTGAG CTGACTTCGT TAGTTTCATC TACAACCTCA AAAACATGTT	240
TTGangnCnT CGTCAGTTCT ATCTGCAACC TCAAAGCAGT GCTTTgagcG CTTCTGTCAGT	300

1170					
TCTATCTACA	ACCTCAAAAC	AGTGTGTTGC	GCAGCCTTTA	ATCAGCCGCC	TAGTCCGCTC 360
TATGGTATTC	ATTAAGTCAA	CATCTCTTGT	TTAAGAGCAC	CAAATCAGGA	AATCTTCTCG 420
ATTCCCTGAT	TTTTTCTATT	TACGTTTTTCG	TGTTGAGCTA	CGTTCGTGCA	AACCATGAGG 480
TAAGAGAACT	TCACGTTCCT	CCAACTCTTC	CTTATGCATA	ATCTTGGTCA	ACATACGCAT 540
ACTAATGGCA	CCAAGGTCAT	AAAGAGGTTG	GGCAATCGTT	GTCAAGTTTG	GACGGGTAAA 600
GCGTGAGATT	TGTGAATCAT	CACTAGTAAT	AATTTCAAAA	TCTTCTGGCA	CAGAAACACC 660
CTTATCAGCC	AAACCGTTCA	AGACTCCTGC	TGCCAACTCA	TCACCTGTCA	CAACTGCTGC 720
AGTTGCATTT	GATGAAATCA	AACGCTCTGC	TAAGGCGTAA	CCATCATCAT	AGCTATATTT 780
AGATTCAAAT	ACCAAACCTT	CACTATAAGT	GATTCCTGCT	TTTTTCAAGG	TTTCCTTGTA 840
GCCAACTAAA	CGAACCTTAC	CATTGATGTC	ATCCACTAGC	GGACCGCTAA	CGAAAGCAAT 900
ACGCTCATTT	TCTTTAGCAA	GGTAACTCAC	TGCATCAATT	GTTGCTTGCT	TATAGTCAAT 960
ATTGACACTT	GGCAACTGGT	GCTCAACATC	GACAGTTCCT	GCGAGAACAA	TCGGAGTACG 1020
TGAACGCGAA	AATTC TGAGC	GAATTTTATC	TGTCAAGTGA	TACCCCATAT	AGATAATGCC 1080
ATCTACCTGC	TTTGAAAAGA	GGGTATTGAC	AACAGAAACT	TCTTTCTCGT	TATCTTCATC 1140
GCTATTAGCT	AGGACAATAT	TGTACTTGTA	CATTTCTGCA	ATATCATCAA	TCCCTTAGC 1200
CAAACTCGAA	AAATAACCAT	TGGTAATATT	TGGAATCACG	ACACCGACAG	TGGTTGTCTT 1260
TTTACTTGCA	AGACCACGCG	CAACTGCATT	TGGACGATAA	TCCAAACGAT	CAATTACCTC 1320
TAGCACTTTT	TTACGGGTAT	TCTCTTTTAC	ATTTTTTATTG	CCATTGACCA	CACGGCTGAC 1380
CGTCGCCATG	GAAACACCTG	CTTCACGAGC	GACATCATAA	ATGGTTACTG	TATCATCTGC 1440
ATTCATTCCCT	TTTCCTGTCC	TTTCTATCTC	ACACATTCTT	TTACAAGTAG	AGGTACTGAT 1500
TGAAGCTCTA	TATCTACTTA	CAAAAGTGAA	GATGTGAAAA	TTTCGTTTTT	ATATTTCTAC 1560
TTATTCCATT	CTATCACTAA	TTGTAAACAC	TTTCAAGTGT	TTTTTGAAGA	TTGATTGAAA 1620
AAATTTTATA	GAAAACCTAG	GTTTAGCTCC	TTGCTACCAC	CTTAGACTAA	ACAAAAAGGA 1680
GGAAACTAAG	CCCTCCTAAA	GTTATAGTAA	AATGAAATAA	GAACAGGATA	AATCGATCAG 1740
GACAGTCAAA	TCGATTCTTA	ACAATGTTTT	AGAAGTAGAG	GTGTACTATT	CTAGTTTCAA 1800
TCTACTATAG	GTATTGTTCC	ATTCACTACC	GTCAATTTTA	GCACATAGTC	TTCATGAAAA 1860
TATTATATCA	TCATAACCAA	CCAGATTCTT	TCGCGATATT	AGCTGCCTCT	GTTCGATTAC 1920
CTGCATCTAG	TTTCGAAAGA	ATATTGGTGA	CATAGTTTCG	GACTGTTCCG	TTGGATAGAT 1980
AAAGTTTGTC	TGCAATTTCT	TGGTTAGAGA	AGCCCTGAGC	AATTCCTTTT	AAAACTGCGA 2040
TTTCTTGCTC	CGTTAATGGA	TTGGGATGCA	TCATCACCAC	TTCCATCAAT	TCAGGCGAAT 2100

1171

ACTCCTTGCG	TCCTTCGAGG	ACGGTGTGCA	AGGTTTGCAT	GAGGTCTGCA	ATGTTTCTTT	2160
CTTTTAATAC	ATAAGCATCT	ACTCCAGCCT	TGACCGCACG	TTCAAAATAC	CCAGGACGCT	2220
TGAAGGTCGT	CACCACAACC	ACCTTTGTTT	CAAGCTTTTC	TGCTCGTATC	CACTCCAAGA	2280
CTTCAAGACC	TGTCTTAACA	GGCATTCTTA	CGTCAAGGAT	GGCGATATCT	ACAGACTCCT	2340
TTTCTAATAG	TTGGATTGCT	TCTTGCCCAT	TCTTGGCTTG	AAAGACAGAC	TCTACATCCG	2400
GTTGAAGCAT	GAGCAACTGG	CACATGGCAT	CTCGCAACAT	ACTTTGATCT	TCTGCGACTA	2460
ATACTTTCAT	CTACTTCTC	TCCTTATAAA	GTAGTCGAAC	CTGCACTTCA	GTTGGATGTT	2520
TCTGACTGAT	TACACTTACT	TCTCCTGAAA	ATGGAAAAAC	ACGATTTCGG	ACTGTATGGA	2580
GCTCATCCCC	GCTTATAGAG	GCAAAGCCAC	AGCCATCATC	TCTCACTGTT	AGAATGAGTT	2640
CTTTCTCTGT	CCGTTCTAAT	TTCAAGTAGA	CTTTAGACGC	TTTAGCATGT	TTGATGATAT	2700
TGGTCACTAA	TTCAAGCAAA	ATCATGGAAG	CCGTTGACTC	CAATTCCTGA	GTTAAGCTAG	2760
ACTTGTCCTAA	GTGATTCTCA	ACTTGAACCT	CAATTCACGC	AATTTCTAAC	ATCTTTTCTCA	2820
CAGTCTCTAG	TTCCGATGTC	AAAGTTCTAG	ACTTAAGATT	TTCCACAATG	GTTCGCACTT	2880
CATTCATGGA	TCCTTGCTGA	TCTGGTGAAT	TTCTTTTAAAT	TCCTTTTCCA	CCTGTGGATA	2940
AGCCTCCATC	TGAAATAACT	GCAAGGCTAA	ATCTGTCTTG	ACACTCAGCA	TAGCAAAGGT	3000
ATGTCCCAGA	CTATCATGCA	AATCCTGACC	GATACGACTA	CGTTCATTTT	CAGCAAGCAA	3060
TAGATTTATC	TGAGCATTTT	GCTTGACCTG	AGCTTCTTTC	AAATCCTCGA	CAATACGAAT	3120
CCGAACCAAT	CCAAAAGTCA	TTAAATCGAC	AAAAGTAAGA	ATTACAAGTA	GATAGAATAG	3180
AAACTCAACT	TCGATTCTCT	GAAAAATCAA	CAGTTGCCCC	ACAACAAGGA	CTTGAGCAAG	3240
AAGAAAAGTC	CAGACATGTA	AAGACTTTAA	ACTACGTACG	CTGAAATGAT	AACTTAAGAG	3300
ATTGGATAGG	AAAAAGAAAA	ACCAGATATA	ATTAACAGCA	ACAAAGGCAG	TATTCCCAAC	3360
TACATAAGTC	AGCATGAGGC	CCCAATATAG	CCAAGATAGG	CGCTGGCTCT	TAGTTGTAA	3420
AACACCCAAA	TATGCCACTA	CAAATAGAAT	ATCAATCAAT	AAATGCCAGG	CAGAAAGCCA	3480
CCCAGTCACT	ACAGACAGGA	TGGGGAAAAAT	CATAAAAAAT	AAACTGATCC	AAAACATATA	3540
ATGTATTCTT	TTCAGTCTTT	CAAGCATTA	GCATTCTCCT	TATGACCTTG	AAGGTAATG	3600
GTCAAACCAA	ACAAAACACT	TGAAAAACA	AGTAAATAAA	CTGTGGCTGA	TAGATTGATG	3660
CCACCCTCAT	TTAAGAAGGT	CTTGAGCAAC	TCCATCAACT	GATAGGTCGG	GAGACACTTA	3720
CCTACTACTT	GCATCCAGTC	TGGAAATAAA	GAGATAGGCA	TCCAGAGTCC	ACCTAAACA	3780
GCCAACCCTA	GATAAAGAAG	ATTGCCACG	ACAGACATCA	ACTGACTAGT	TGGTAAGAGA	3840

1172

GTCAAGGTCA AACCAAGCGC TACGAAGGCA ATACTTCCTA CTATCAGCAA AAGTGCAGCC	3900
CCAATCCAAT TTCCAAGAGA CATGTCCACA CCTCTTACAA AATGCCCAAC TGAGAAAACC	3960
ACCAAGATTG AAACCAAATA ATCAACCAGC ATACTTGTTA TCTTTGATAG ATAATATTCT	4020
ACCATATTTA CAGGGCTATG ACGCAATGTT TTCTGCCAGT TGTGATCTT GTCGGTATGT	4080
AAAACAACTG GGAATGAGAA GATAGCTGTT GACATCATGG AAAATGCAGT CATGGAGATA	4140
AGATAATCAC GCATAAAATT CGCGAGTTCA CCTGGTGTGT CCTGATAGAT ACCAGAAAAA	4200
AATAAATAGA AAGCCGTCGG CATCCCTACT GACAATAGAT AATAGATCAA TTGTCGTTTG	4260
GTCAATAAAA ATTCTATCTT ACTAAGTGCT AGCCATCGTT TCATCTTAGT TATCTCCCTT	4320
CTGCGTTTCT TCAAAGATTG TATCCAACAA ACTACGATTA TTAACCTCAA TTTCTTGTAT	4380
GCCACATCCT GCTTGAACATA ACAGTTCCCA AAAAGCATCT GCTTCGCGTG TGACTIONTG	4440
TAGAGCATCC TGTTTTTGTG ACCAGTTTTTC AACCAAGTTA GACTGCTCAA TGACTTCCTT	4500
GTATGCCAGA GGAAGGATAA AATGCTTTTC AATTCCCTCA CTACGCATAG CTAGAGGCGT	4560
CGTATCACGA ATCAACTCTC CCTTATTTAA AACCAAAATC CGGTCAGCCG TATGCTCTAC	4620
CTCTTCAATA TAATGAGACG AATAGAGAAT CGTGACTCCT TGCCTTTTA GGTCCCGAAC	4680
GATTTCCCAA AAGCGTTGAC GAGTTGAAGT ATCCATGGCA GCAGTTGGTT CATCTAAAAA	4740
GACAAGCTTT GGTGCCCCAA TCAAGGTCAA GACAAAAGAG AAGAGACGCT TTTGCCCCGC	4800
TGACAATTTT TCTGCGAATT GCTCTTTTGT TTGCTGGTCA AACTGCAATA GTTGATCGAT	4860
TTCTTGATCG CTCAAGGAAT TTGGATAGAT ACGTTGAAAG AAAGCAATCA ACTCTTTGAC	4920
CTTTAATTTT TGAACGATGA CATTTTCTTG AGGCAGATAA CCTCTAATAT AGTCTAACTG	4980
AGAACTCGTC ACTGACAAGC CTTGGATGGA TACTTGACCG CTTGTGACCA GTTTATCTCC	5040
AAGCAGACAG TCCAAGAGTG TGGTCTTCCC AGCACCATTG GGCCCAATCA AGGCGACGCA	5100
TTACACCTCA GCTACCTCAA AGGAAATACC CTTCAAAATA GCCTTGCCCT TGATGTTTTT	5160
ATTTAGGCTT TCTACCTTAA TCATATTCAT GATATTCTCC TTTCAACCAC TCCATTCTCA	5220
TAAGGAAAAC GACGAAAATC ATAAATCCAA ACCCCAAAGC ACCACGAATG AATTGGCGAA	5280
gCAAGGTTTG GTCAAACCAA CTGTAAACA TTTCCACTAA CCATACCAAG AGTGACAGGC	5340
CGATAAAGAA ATAGATGATC CCTCTCTTCA TTCTCAAGC TCCTTTTTCA CATCTCCGAC	5400
TAATTTCAAA CCTTCTCTAA CAAGCCAAGA CATCATTTCA AAGCCAGCAA AGAGCTCCCA	5460
AGGAAAATGA TAGAACTCT CATCCAATCC CGAAAACATG AGTTAGGTCA TAACTCCTGC	5520
TACTACTAAA CTCACGCGA TAATCATTTT ATTTCTCATC TCTTCTTCCT CCATTTCATA	5580
CTACAATTAT AGTCTTTTGA AATCAGAGGA GACAGAAGCT TCTGTCACTA GAAAATATGA	5640

1173

CAAATGTCAT AAAAAATTCT GTTCAAAACA AGCAAGATAC ACTATACAAT AAAACACAAT 5700
 TAGAAAAATC TAAGGCAACT TCCTCAAAAG AGATATCAAA CCCAATTCAC ACCATAATGT 5760
 AAATAATAC TTATTTAAAA TCAAAAAGAG TAGAAATTTT TATCAGACAA ACACATATAT 5820
 AGTGTATTGA ATCTATAACA GTAGGCCTTA AATACTAAAA TATTTCTATA AATTAATTTA 5880
 ACTTTCCTGA TAGAGCTGTT CATATCTTAT TTCAATTCCTC TAAATTATAC GTTGAACAAA 5940
 ACCCTTCTAT TTCTTTCTTA AAGATTTATA AGAGTTATAA AATCTGTTAA ATTTCAATGT 6000
 GTATACCTAA ACTACGGTAT TTATTGAAAA GACTGGAGAC AAAAAGTATA CGCTGCCAAA 6060
 ATGAATTACT GAAAAATCAAA AAAGAGAGAA CCAAACCTGAT TCCCTCTTAA TGTATATAAT 6120
 ATCTAGTTT AAAAATACAC ACTCACATAT CTCTGTAATG AATCGGGAAG ACAGGATTCG 6180
 AACCTGCGAC ACCTTGCTCC CAAACCAAGC ACTCTACCAA GCTGAGCTAC TTCCCGAGTT 6240
 AAATAGAAAA ATGCACCCTA GAGGAGTCGA ACCTCTAACC GCCTGATTCTG TAGTCAGGTA 6300
 CTCTATCCAG TTGAGCTAAG GGTGCTCCAT ATTATGCCGA GGACCGGAAT CGAACCGGTA 6360
 CGATCGTTAC CAATCGCAGG ATTTTAAGTC CTGTGCGTCT GCCAGTTCCG CCACCCCGGC 6420
 CTCTCTAAGC GAACGACGGG ATTCGAACCC GCGACCCCCA CCTTGGCAAG GTGGTGTCTT 6480
 ACCACTGAAC TACGTTTCGA CTGTTTTCTT CTATCTAAAA ATGCCGGCTA CATGACTTGA 6540
 ACACGCGACC CTCTGATTAC AAATCAGATG CTCTACCAAC TGAGCTAAGC CGGCTCATTT 6600
 GTTATATCTT AATGCGGGTT AAGGGACTTG AACCCCCACG CCGTTAAGCG CCAGATCCTA 6660
 AATCTGGTGC GTCTGCCAAT TCCGCCAAAC CCGCATATAT GACCCGTACT GGGCTCGAAC 6720
 CAGTGACCCA TTGATTAAAA GTCAATTGCT CTACCAACTG AGCTAACGAG TCTAAAATAA 6780
 cTTGCGTTAC CTAAACGGT CCCGACGGGA ATCGAACCCG CGATCTcGCC GTGACAAGGC 6840
 GACGTG 6846

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GAATTCATTT TAAATAAAGA TACGGGAGAG GTAAGTGAAT TAAAACCTCA TAGGGTAACT 60
 GTGACCATTC AAAATGGAAA AGAAATGAGT TCAACGATAG TGTCGGAAGA AGATTTTATT 120

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TTACCTGTTT ATAAGGGTGA ATTAGAAAAA GGATACCAAT TTGATGGTTG GGAAATTTCT	180
GGTTTCGAAG GTAAAAAGA CGCTGGCTAT GTTATTAATC TATCAAAAGA TACCTTTATA	240
AAACCTGTAT TCAAGAAAAT AGAGGAGAAA AAGGAGGAAG AAAATAAACC TACTTTTGAT	300
GTATCGAAAA AGAAAGATAA CCCACAAGTA AACCATAGTC AATTAAATGA AAGTCACAGA	360
AAAGAGGATT TACAAAGAGA AGAGCATTCA CAAAAATCTG ATTCAACTAA GGATGTTACA	420
GCTACAGTTC TTGATAAAAA CAATATCAGT AGTAAATCAA CTACTAACAA TCCTAATAAG	480
TTGCCAAAAA CTGGAACAGC AAGCGGAGCC CAGACACTAT TAGCTGCCGG AATAATGTTT	540
ATAGTAGGAA TTTTCTTTGG ATTGAAGAAA AAAATCAAG ATTAAGATAA AAGCTATAGA	600
AAAAATGGT TTATGTACTG AGATTAGATA GTGAGGTGAT GACATAGTTT TGTGAAAATA	660
GCCATTTATA ACTCAATTAT TTAGTTTACT TTACTTTACT AGTGATACTA TTTGGAGTTA	720
TTAATGGACT TAGTTTATAT AACTAATGAA TTGATTGAAA GGGTTAGTAT TGACAATATT	780
GGTCATATTG ACTAGAAAAT AGAGTCTATC AAAATTTAAA GGCTAATAGA GGTGATGAGA	840
CAATTCGGC TCTTTGTCAA CTGTAGTGGG TTGAAGTCAG CTAAGCTCGA GAAAGGACAA	900
ATTTGTCTT TCTTTTTTGT ATATTCAGAG CGATAAAAAT CCGTTTTTTG AAGTTTTCAA	960
AGTTTCGAAA ACCAAAGGCA TTGCGCTTGA TAAGTTTGAT GAGATTATTG GTCGCTTCCA	1020
GTTTGGCATT AGAATAGTGT AGTTGAAGGG CATTGACAAT CTTCTCTTTA TCTTTGAGGA	1080
AGGTTTTAGA GGATGAACTT GATTCAGATT GTCCTCAATG AGTCCGAAAA ATTTGTCAGG	1140
CTCCTTATTC TGAAAGTGAA AAAGCAAGAG TTGATAGAGA TTATAGTGGT GTTCAAGTC	1200
TTCTGAATAG CTCAAAAGTT TATCTATAGT AGATTGAAAC TAGAATAGTA CACCTCTGCT	1260
TCTAAAACAT TGTTAGAAAT CGATTTGACT GTCCTGAATG ATTTGTCCTG TTATTATTTT	1320
ATTTTACTAT AAATCCACGT TTACGAATCT CTTTCCACAC TTGTTCAATG GGGTTCATCT	1380
CTGGTGTGTA TGGAGGAATA AATGCAAAAC CAATATTAGT CGGAATCTTT AAGGTAAGTT	1440
ATTTATGCCA TATAGCATTG TCCATAACGA GTAAAAGATA ATCATCTGGA TAAGCTTGTG	1500
AAAGCTCCTA TTCCTAAAGC CCCTTTATAA CCTCTTGCGA GAGAGACTAT TGAAGTACCC	1560
CTTACTTCAT GCGGATGAAA CTTCTTATCG GGTCTAGAG AGTCATAGCC ATCTGACCTA	1620
CTATTGGACC TTTTGTCTGT GGAAAGTTGA GAATCAAGCA ATCAGCTGT ACCATCATGA	1680
TCAGAGTCGG AGTGGTTCGG TAGTACAAGA ATTCCTAGGA GATTATTCTG GCTATGTTCA	1740
TTGTGATATG TTGCGGCAGT AACTTAGGAC TTTAGTCCTC TAGTTCTGCC TATGCGATAG	1800
CAGTCCAAGG TTTAGGAGCA AGGCGACGCT AAGCTTGGTA AACTGCGAAC CGCTAGAAGC	1860
TTATCGTCAA CTGGAAGAAG CTGAACTTGT TGGATGTTGG GCGCATGTGA GAAGGAAATT	1920

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TTTTGAAGCG ACCCCCAAGC AAGCAGATAA ATCATCCTTA GGAGCTAAAG GTTTAGCTTA 1980
 TTGTGATCAG TTATTTTCCT TGGAAGAGAG CTGGGAGGCT TTGCCAGCTG ATGAACGACT 2040
 ACAGAAACGT CAAGAACATC TCCAGCCCCT AATGGAAGAC TTCTTTGCTT GGTGCCGCCG 2100
 TCAGTCAGTT TTAGCAGGTT CAAAACCTAGG AAGGGCAATT GAATACAGCC TCAAGTATGA 2160
 AGAAACCTTT AAGACTATTT TGAAAGACGG ACATCTGGTC CTTTCCAATA ATCTAGCTGA 2220
 ACGCGCCATT AAATCATTGG TTATGGGACG GAGTAAAAGA GTCCAGTGGA CTCTTTTAGC 2280
 CTGAGCTCAG TTTAAAAAAG CGAGGGTGGT TATTTTCTCA AAGTTTGTAA GGAGCTAAAG 2340
 CAAGAGCTAT TGTTATGAGC TTGTTGGAAA CAGCTAAACG TCATCAATTA TAGTGCGTTG 2400
 AATCTATAAC AGTACGCATC GACTGCTAAA ACATTTCTAT AAATCAATTT TCCTTTCCTA 2460
 ATCGATTGTG TCATATCTTA TTTCAATCCA TTATAAATAG CGAGAAATAT CTATCCTATC 2520
 TTCTAGAATG TCTTCCAAAC GAGGAACTC TCGTAAACAA AGAGGTTTTA GAGGTTTATT 2580
 TACCATGGAC TAAAGTTGTA CAAGAAAAGT GCAAATAAGA AATCTCCAGA TTAGGAACCTA 2640
 TCCGTGAGTT CACTAATCTG GAGATTTTTC AATAGATTCG TTATTGGGCG GTTACGATAT 2700
 GATcACTACT TCGTCAGTCT TATCTACAAC CTCAAAACAG TGTTTTGAGC AACCTGCGAC 2760
 TAGCTTCCTA GTTTACTCTT TGATTTTCAT TGAATATTAG AACAGAAAAA ATGCTTGGAG 2820
 TATTTGTTTG TGTGTTTATT TTTATATAAC AAATATAAAA CAAAATAAAA ATATAAAAAA 2880
 AGAGACAAAA AAGAACAGAA AGTAATTGAC A 2911

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6854 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GAAAATAAGT CTTGACAGAA AGCGCTATCA ATGATAGAAT GAATTCAGAT AAAAAGATTT 60
 ATTTTAAAAA CAAAAATGAA ACGTTTCAAA AAAAGAAATA AAGAGACAGC GCCAAGCGCT 120
 ATCTTTTCTA GAAAAAATG AAACGTTTCA AAAAAGGAGG TTGCTATGAA TAGCAAAGCG 180
 AAGCAAGTTT CTCTTTGGGA AAGAATCAAG AAACAAAAAC TCTTGTTATT GATGACTGTC 240
 CCCGGTTTAG TTTTAACCTT TATCTTTAAA TACATCCCTA TGTATGGGGT TTTAATCGCA 300
 TTTAAAGATT ACAATCCTTT AAAAGGAATT TTAGGGAGTG ATTGGATTGG TTTTCTGAG 360

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TTTACAAAAT TCATATCCTC TCCCAACTTT GGTATCTTGT TAGCCAACAC ATTAAAATTA	420
AGTATCTATG GTTTATTGCT TGGCTTTTTA CCACCAATCA TTCTCGCGAT TATGCTCAAT	480
CAACTCTTGA GTGAAAAAGT CAAAAACGA ATTCAGCTCA TTTTATACGC ACCAAACTTT	540
ATCTCAGTCG TTGTTATTGT CGGTATGATT TTCCTCTTCT TTTCAGTGGG AGGACCAATC	600
AACAATTTTC TTTCTATGTT TGAATGAAG GCTGACTTCT TGACAAATCC AGACTTCTTT	660
AGACCTTTAT ACATCTTTAG TGGTATCTGG CAAGGAATGG GCTGGGCTTC AACGCTCTAC	720
ACGGCAACAT TGGTAAATGT AGATCCAGCC TTAGTAGAAG CAGCCCGACT GGATGGAGCC	780
AATATCTTCC AACGAATCTG GCACATTGAT ATTCCAGCTC TTAAGCCTAT TATGGTTATC	840
CAATTTGTTT TAGCTGCAGG TGAATTATG AATGTCGGAT ATGAAAAAGC ATTCTTGATG	900
CAGACATCGT TAAATTTGCC AACTTCTGAA ATTATCTCGA CATATGTCTA TAAAGTTGGT	960
CTTGATPCAG GAGACTATTC TTAATCAACA GCGGTTGGTT TGTTTAATGC AGTGATTAAC	1020
GTAGTATTGC TTGTTGCAGT TAACCAATC GTTAAACGCA TGAATAATGG TGAAGGAATT	1080
TAAGGAGGAA AGTATGAAAA ATTCGATTAT GGATACAAAA TTTGATAGAC GTATCTTACT	1140
CTTAAATAAA ATCATTATTG TCTTTATCGT TTTGATGACT TTGCTTCCTT TACTTTATAT	1200
CGTCGTAGCA TCCTTTATGG ATCCTAAGGT TCTGGTTAGT AGAGGGATTA GCTTTAATCC	1260
AGCCGATTGG ACTGTAGAAG GTTACCAGCG TGTATTGAGT GACCAATCTA TTCTAAGAGG	1320
TTTTATCAAT TCTCTACTAT ACTCTTTTGG ATTTGCAGCT TTAACAGTCT TGCTATCTGT	1380
GTTTACAGCT TATCCTCTTT CTAAGAAAGA CTTGGTTGGA CGTCGTTGGA TTAATACTTT	1440
CTTGATTGTA ACTATGTTCT TTGGTGGTGG TTTAGTCCCA ACTTACTTGC TCGTAAAAGA	1500
ATTGGGAATG CTCAATACTC CATGGGCTAT CATGTGTTCCA GGTGCTGTGA ACGTTTGGAA	1560
TATTATCTCT GCTAGGGCCT ATTTCCAAGG ATTGCCTGAA GAATTAGTTG AAGCTGCTGT	1620
CATTGATGGT GCAAATGATT TACAGATTTT CTTCAAAATC ATGCTTCCTC TTGCAAAACC	1680
AATTATGTTT GTTCTCTTCC TTTATGCTTT GTAGGACAG TGGAACATCAT ACTTTGATGC	1740
AATGATTTAT ATCAAGGATC CAAACTTGGA ACCATTGCAA CTTGTACTTC GTAAAAATCT	1800
CATTGAGAGC CAACCAGGTC AAGACATGAT TGGAGCACAA GCGGCTATGA ATGAAATGAA	1860
ACGTTTAGCT GAATTGATTA AATACGCAAC TATTGTCATT TCCAGCTTGC CATTGATTGT	1920
TATGTATCCA TTCTTCCAAA AATACTTTGA TAAAGGAATT ATGGCTGGTT CACTTAAAGG	1980
ATAAAAAAAG AAAAAATAAA AGGAGTTTTC TCATGAAATT CAAAACATTC TCAAAATCAG	2040
CAGTTTTGTT GACAGCTAGT TTAGCAGTAC TTGCAGCCTG TGGCTCAAAA AATACAGCTT	2100
CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCCCCTG TCAAGAAAAG AAAACATTGA	2160

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AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC AAATGAAAAG TTAATTTTGC	2220
AACGTTTGGG GAAGGAAACT GGCCTTCATA TTGACTGGAC CAACTACCAA TCCGACTTTG	2280
CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTTACC AGATGCTATC CACAACGACG	2340
GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG TGTATTATT CCAGTTGAAG	2400
ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAATTTT GGATGAGAAA CCAGAGTACA	2460
AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT TCCATGGATT GAAGAGCTTG	2520
GAGATGGTAA AGAGTCTATT CACAGTGTCA ACGATATGGC TTGGATTAAAC AAAGATTGGC	2580
TTAAGAAACT TGGTCTTGAA ATGCCAAAAA CTACTGATGA TTTGATTAAA GTCCCTAGAAG	2640
CTTTCAAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA TGAAATTCCA TTTTCATTTA	2700
TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTCG TGCATTTGGT ATAGGGGATA	2760
ACGATGATCA TTTAGTAGTA GGAAATGATG GCAAAGTTGA CTTTCACAGCA GATAACGATA	2820
ACTATAAAGA AGGTGTCAAA TTTATCCGTC AATTGCAAGA AAAAGGCCTG ATTGATAAAG	2880
AAGCTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAGG TCATGATCAG AAATTTGGTG	2940
TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA CGAAAGTTAT GATGTTTAC	3000
CAGTACTTGC TGGACCAAGT GGTCAAAAAA ACGTAGCTCG TACAAACGGT ATGGGATTTG	3060
CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT AGAATTGACA GCTAAATGGA	3120
TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA CTGGGGAAC TACGGAGATG	3180
ACAAACAACA AAACATCTTT GAATTGGATC AAGCGTCAAA TAGTCTAAAA CACTTACCAC	3240
TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA AGTAGGAGGA CCACTAGCTA	3300
TCCTAGATTG ATACTATGGT AAAGTAACAA CCATGCCTGA TGATGCCAAA TGGCGTTTGG	3360
ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT CAATAACTAT CCAAGAGTCT	3420
TTATGACACA GGAAGATTTG GACAAGATTG CCCATATCGA AGCAGATATG AATGACTATA	3480
TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT TGATACTGAG TGGGATGATT	3540
ACAAGAAAGA ACTTGAAAAA TACGGACTTT CTGATTACCT CGCTATTAAA CAAAAATACT	3600
ACGACCAATA CCAAGCAAAC AAAAAGTAGA GGTGATTAT GGGAGATAAG AAATACACAG	3660
TAGAAAAAGC CAATCGTTTT ATAGCAGAAA ATAAACATCT CGTTAATACT CAATATAAGC	3720
CTGAAGAACA TTTTTCAGCT GAGATTGGTT GGATCAATGA TCCAAATGGA TTTGTCTATT	3780
TTCTGTGAGA ATACCATCTC TTTTATCAAT TCTATCCATA TGATAGTGTT TGGGGGCTTA	3840
TGCACTGGGG ACATGCTAAA AGTAAGGACT TGGTGACTTG GGAGCACTTG CCAGTGGCAC	3900

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TTGCTCCTGA CCAAGATTAT GACCGAAATG GTTGTTCCTC AGGCTCTGCC ATTGTCAAGG	3960
ATGATCGCCT CTGGCTCATG TACACTGGAC ATATCGAAGA AGAAACCGGT GTCCGCCAAG	4020
TGCAAAATAT GGTATTTTCA GATGACGGGA TTCACCTTTGA AAAGATTTCC CAAAATCCAG	4080
TTGCAACTGG ATCAGACTTA CCAGATGAGT TGATTGCTGC TGATTTCCGT GATCCAAAAC	4140
TCTTTGAAAA AGATGGACGC TATTACTCCG TAGTAGCTGC CAAACACAAG GATAATGTGG	4200
GCTGTATCGT TCTACTAGGG TCCGATAACC TAGTAGAATG GCAGTTCGAA TCCATCTTTT	4260
TAAAAGGGGG AGAACACCAA GGTTTATGT GGGAAATGCC AGATTACTTC GAGTTAGATG	4320
GGAAAGATTG CCTTATTATG TCACCCATGC GTTATCAGCG TGAGGGAGAC TCATATCATA	4380
ACATCAACTC ATCGCTTTG TTCACGGTA AGGTAGATTG GAGAGAAAA CGTTTTATCC	4440
CAGAATCAGT TCAAGAAATT GATCATGGCC AAGACTTCTA TGCGCCTCAA ACATTGTTGG	4500
ACGATCAAAA TCGTCGTATC CTGATTGCTT GGATGCAGAC ATGGGGCGT ACCCTTCCAA	4560
CCCATGACCA AGAACACAAG TGGGCATGTG CCATGACTCT ACCTAGAATT CTAAGATTGG	4620
AAGATGGCAA ACTAAGACAA TTCCCTGTTA AAAAAGGCCA ATATCAAATC CAAATAGATA	4680
AAGATTGTCA TTACCACTTA GGAAATGATA TAGATTATCT TGAATTTGGT TATGACAGTA	4740
ATGCGCAGCA AGTTTACATT GATCGTAGCC ATCTTATCA AAAAATTCTA GGTGAAGAAG	4800
AACAGGACAC TAGTCGACGG TATGTAGATA TTGAAGCTAA AGAATTGGAA GTTGTCTTAG	4860
ATAAAAATTC CATCGAGATT TTTGTCAATC AAGGTGAAGC AAGCTTGACT GCAACTTATT	4920
ACTTAACGGT GCCAGCTGAG CTATCACGAA TTGATTAAAA ATTAAGTTAT TTCTCCTAAA	4980
GAAAAAGTTC TCTTCTAAA ATAGTGGAAA GAGGACTTTT TGTGTTTTGG GTATATAAGC	5040
TTAGTTTATG GTATTTGTAA AATTGGTGTG GGATTATGAT TTAAGCTAGT TTTCTAAAGA	5100
ATTTGAAAAA AATTTTATTT AAGCAAAAA ACCTTGGTTC CAAGGCTTTT CCTGTTGTAT	5160
TTAGATGCCC CCTACAGGA TTGTAGGAGA TATGTTGCTT AGATGTTCTT GATTTTCTGG	5220
TGTTTTGTAA CGTTTAAATG AGTTTTTTGA GTTGTGTTGG GGGGCGTTGC CCGGCAATTG	5280
CCCGACTTAT TGCTTGAAAA AGAATTTAAA ATATAGTATA GTTAATTATA GATTAACACT	5340
TGCTTGAGAG AACTGATGAA GAACAATGAA AGATTAGGTA TTAAATTAAG TAGAGATAGC	5400
GTTTTAGGAT TGAGGGAAGT TAGAAGGCTT TATTTAGGCA GTTCAGATAT CCCAGTTTCT	5460
GATGGCTATG TGATTGAAGT TGCTTATAAC CAGATATCAC ATGAGATTGA TATTATTGAT	5520
TGGGTAGAGT TGAACAAGTC AAAAATTAAG ATAAGTGAAG TTAGTGAAAG CGTGGATATA	5580
GATGCCACTA GCTTGAGAAC AACTTTGACT TTAGACACAT TAGTATATGA AGGTATGAGA	5640
GATATACAGT TAAAGTTGAG AGAGCTTACA AAGGGGAGAG TATTCTTTTC ATTTGTAGTG	5700

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AAGTTAGTTT TGTTCGCTTC TATTTTAAAG AAAAAAGATT TACTAGAAAA ATTTCAAGAA	5760
AAGTGTTAAT CAAGTATTGA CACTTTATCT GGATTTCCGT ATAATATGCT TAGAAAGGAA	5820
TCTTTCTAAA TTTTTTCGT CCTTATGTGT TAATCAAAGA CGAATACAAA AACATATTTT	5880
TTTACTCTAA AAAGTGTTAA TCAATGATGT ATTTGTTAGA GAGGTAGATA AATGGAATTG	5940
AGAGCACCAC CAGTTATAAT AGTATAAAAC GTATAATAAA AATATTTTAA CTTGAATTAT	6000
AGAAAAGGAG AAACAAATCA TGAAACAAAA ACAACCGATT GTTCTTAGAA CGAAACAACA	6060
TACATTTGAA GAGCTTATTC AAGACCAAAA GTTAGAAAGA TTGGCTAAGT TGTCGCCCCGA	6120
TTTGTTGGA AGGTATGGTT TTA CTGCTAG CTGTGCGTCT TCATTTGCGA ACTTGATTAA	6180
AGAAGCGTAT GGGGGTAAAA ATCTAAACGT AGTTTATGCG AGTCGGATGT TGGCTCTCTG	6240
GAATATTGCT TGCAGTTGTT ATCATAAGGC TGATGGGTAT TCTTTAGCAG ATGCGCTTTT	6300
TAGTGATAAA AAAATTGTGC TAGATTCTTA CTATTACCAC AAGAATACCT CTAATACCAT	6360
AACTAGTGAT GTGATAAAAG ATGTTTACGA TAATTATAAT AATTATATGG TTTTAACTCG	6420
AGAAGCGACA CCTGAATACA TTTATGTTGT ACAAACTGAA ATGCCAAAAG ATTCAGATTT	6480
ATATTTTAT ATTAGAGAAG TTCTGGGATT ATCGTTTAGT ACCATGCATT ATGCATTTTT	6540
AGTCAAGGTT CTTGCAGGAG CGCTTGCTAG AAAATATAAG CCATATCGAA ATTGAATTAT	6600
TTAAATTTAT ACTCTTCGAA AATCAAATTC AAACCAAGTC AGCTTCGCCT TGCTGTACTC	6660
AAGTGCTGTC TGTGGCTAGC TTCTTAGTTT GCTTTTGTAT TTTCATTGAG TATTACTCTT	6720
ATGGTAGTTA TTTATGGCAT AATAATATTG ATTTGGGAGT TATAGCGAAA ATTTTAGGTT	6780
CTATAATATT TGTAGTGGGT AAACCACTAT AGATATTATG GAGCCTATTT ATTGTAGAAA	6840
AAAGTCCCAT ATGA	6854

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3895 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

TCCTTGCTAA GTTTATACTC AATGAAAATC AAAGAACAAA CTAGGAAGCT AGCCACAGGT	60
TGCTCAAAGC ACCGCTTTGA GGTTCAGAT AAAACTGACA CGGTTTGAAG AGATTTTCGA	120
AGAGTATTAA TTTACATAAA TAGCCAGTGT TTGATAGGTT TTGAGTAGAA TTTTCTCAGA	180

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CACTTCTGCA	TCTTCATAGT	TTGATATCAA	AATCTGTCCA	TTTGGTAGA	CTGCTGGCAA 240
GTCGATTTC	CTTCTTTAGC	ATAAAAGTTA	TTGAGCACTA	GTAACCTTTG	ATCCTCAAAC 300
TGGCGTTCAA	AAGCGTAGAC	TTGTTTGCTA	TCTTCAAAGG	CTGGTTTGTA	ACTTCCTTCT 360
GAAATGATTG	GCATTTCCCT	ACGCATCGAA	TCAAGTCTTG	ATAGAAGGTA	AAAATCGGAC 420
CCTGGATTTC	ATTTTCTACA	TTGATGTATT	TATAGGATTT	ACCAGCTTTC	AACCAAGGAG 480
TGCCTGTTGA	AAATCCTGCA	TTTCCGAAG	CATCCCCTG	CATGGGAATG	CGTGAATTAT 540
CACGCGACTT	AGCTTGAATA	ATCTGGAAGG	CTTCTTGCTG	ACTCTTTCCT	TCTTCTAAGA 600
GCATCTGATA	GGCATTAAAG	GATTCGACAT	CCACATAATC	AGCCATAGAA	TCATAGTCTG 660
GGTCAATCAT	CCCGATTTC	TCACCCATGT	AGATATAAGG	TGTCCCACGT	GACAGGTGAA 720
TGCTGGCTGC	TAGCATGGTG	GCTCCTTCCT	TGCGGAAGTT	TTGAATATCG	ACAAAACGGT 780
TCAAGGCACG	TGGTTGATCG	TGATTATTCC	AAAAGAGGGC	ACTCCAACCG	TCTTTATCAC 840
TCATTTCCTT	ACCCCAACTA	TGGTAAAGAC	TCTTCAACTC	TTCAAAATCA	AAGGGAGCCA 900
AGGTCCACTT	TTGTCCATCC	TTATAGTCCA	CCTTGAGGTG	ATGAAAATTA	AAGGTCATGG 960
ATAATTCCTG	ACGATCAGGC	GACGAATAGA	GGACACAGTT	TTCCATGGTG	GTAGAAGACA 1020
TTTCCCCAAC	TGTCATAAAG	CTATCGTCGG	ATCCAAAAGT	GGCTTG GTTC	ATCATACGCA 1080
AATAGTTATG	AACGATGGGT	TTGTCTGTAT	AAGCTGGCTT	CCCTTCATTT	TCAGGACAGT 1140
CCACTGAAAC	CTCGTCCTTA	CCGATCAAAT	TGATCACATC	AAATCGGAAA	CCTTTGACAC 1200
CCTTGTCGCG	CCAGAAATTA	ACAACCTTGA	AAAGCTCCTT	ACGGACATTG	GAATTGCGCC 1260
AGTTAAGGTC	AGCCTGGGTC	TCATCAAATA	GGTGAAGATA	GTATTTCCCA	GTATCCCCGA 1320
AAGGCGTCCA	TGCAGAACCA	CCAAACTTAG	ACTGCCAATC	TGTTGGTTGG	TCTTGGATGA 1380
AGAAAAAGTC	TTGATAATAC	TTATCACCAG	CTAGGGCTTT	CTGAAACCAT	TCATGCTCTG 1440
TCGAACAATG	ATTAAGTACC	ATGTCCAGCA	TAAAGTCAAT	CTTGTGCTCT	TTACCGACAC 1500
ACACCATTTT	CTCAAAATCA	GCCATATCAC	CAAAAAGAGG	ATCCACTGCC	ATATAATCTG 1560
AAATATCGTA	ACCATTATCC	CGTTGAGGGC	TTGGATAGAA	TGGATTGAGC	CAGACCATAT 1620
CCACACCTAG	TTTGGCTAAA	TAGGGAATTT	TTTCGATAAT	CCCACGGAAA	TCCCCAATAC 1680
CGTTTTCAGT	GGTGTCTTTG	TAAGATTTTG	GATAGATTTG	ATAGACTACT	TTTCCTTTAT 1740
CAAGTGTCAT	CTGTTTCTCC	TTTTCTGATA	AAAGGGAGGA	AGCAGTCTTC	CGTCCCTATT 1800
TGTGCTATTT	CAATTATACT	CAATGAAAAT	CAAAGAACAA	ACTAGGAAGC	TAGCCACAGG 1860
TTGCTCAAAA	CACTATTTTG	AGGTTGCAGA	TAGAGCTGAC	GTGGTTTGAA	GAGATTTTCG 1920
AAGAGTATTA	GATTCGTGTA	GCGACCATGA	GAGATGCTCC	AGCTTGGATC	GTTGTCGGAT 1980

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AAGTTCGGG AATAGTCGCT GTATAAGCAT CTTGGTTGGT GATGATAACA GGAGTTTCTG	2040
TCACCAGACC TGCAGCCTTA ATGACATCCA TATCAAAACG AATCAGTTGC TGACCAACTG	2100
TAACGTGATC TCCTTGGA CTACAAGACTTT CAAAACCTTT GCCATCAAGA CCTACTGTAT	2160
CCATACCGAT GTGGATGAGC AATTCAACTC CCTCGTCAGA GACAATGCCG ATGGCATGCT	2220
TGGTAGGGAA AAGAACCGTC ACTGTCCCAT TAACTGGAGA GGTCAACTCA CCTTGGCTTG	2280
GTTCAATGAC TAGACCTTGC CCCATGACAC CTGATGCAAA AATAGGATCC GTCGCTTGAC	2340
TCAATTCTTT CACTTGGCCA GTTAGTGGGC TGATAATTTC TACCGAAGTA AGTTCTACTG	2400
GTTCATGGTT CACAAATTCT GCTTCTTCTT GAGCAACGAA TTCTGCCTGC AAGTTCGTAT	2460
CGCCCTCTGT TTTTGTAAG AGACCAGCCT TCGGAAGAA GAAAGTCAAG AGCATTGGAA	2520
CAACAATCGC AACTAGCATA GTTCCTGCAA ATGGCAGCAT GTATTGAGGT TGAATAGAGA	2580
GAATACCTGG CAAACCACCG ATACCAATAG AAGCCGAGT TACATTAAAA GTAACGGATA	2640
ACATGCCTGC AAGGGCTGAA CCAGTCATCC CAGCAACAAA TGGATAAATA TATTTTACGT	2700
TAACCCCAA AAGAGCTGGT TCTGTAACAC CGAGATAGGC TGAAATGGTT GCAGGAAGTG	2760
AAACCTGAGC CTCACGCTCA TCATGGCGAT GCATGAAATA ATAGGCAAAC ACGGCTGAGC	2820
CTTGAGCAAT ATTAGAAAGA GCAATCATTG GCCATAGGGC AGTGCCACCA GCATCCGCAA	2880
TCAATTGTGT ATCAATGGCA TTGGTCATAT GGTGCAGACC TGTGATGACA AATGGAGCGT	2940
AGAGGGCGCC AAAAAATTGCA CCGAAGAGCC ATTTAACTGG ACCAGTTAAA CCTGCCAAGA	3000
CAACTGATGA AAGTCCTTGT CCAATTGTCC AACCGATTGG TCCCAAAACA GTATGAGCCA	3060
AAATCAAGGC TGGAATCAAT GACAAGAAAG GTACAAAAAT CATAGAAATG ACTTCTGGGA	3120
TATGCTTGTG CCAGAAGATT TCAAGATAAG ACAGACTCAA ACCTGCAAGC AAGGCTGGGA	3180
TAACTTGGGC TTGGTAACCG ATACGATTAA CAGTAAAATA GCCAAAATTC CAAACCCAGT	3240
TTGCCGCGAT ATCAGCTGCT GGCCTTGAAG CAACCGCATA GGCATTGAGC AACTGAGGCG	3300
ATACCAAACA GATTCCGAGA ACAATTCCCA AAATTTGGCT GGTTCCTATC TTACGAGAAA	3360
CAGACCAAGT AATCCCTACT GGTAAGAACT GGAAGATAGC TTCACCAGGC AACCAGAGGA	3420
AGTGATTGAC ACCTGCCCAA AACTGAGAGG ATTCTGTGAT GGTCTTGCCA TCCAACATCG	3480
ACCAATGGAC ACCTTCCAAG ACATTACGGA AACCGAGGAT CAATCCTCCG ACTATCAAGG	3540
CTGGAATAAT CGGAGTAAAA ATCTCCGCCA GAGTGGTCAT AACACCTTGG ACCACGTTTT	3600
GATTACTCTT AGTGTCAGAC TTGGCTGCTT CTTTGAAAC ACCCTCAATA CCTGAAACGG	3660
CTGTAAATC ATTATAAAAG ATGGGCACGT CATTTCCAAT GATTACCTGA AATTGACCTG	3720

1182

CATTTGTAAA GGTTCCTTTA ACAGCTGGAA TTGACTCGAT AGCTTTAACA TTAGCCTTCT	3780
TATCATCTCC TAAAACAAAC CGCATCCGTG TCGCACAGTG AGTTACGGCA GTCACATTTT	3840
CTTTCCTCC GATTGCCTGA AGCAGATCTT TGGCTTCTTG TTCAAATTTT CCCGG	3895

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3936 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

AGGATCGCCG CTCCAGCTAC TAAGTCTCGT GCAGTGCCGA TTTATCAAAC AACATTTTTT	60
GTTTTTGATG ACACGTAGGA AGGTGCCGAT CTGTTTGCCT TGAGGAAACC AGGGAACATT	120
TATACTCGTA TCACCAATCC TACAACAGCT GCCCTTGAAG GTGGTGTGA AGCGCTAgcA	180
ACAGCATCAG GTATGACTGC AGTGACTTAT ACGATTTTGG CGATTGCCCA TGCTGGTGAC	240
CATGTAGTGG CTGCTTCGAC TATTTACGGT GGAACCTTCA ATCTTTTGAA AGAACCCCTT	300
CCTCGTTATG GTATCACAAC AACCTTTTTC GATATTGATA ATTTGGAGGA AGTAGAAGCA	360
GCTATCAAAG ACAATACCAA GCTTGTCTTG ATTGAAACCT TGGGTAACCC CTTGATTAAT	420
ATTCCAGACC TGGAAAACT GGCAGAGATT GCTCATAAAC ATCAAATCCC ACTTGTGTCA	480
GACAATACTT TTGCAACACC TTATTTGATT AACGTCTTCT CTCATGGCGT TGACATTGCC	540
ATTCACTCTG TGACTAAGTT TATCGGTGGG CATGGTACAA CTATTGGAGG AATAATTGTC	600
GATAGTGGTC GTTTTGACTG GACGGCTTCA GGGAAATTCC CTCAATTGTG TGACGAGGGT	660
CCAAGCTGCC ACAATTTGAG CTATACTCGT GATGTGGGTG CAGCAGCCTT TATTATAGCT	720
GTTTCGAGTC AATTGCTTCG TGATACAGGT GCAGCCTTGT CACCATTCAA TGCTTTCCTC	780
TTGCTACAAA GACTTGAAAC CTCTTCACTT CGTGTGGAAC GCCATGTACA AAATGCTGAG	840
ACAATGTGTG ATTTTCTTGT CAACCATCCT AAGGTAGAAA AGGTAAATTA TCCAAAACTT	900
GCAGATAGTC CTTATCATGC CTTGGCTGAG AAATACTTGC CAAAAGGTGT CGGTTCATC	960
TTTACCTTCC ACGTCAAAGG TGGCGAGGAA GAAGCACGCA AGGTCATTGA TAATTTAGAA	1020
ATCTTTTCTG ACCTTGCAAA CGCGGCAGAT GCTAAATCGC TTGTTGTCCA TCCAGCAACA	1080
ACCACTCACG GTCAATGTG AGAAAAAGAC CTAGAAGCAG CAGGTGTCAC ACCAACTAA	1140
ATTTCGTTGT CAATCGGTCT TGAAGATGTA GAAGATTTGA TTGAAGACTT GCGCTTGGCC	1200
TTGGAAAAAA TTAAAGTAA AAGAAGATAA ACAGTGGGCT TCGACTCACT GTTTTGTATT	1260

1183

TTCCCTCAGG CATGATATAA TGGTTACAGA AGTCTAGAAA GAGGAACGAT ATGAACGAAA	1320
TCAAATGTCC CAACTGTGGG GAAGTCTTTA CAGTAAATGA GAGTCAGTAT GCCGAACCTCT	1380
TGTCCCAAGT GAGAACGGCA GAGTTTGATA AGGAACCTACA CGATAGGATG AAGCAGGAAC	1440
TGGCCTTGGC TGAGCAAAAG GCCATGAATG AGCAACAGAC TAAACTGGCT CAGAAGGATC	1500
AAGAAATTGC GCAATTACAG AGTCAGATCC AAAACTTTGA TACAGAAAAA GAATTGGCCA	1560
AGAAAGAGGT TGAACAGACA AGCCATGAGG CTCTCTTGGC TAAGGACAAG GAAGTACAGC	1620
TCTTAGAAAA TCAGTTGGCT ACCTTGCGTT TGGAGCATGA AAATCAACTA CAAAAGACCC	1680
TTTCTGACCT AGAAAAAGAA CGGGATCAGG TTAAAAACCA ACTACTTTTG CAGGAAAAGG	1740
AAAATGAATT ATCTTTGGCT TCTGTTAAGC AAAACTACGA AGCCCAGCTC AAGGCAGCTA	1800
GTGAACAAGT CGAGTTTAT AAGAATTTA AGGCTCAACA ATCTACAAAA GCGATTGGGG	1860
AAAGCCTAGA ACAGTATGCA GAGAGTGAGT TTAACAAGGT TCGTAGTTTC GCCTTTCCAA	1920
ATGCTTACTT TGAGAAGGAT AACAAGGTCT CTTCGCGTGG GTCTAAAGGG GACTTTATCT	1980
TCCGTGAGTG TGATGAAAAT GGAGTTGAAA TCATTCTAT CATGTTTGAG ATGAAAAACG	2040
AAGCGGACGG AACAGAGAAG AAGCACAAGA ATGCAGATTT TTACAAGGAA TTGGACAAGG	2100
ACCGTCGGGA GAAGAACTGT GAGTATGCCG TTTTGGTGAC CATGCTTGAG GCTGATAATG	2160
ACTACTTTAA CACAGGGATT GTTGACGTCA GTCACGAGTA TGAAAAAATG TATGTTGTTC	2220
GTCCTCAATT CTTTATCCAA TTGATTGGTC TCTTACGTAA TGCGGCGCTA AATTCCCTAA	2280
AATACAAGCA GGAGTTGGCC TTGGTTCGCG AGCAAAATAT TGACATTACG CATTTTGAGG	2340
AAGATTTGGA TGCCTTTAAG CTAGCTTTTG CTAAGAACTA TAATTCAGCT TCGACTAACT	2400
TTGGAAGAGC TATTGATGAA ATCGACAAGG CCATCAAACG CATGGAAGAG GTTAAGAAAT	2460
TCCTGACCAC ATCTGAAAAC CAACTCCGTT TAGCTAACAA CAAATTGGAA GATGTCTCTG	2520
TTAAAAAATT GACCCGAAA AATCCAACAA TGAAAGCGAA GTTCGAAGCA CTGAAGGGGG	2580
AGTAGAAAGC AAAAATGAAC GGTATTATTA ACTTAAAAA GGAAGCAGGA ATGACCTCGC	2640
ATGATGCGGT TTTTAAACTG CGTAAGATTT TGGGAACCAA GAAAATTGGT CATGGTGGA	2700
CCTTGGATCC GGATGTGGTG GGTGTTTTGC CGATTGCGGT TGGCAAGGCG ACACGCATGG	2760
TCGAGTTTAT GCAGGACGAG GGTAAAGATCT ATGAGGGGGA AATCACTCTG GGCTATTCCA	2820
CGAAGACTGA GGATGCTAGT GGGGAAGTGG TCGCAGAAAC CCCTGTTTTG TCTCTCTTGG	2880
ATGAAAAGCT TGTTGATGAA GCGATTGCTA GCTTGACTGG GCCTATTACT CAGATTCCCC	2940
CTATGTATTC GGCAGTTAAG GTTAATGGTC GCAAGCTCTA TGAGTATGCG CGTGCTGGTC	3000

1184

AGGAAGTGGA GCGTCCAGAA CGTCAGGTGA CCATTTATCA ATTTGAGCGA ACAAGTCCGA	3060
TTTCTTATGA TGGCCAACTT GCGCGATTCA CTTTTCGTGT AAAATGCAGT AAAGGGACGT	3120
ACATCCGTAC TTTGTCAGTT GATTTGGGTG AAAAGCTTGG TTATGCGGCT CATATGTCCC	3180
ATTTGACTCG TACTAGTGCT GCTGGCTTAC AATTAGAAGA CGCTCTTGCC TTGGAGGAAA	3240
TTGCTGAAAA AGTAGAGGCT GGGCAATTAG ATTTTCTCCA TCCTTTAGAG ATTGGGACAG	3300
GTGACCTTGT CAAAGTTTTC CTAAGTCCAG AAGAGGCTAC AGAAGTTCGC TTTGGTCGTT	3360
TTATTGAGCT AGACCAAACG GACAAAGAAC TGGCTGCCTT TGAAGATGAT AAATTGTTAG	3420
CCATTCTAGA AAAACGGGGC AATCTCTATA AGCCAAGGAA GGTTTTTAGC TAGATCGTTT	3480
AGGAATAAAA ATCGGGTGAT AGATAACAAT TGCTTGATAA AACCCCATAC TAATAGTAGA	3540
ATGGTTTTGG GAATTATAAT ATTCCAATTG TTGCGAGTTG TAGGTACTCA AATAATCTAT	3600
ATAGAAATTT AGAGGTGTGA AATGAAGCAA TTAAAAATTC TTTCAGATAA ATATTTAGAG	3660
TCCATTACAG GTTCTGATGG GAACTTAGGC CCAGGATTTG GTGTGATAAT TCCATGATGC	3720
GAAATGAGTT TCGAGAAAGG GTGGAGCAAC TTCTTCAACA AAAAGAAATA AATGAAAATA	3780
GTGAGTTGAG TCACCTGTTT CGTCTTGCTA TACAAAATTT AGACAGAAAT GAAAAATACC	3840
AATCGGTCAT GGCCAATTTG AGTCAAGGGT TGTCACTTTA CCTCATGACG CATCATTACC	3900
AGGCACCTAA GTCTGTCATT GATTTTGGTT TATGGA	3936

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

CATCCAGCAA CTGCTCCTCT GAGCGTTTCA AAATTGATGT AATTTTCTA GTTTTTCTA	60
ATAAATGTGC CATTTTTCAC CTCGAATTTA ATCGCTATCA TTATAACATA AAAACGTCTC	120
TTTTTCAATA ATTATCTGAA AATTCCTTAT TGACTTGCAT TGACTTACAA TTTAATTA	180
AACCAGAATA TTTTAAATTA AATTGTTCTT TTTCTATTGA CAAGTTGCCT ATTTTGTGT	240
ATCATAATAT TATAAAAGAT AATATAATAA TTTTATTTGT CTTTTCACAT TCGGTCTCCT	300
TATATAAAAA AGCGATTCAT TTTGAACCGC TTTTCTTAT TTATCGCCTT TGTTACGAAT	360
AACAAAGCCT GTTTGCTTTT CGCTTAAAGT ATTGCGTGGT TTTTATTAT CCTTACGGTA	420
ACGTTTTTCC TTATCAAAAC GATCGTTGCC ACGACTTCCT TTTTGAAC TATCACGGCG	480

1185

ACCATTGCCA CGGCGATCAC GCTCTCGACG GTCGTCCCCA CGACGGCCTC CACGACCTCC	540
CTTAGCTTTA CCACCGAAAC CATTACCTGA TGGTTTAAAC GGTAGTGGtT TTTCACGTGC	600
AATCTCCACT TCTGGAAGGC TATCTGGGTC TTGGACTGTC AGACTCAAGA TATACATTGC	660
CAATTCTTCT GGAGTAAACT CAGCAGCCAA TTGCGGAGCA TCCTTACCAA ATTTCTCAAA	720
GTTGGCACGA ATGGTTTCAT CTGCAAAATC ACGTTCGATT TTCTTGAGAG CTACCTGTTT	780
TTTTGATTGG AAGGATTCTT CTACACTTGC AGGTTTGAGA CCTTTCATGC GTTTCCTTAGT	840
CAAGTTTTC AATGATTGAA GGTAACCCAT TTCGTTTGA GCAACAAAAG TAATAGATTG	900
ACCTGACTTA CCAGCACGAC CTGTACGACC GATACGGTGA ACATAACTCT CAGGATCTTG	960
TGGAATATCG TAGTTGTAGA CATGGGTCAC ACCTGAAATA TCCAAACCAC GCGCTGCAAC	1020
GTCTGTGCGA ACCAAAACAT CAAGATTGCC ATTTTTTAAAG TCACGAAGGA CACGAAGACG	1080
TTTGTTTGG TCTAGGTCGC CATGAATTC TTCTGCACGG AAGCCACGAA TTTTCAAACC	1140
ACGAGTCAAT TCATCCACAC GCGGTTTGGT ACGACCAAAT ACAATAGCGA GTTCTGGTTG	1200
TGCCACATCC ATGAGACGAG TCATGGTGTC AAATTTTCT TGTTCCTTAA CACGGATATA	1260
GTACTGGTCA ACCAATTCTG TTGTCAATTC CTTAGCCGCA ATCTTGACAT GTTCAGGGGC	1320
TTTCATAAAC TGAACACCGA TACGTTTGAT GGCATCTGGC ATAGTTGCTG AGAAAAGCAA	1380
AGTTTGACGG TTCTCAGGTA CACGGGAAAT AATGGCTTCG ATGTCTTCAA GGAAGCCCAT	1440
GTTAAGCATT TCATCCGCTT CGTCAAGGAT AAGGGTTTCA ATGTCTTGTA ATTTCAAGGC	1500
CTTGCGTTTA ATCAAGTCCA AGAGGCGACC TGGAGTCCC ACCACAATAT GGGCACCAGA	1560
TTTAAGAGCC TTAATTGTG TTTCAATGCT TGATCCGCCA TATACTGAAC GGAATTGAC	1620
TCCCTTACTA CGACCAAAGC GGAAGAGTTC TTCTTGACTT TGGACAGCTA GTTCACGAGT	1680
TGGAGCGATG ACCAAGGCTT GGATAGTCGC TTCTTCTGTA CGGATTTTTT CAAGGGTAGG	1740
CAAGCCAAAG GCTGCAGTTT TTCCTGTACC AGTCTGAGCT TGACCGATAA CATCCTTGCC	1800
TTCAAGGGCC AAAGGAATAG TTTGTCTTGT GATAGGACTA GCTTCTACAA AACCAGCTTT	1860
TTCAATTTCT GCTAGCAAAT CAGCAGACAA GTTTAATTCA TTAAATTTCA CGTTATTCTT	1920
CTTCTCAAAG GTGGTGCGAA GCCACCCTAT AGGGCTTAGT TTATACTTTT CTTTTTATGA	1980
CGTATTTTCA TATACTAGA TATAAAATCG TGTGCTTCT TTTCCACAAA AGAAAAGTAC	2040
TGTTTTCTTT GCAACCTATC TAGTATAACA CAAGACCAGA GCAAAAGATA GCCCCATTTT	2100
TACAGAAAAT CATGTAAGCG CTTTTTGACT TTCTTTTTTG ATTGAACGAC CTAGATAATA	2160
AGACAAAGCC AAGGCGATAC TGTATAAAAT GAGAAAAACG AACAAGGTTT GTGTGTACGA	2220

1186

ATGAGCCATT TTATAAGTCT CTGCTAATAA AATAGGTCCC GCTAAACCAG CCATTGCCCA	2280
AGCTGTTAAA ATATAACCAT GCAGAGCGGC CAATTCCCTTG GTTCCAAAAA TATCACTGAG	2340
ATAAGCTGGA ATCAAAGAAA AACCAGCTCC ATAGCAAGTC ATCAAAATAG ACATAGCAAC	2400
TACAAATAAA ACGGAATCTG TAAAGAGCCA AAGTGAGAGA GAAAAGAAAA GATTGACAAG	2460
CAGTAATATA CTAAAGGTTA GAGGGCGACC GATATAGTCA GACAAACTCG CCCAGAGCAA	2520
GCGACCAAAT CCATTGAAAA TCCCCAAAAC ACCCACCATT ACTGCTGCAT GACTTGTTAGA	2580
CAAGCCAGCC ATCTCCTGTG CCATTGGCGA TGCCGCTGAA ATTAAGCCTA AACCACAAGC	2640
TATGTTGATA AAGAAAATAA TCCAAAGCAT ATAAAACCGA TTGCTTTTTA GAGCCTGATT	2700
TGCAGCCATT CCTTGCGTCA AAGAGGCTGT TTTTCTTTC CCTGAAGAAG ATAAAATTGC	2760
AAGCTCTTGC TCATTTGGAC GCTTAATGAA TTGTGAAGCT AGGAGCATGA TAATAAGTA	2820
ACTTGCTCCT AAAATATAAA AAGTTTCTAC AAGCCCTACC CCTGCGATGA GGTGTTGCGC	2880
TATGGGACTA GTCAATAAAG AAGCAAAACC AAACCCATA ATCGCTAAAC CTGTTGCGAG	2940
ACCACGTTTA TCAGGAAACC ATTTTATAAT CGTCGACACA GGGGTAATAT AGCCTGCTCC	3000
CAAACCAAGC CCACCTAAAA TGCCATAAGC GAGATACAAC AACCACAGCT CTGACGGTCT	3060
ATTGCAAATC CTGTTAAGAT ATTTCCACCT GCGTATAGAA AAGCAGATAG ACTTCCCATG	3120
ACTTTCGGAC CAAATTTTTC TACCAAACGC CCCATAAATG CAGCCGATAA GCCCAAACAA	3180
AAGATTGCTA GACTAAAGGC GAAGGCAACA GAAGCCTGAT CCCATCCCGT	3230

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5096 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CCTATGAAGA CTGTCCCAAC TGGGTGTCCT TCTAGGCTAT CTGGTCCTGC CACTCCAGTC	60
AAACTAATTC CAAAATCAGA CTGGGTCTTG CTTCGTGCCT GCTCAGCCAT CTTCTGAGCT	120
GTAAATTCAG ACACCACACC ATGTTCTTCC AAATTCCTTG CAGGAATATC CAACATCCTT	180
GATTTTTCCT CCAAGCTATA GGTCACAAAA CCACCCTTAA ATATACTGA AACTCCAGAA	240
AAATTCGCCA CGGTAGCTTG GAAAAGACCT GCCGTCAAAC TCTCTGCAGC CGCGATGGTT	300
TTCCCTTGCC TTTTCAGTTC TTCTACCACA ATGCTGGCTA AACTAGTTTC TTCCCCATAA	360
CCATAGCAAA AGTCTCGTAA AGAAATTCCT TCGAAAGTCT GGCAGTCCAA GATTTGATTT	420

1187

TCCAAGATAT CCAGCGCTTG ATTCGCCTCT TCTTGACTGC TAGCCTTTGT TGACAGACGT	480
AGAGTGACTT CTCCTGTCTT GGCATAAGGG GCCAAGGTAG GATCGATCTG ATTATCAATT	540
AAATCAGCCA AAATCGTAAC CAACTGGCTC TCGCCAATCC CAAAGAAACG AAGAACTCGG	600
GAATACAGCT TGCTCCCTGT CATCAACTTG GGTAGAAGTT GGTTTAAGAC CATGGGTTTC	660
AATTCACTTG GCGGACCTGG AAGGACGACA TAGGTCAC TC GTCTACTTC TAATTTTCCT	720
CCAACAGCCA GTCCTGTTTC GTTTGGCAGT GGAATCGCTC CTTCTACAAT TTGAGCTTGT	780
CTTTCGTTAT TCGGTGTTTC GGCATAGTCT GGTGCGAGGG TAAAAAAGAT ATCCAACCTC	840
TCCTGAGCCT GAGGATCAAA GACTAATGCT TTCCCTAAAA ATTTAGCTAG GGTGTGTTTG	900
GTTAGGTCGT CCTCAGTTGG CCCCAAACCG CCTGTCAAAA TCACCAGACT GCTACGTTGA	960
CTGGCAATCT CAAGCAAAGA CAAGAGACGA ACTTCATTGT CTCCTACAGC CGTCTGAAAA	1020
TATACATCTA CCCCAATCTC AGCTAGTTTT TCCGACAAAA ACTGGGCATT GGTGTGACA	1080
ATCTGCCCTG TCAAAATCTC TGTTCACA GCAATGATTT CTGCTTTCAT GTTTCCTCCT	1140
ACCTATCTAT TCGTATTTTT TTGAAAAAAT CGCAGGAATT TTCCTACGAT TGATTTTTTT	1200
ATTTGTATCA AAAGTTAATT ATCTTCATCA CCAACAGGTG CTCTGCCAAA TAAATCTTCA	1260
AATAAAACCG CATTGGTTTC AAGCTGAGTA ACTTCTTCTT GTCCCAAAGA ACGTCGGAGT	1320
AGATTTTGCA TTTCACACAT ATGTGCTCTC GAAACAATCT GGTAAGAAAC ACCTTGAAGT	1380
ATCTCTCCTT CACCCTGCAA CTGCTGAGTT TCAATGGTTT TAAATGAATC TTTATAGCCT	1440
AGCAAGTTAG GGATACTTTT TGCAGACAAA TCAATATTGG TCTGCATATT GTCAC TCAA	1500
GCTTTTAGAA TCTCTTGATA ATGACCAATG CTATTTAAAC TGAGAGCTTT TTCCATGACT	1560
TTTTGAATAA CTTACAGTTG ACGTTTTTGA CGACCATAAT CCCCTCAGG ATCTTGGTAA	1620
CGCATTCGTG CATAGACTAG GGCTTCTTCT CCCCCAATAT GTTGCTCCCC AACACCGATA	1680
GAAATAGTAT TAAATCTTTC TTGGTCACTG ATAGAAATTG GGAAACCTAG GATATTATTG	1740
ACTGTAATAC CTCCTACTGC ATCCACTAGT TTTTGCAATC CTCTCATATT GACCATCACA	1800
TAGCGATCAA TATGGATATT CATCATTTTT TGAATGGTTT CTATAGCAAG CTCTGCTCCA	1860
CCATCTGCAT ATGCTGAGTT CAGTTTCGCT TCATGAGCCT GACCATTCCC TGATTCAATG	1920
CGCGTCAGAA TATCCCGCTC TAAACTCATC ATTGTTGTTT TTTTCGTTTT AGGATTCACT	1980
GTCATCAAGA TCATGCTATC ACTTCTACCG ACCCAAGTTT CAGTTCGTTC AACATTTCCG	2040
GTGTCCACTC CCATTAACAG AATGGTTAGA GGTTCAGTCG CTTCAATAAC CTTGGTTTCT	2100
TCACCGATTT TTTTATAGGT TTTAGCTAAG GTTCTGTGCC CTTGTTGATA AATAGTATAA	2160

1188

GCAAAAACAC	CTACTCCTAC	TACAGTTACA	GAAAGTAAAG	CTAGCACCAT	TCCAATAATT	2220
TTTTTAACCA	TATTTCTACT	AACCTATCAG	TTTACCCATC	AAGTAAACAT	CGATAAATTT	2280
CCCTTCTTCT	ATATATGCCC	CACGCTCTTG	GCTACCTTCA	ATGACAAAGC	CATGCTTTTG	2340
ATAAAGATGG	ACTGCTGCTT	GATTACGAGT	TTGGACAGTC	AGTTGGAGAC	GACGCAGAAT	2400
GCCACTTGCT	TGTGCCCAC	CTATCGCTTC	TTCTAGCAAC	AAACTTCCCA	AGCCATTATT	2460
CCAATATCTT	TTTCCAATCA	CAATGAAGAG	ATCTCCAATA	TGACGGACTC	TCTTACGCTG	2520
ATCAGCTGTA	ATATTTACAA	TACCAGCAAT	TTTGCCATTT	AAGAATGCAA	GTAAGGTTAT	2580
CTGATTGTCC	GAAC TAGCTT	GCTTGTGAG	GAATATTTCC	ATCTCCTCAC	TAGTCAAGAG	2640
AATACCATCT	CCGTCTAGGC	TGGTAAAGTC	TGTCTCCAAA	CTCACACGAT	TTAAAAAGGC	2700
CACTAATTCA	GCTGCATCTT	TGGGCTCTGC	TTCCCTAATG	AGCAATTCAT	ACTCCATATT	2760
GAAGCTCCTC	TAACAATTTT	TCAGCACGCA	AACCTTTTGC	CTGAAAATTT	AAACGGCGTC	2820
CATCTGCTTC	TTTTAGAATT	TCCAATTCTA	AATAAGCATC	TGGCAAGGCA	TCTCCTAAGA	2880
GATTTCCCCA	CTCAATAACA	GTCACGCCGC	CACCAAAGAT	AACTCATCC	AAGTCGATAG	2940
AATCAGCATC	TCCTTCAATA	CGATAAACAT	CTAGGTGATA	AAGTGAAGT	CGACCTTCAT	3000
ACTCTCTCAC	GATAGTATAG	GTGGGACTTT	TAATCATTTG	AGAAATCTGT	AATCCTTTTG	3060
CAAGTCCTTT	AGTAAAGGTC	GTTTTACCTG	CACCCAGTTC	TCCAGTTAAG	ATTAAAAACAT	3120
CATTCTTTGC	TAATAGATGG	CCCAAACGCT	CCCCTAAGGC	TTGCAACTCT	TCTTCATTTT	3180
TTGTGTACAT	ACTCTTATTA	TACCAAAAAC	TTTTCTTTTG	TGTCTATTTT	CCTACTAAAC	3240
TTATCATCAT	AACATCCATA	AAAAACAGGC	TTTCTCTAAA	AGAAAATGAG	CGTAACAATG	3300
ACCAATACAA	GATCTCGGAA	AATATGACCA	TAAAAGGAAA	CTTCCTTCTT	AACCGAATTT	3360
GGGACAAGAT	AGGCTGCAAA	AAACAAGCCC	AGTCCAATAT	AAATCAGAAG	TGAGACAATG	3420
GTCATTGGAT	TTCTTAAGAA	AAGAAGTGTT	GCTAAAATAG	TCACCAACAC	TGTCTTTTTT	3480
CTGTCCAGCA	TAGCAAGAAA	ATCGCGCACG	TATTTTTTCA	AGGGTAAAAA	AATCAGCAAA	3540
TCTAGCCCAA	ATAGGAAAAA	GAAGGATGGC	AATAAAAAGT	CAACTAATTC	TTGCTGCAGC	3600
GTATTTTTGA	TGAACAAGTT	ATCTGACAAA	ACAAGAACAG	CTCCTAACAA	ATTAATTAAG	3660
AGTAACATAC	TGTAAAAAAG	CTTCACCGAC	TTCTTACTGG	CTAGGACACT	ATGGACTTCT	3720
TGCTTACGGG	TATAAAGATA	ATTTACTCCA	GCACAGATTC	CTGAAACGAA	AACCATGCTT	3780
CCGATGAAAA	AAGCTGTACT	TTGTTTAAAG	GACAAGATGC	ATTCCTTCCA	TAGGAAACAG	3840
CTACTCAAAC	TGATTTGAAT	TAAAGCTAAC	AAAAATAAGA	TTCTCATTGA	TTTCATCTTC	3900
TCTCTCCCTT	CCTACCAATC	ATTATACTAG	GAGAAAAGAG	AGAACTGTTT	CTAATCTTCT	3960

1189

CAAATGTCTC TTTAAGACGC TAAACAAACA CTAGAGACTA ATACTCAATG AAAATCAAAG 4020
 ATCAAACCTAG GTAGCTAGCC ACAGGTTGCT CAAAACAGTG TTTTGAGATT GCAGATAGAG 4080
 CTGACGTGAT TTGAAGAGAT TTTCTGAAGAA TATAAATTTG AAATCATGAA AATCCGTCAA 4140
 ACGGGTGGTT GTTTTGTCTC GCACCTCACG GAGCGAGACG GACTCAGAGT CACATAATTA 4200
 TAAGGCTGAT AGTATTAATC TAACTATCAG CcTmCAGGTT ATTTAACGTT TCAGAAAAAC 4260
 TATAATGTCA AGATTAACTA AACAGTATCT AGTTCCTTCA AATAATTTTC TATCTTCATC 4320
 AACATTAAAG GATTGTTATA AATCTTACAT AACTCTCTTG CTTCTATATA ATAATTTTTC 4380
 ACTTGTTCTC TGTCTAGAAA TTTGGCTCCA GCATTTCCTA CAAGAATAAG TAGAGGAGCC 4440
 AATTGGTAGC TTGTCTGTCT TTGTTTACAG AGTTCAATCG TTTCAAGAGC TTCTTGGATG 4500
 GCTTCATTAT ATTTTTCCTT TGATACTAGG TAGTGAGCGT AGTTGTAACG AACTCTGATG 4560
 TAGCCAAATA AAAACTCTTG ATGGTCCAAA TTTTGTGTCT GATACAACTC TATTAAATGA 4620
 GAGTAGTTTG CCTCATATTC TTGTTACGA CCCACTAAGG AATAGAAAT AGATAGAGTA 4680
 TTCAACGCCT TTAAATAAAT CAGAGTATTT GAAGAGACTT TTAATAATAT ATTTTCCAAT 4740
 GACGAAATTG CCTCACACTT ACTGTCATAT TGATAGAAGT CAATTATAGA TTTAATCCAT 4800
 TCAAGGTAAG TTCGGTCTTC TAATGTTAGA AAAGTGCTTC GTTCTACTTC TATTTTATAA 4860
 AGATATTCTA AATCGTCATA ATTTCTGTCA TCTAATAGGC GAGCAGATAG ATGTTTGAAA 4920
 TTAGAGAGGT TAGACTTAAC TTCGATTTGT TCATTGAAAA AGTAATCCAA AGGGACTTCA 4980
 AGTCGTTGAG AGAGTTTGAA TAACAAGTCT GCGGAGGGAA TAAAATGACC TCTTCAATT 5040
 TTACTAATCT GGCTTTGTTC ACAAATTCCT TCTGCAAGAG TTTGTTGGGA GAGTCT 5096

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

ACAAGATAAA AATAAAGGAT TACAATGGGG AATATAAAGT AAACCGGTAA ACCTAAAAAG 60
 AAAGGAGAAA AGATGAAAAT TGTACTTGTA GGCATGGAC ATTTTGCTAC AGGGATTTAT 120
 AGTTCTTTAC AATTGATTGC AGGTAATCAA GAAAATGTGG AGGCGATTGA CTTTGTGGAA 180
 GGAATGTCAG CAGATGAACT CAAGCAAAAA ATCTTACTTG CAATTTCAAA TGAAGAAGAA 240

1190						
GTTTTAATCC	TAAGTGATCT	CTTGGGAGGA	TCGCCATTCA	AGGTTTCTTC	TACCATAATG	300
GGAGAAAATC	CAGCCAAGAC	AATGAATGTT	CTCTCGGGTT	TGAACCTAGC	CATGTTAATG	360
GAAGCAGTCT	TTGCTAGAAT	GGCTCATAGC	TTTGATGAGG	TTGTTAATAA	ATCAGTAGTG	420
GCGGCCCAGG	GCGGAGTCGT	AAATGGTAAA	GAATTGTTTT	CAACGGATGC	AGAGGAAGAG	480
GAAGAAGATT	TCGAATCGGG	TATTTAAAGG	GTAAAAGAAT	GATAAAAAAG	GTTACGATTG	540
AAAAAATAAA	ATCGCCTGAG	CGCTTCTTAG	AAGTACCACT	TCTGACGAAA	GAAGAAGTCG	600
GCCAGGCAAT	CGATAAGGTT	ATTTCGGCAGT	TAGAACTCAA	CCTTGACTAT	TTCAAGGAAG	660
ATTTCCCGAC	GCCAGCTACC	TTTGATAATG	TCTATCCAAT	CATGGATAAC	ACGGAATGGA	720
CCAATGGTTT	CTGGACAGGA	GAACGTGGT	TGGCTTATGA	ATACAGTCAA	CAGGATGCAT	780
TTAAAAACAT	CGCTCATAAA	AATGTTCTTT	CTTTCCTGGA	TCGTGTCAAT	AAGAGAGTAG	840
AATTGGATCA	CCATGATCTC	GGCTTCTTGT	ACACACCGTC	TTGTATGGCT	GAATATAAGA	900
TAAATGGAGA	TGGAGAGGCT	AGAGAAGCAA	CCTTGAAAGC	TGCAGATAAG	TTGATTGAAC	960
GCTATCAAGA	AAAAGGTGGT	TTTATTCAAG	CTTGGGGAGA	CTTGGGCAAG	AAAGAGCATT	1020
ACCGTTTGAT	TATCGACTGC	TTGCTCAATA	TCCAACCTCT	ATTCTTTGCT	TATCAAGAAA	1080
CAGGCGATCA	AAAATACTAC	GATATTGCAG	AAAGCCATTT	CTATGCTTCA	GCTAATAATG	1140
TAATCCGTGA	TGACGCTTCG	TCCTTCCACA	CCTTCTATTT	TGATCCTGAG	ACAGGTCAAC	1200
CCTTTAAAGG	TGTAACGAGA	CAAGGGTATA	GTGATGATTC	ATGCTGGGCA	CGTGGTCAAT	1260
cATGGGGAGT	CTATGGTATT	CCTTTGACTT	ATCGTCACTT	AAAAGACGAG	tCCTGCTTTG	1320
ACTTGTTTAA	GGGTGTGACC	AATTATTTCT	TGAATCGTCT	GCCAAAAGAT	CATGTGTCTT	1380
ATTGGGATTT	GATTTTAAAT	GATGGTAGTG	ATCAATCACG	AGATTCTTCA	GCAACAGCTA	1440
TCGCCGTCTG	TGGGATTCAT	GAAATGCTAA	AACATCTCCC	AGAGGTGGAT	GCTGACAAAG	1500
ATATTTATAA	ACATGCTATG	CATGCCATGC	TTCGTTCCCT	GATCGAACAT	TATGCAAATG	1560
ATCAATTTAC	CCCTGGTGGG	ACAAGTCTCC	TCCACGGTGT	GTACTIONG	CATTGAGGTA	1620
AAGGAGTGGA	TGAAGGCAAT	ATCTGGGGTG	ACTACTATTA	CCTAGAAGCC	CTTATCCGTT	1680
TCTACAAAGA	CTGGAACCTA	TATTGGTAGG	AGGAGAAATA	TGACAATGCC	AAATATTATT	1740
ATGACCCGTA	TCGATGAACG	GTTGATTCAT	GGACAAGGAC	AAC'TTGGGT	AAAATACCTA	1800
GGTTGTAATA	CGGTCATTGT	TGCCAATGAC	GAAGTAAGCA	CGGACAAGAT	GCAACAAACT	1860
CTGATGAAAA	CAGTTGTGCC	AGACTCAGTT	GCCATGCGTT	TCTTCCCTTT	GCAAAAAGTG	1920
ATTGATATCA	TTCAACAAGC	TAATCCTGCT	CAAACGATCT	TTATCGTTGT	AAAGGATGTG	1980
AAGGACGCTT	TAACCTTGGT	AGAAGGTGGT	GTCATATCA	AAGAAATCAA	TATTGGGAAC	2040

1191

ATTCACAATG CCCCTGGTAA AGAGCAAGTG ACACGCTCCA TCTTCCTGGG TGAAGAGGAC	2100
AAGGCGGCCC TCAAGGAATT GAGCCAACT CATCAAGTAA CATTTAATAC GAAAACAACT	2160
CCAACAGGAA ATGATGGAGC TGTTCAGTC AACATTATGG ACTATATTTA ACAGAGGAGA	2220
TCGTTATGTC GATTAATGTA TTTCAAGCGA TTTAATTGG ATTATGGACA GCTTCTGTT	2280
TTAGTGAAT GCTGTAGGA ATTTACACCA ATAGATGTAT TGTTCGTCA TTTGGTGTCG	2340
GAATTATTCT AGGTGATCTG TCATGCTCTT GCAATGGGAG CCAATGGTGA ATTGG	2395

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CCTTCTTAG AGGTAAATTT TGCAAAATCG TCGATTGTTA TATAAGGATT ATTATAGAGA	60
CTGTTGCGAA AGAATCTCTG ATATGTTTTT GAATCTTTTG AATACAAAAC TATCTCTCTA	120
ATAGCATGTC CATCTGTTCC ATCAATTGGT AAACATACCG TAACTAGAAA AAGAATTATA	180
TTCAAAATAA AAAATTCTGA TGCGTACGGC ACAAATCCCA AAAGTGCTAA TATTGCGACA	240
ATTAGGTTAG CTCCACCTCC CCCAAGAAG TAGAACACCA AATTCCTATC ACTATTTTTT	300
TCATTAGTAA TGTTTCTATT ACTCATTTGA CAATAACCGA ATGCTAATAA CACTGGAAAT	360
TTGAAATATA TTTTTTTTCT GAAATAGAAG AAAAAGGGAG TAGCAAGCAT CTCTAGTTTA	420
TAAGATAAAC ATCTTCCCAC TAAAAAATGA CCTAGTTCAT GTAATGTAAT TGATATTAAC	480
GAAATTAAAA TCAATCGAAA ATAATAGATT AATGAATCAT TTGGAAAAAT TATCAATAAT	540
AGGAACAATA ACGGAATCAA ACATAAATAT ATGACAGAGT TATTTAATAT TTTCAACATA	600
ATACCATTCC TCTAAACTAT TAGCTTCAAA AAGGCGTTTT TTCTCCCAAT ACATCTTCTC	660
AAAATGTTTCG GAATCATAAT TTTCTAAAAA TAATTTTAtG TCTGGTAAGC TCTTCTTGA	720
TAATCCGTTG TTTTGTACTT AATTTTCCCT TCAAGTACAT CTTCAATTTT ATAAGTTGCC	780
TCCATCAACT GAGCCTCTGC AATATCTTTG AGTGAATTGG TAATGAAAC TTGGTGTAAT	840
ATCTGTCctS CCATATATGA AAATATATCT CTAAGATATT CTGACACATT ATCAGAGCCG	900
TTACTCTCAG CAACATCTAA TGTTACAACA AACTTTCCAG CTAATCGAAA AAGATGGCTC	960
CACCCCCCAA TCCTTTCAAT AAAGTTTTTT GTGTCCACAG ATACGTTTTG TAAATATACA	1020

1192

GGAGAAGAGA TAATTATAAT ATCAGACTCT AATAACTCTT TTTTATAAC ACCTCCATCA	1080
TCAGCATTAC TTGCCTATC AATTCCTTTC TTAAACAACT CTTCTGAATC AGAATTAGAT	1140
ATTTCTAGCT CTGAATTGAA AGGTGTCCTG AAAGATATAT CAACATTATT TCTACTAGAA	1200
ATGATACTTG AAAGTCTCTT AGTATACTCT AAAGTCTTAG AGTTATGATT TCGCACTCCT	1260
GCATATATAA ATATTTTATT CATTTTAATT CATCCTCTCA ATTTGAATTT AGTAGATTTT	1320
TCAAGATAGT ATGGTACAAA AACAGACTTT TGTGACTCA CATTATTACA TATGTTTGT	1380
ATTAAACCAA AATCAATACT ATTTTGGAG TAATTTTGAT TTTAGTTTAA AATCATTTCT	1440
ATAACAGTAG CATATACCTC AAGCCGTTTA GCAATTAGAA TAGAACTTTT CTTTATTATA	1500
TTATTATCTC AACGAAAAGC TACACTATTA AAAATATTTT ATAGAATTAC ATATTAAACT	1560
AGTCAATCTT GGTATTTTTA TATTGCTTAA TGAGTGGACA CCTCTATTTT AGAAACAAAA	1620
CTATAAATTA AGCTAGATTT CAAGTAATGA GGGGATAACT ATCTTTTGT CATTCTGATT	1680
CAGTGCATA TACCTTAAAA AAGTATAAGC AATACCAGTC ACACCTGTAT ACAAAGAAAA	1740
ATCTGGGAAA TTGCTTGTTT GGACGATACG ATACTCTCCT TCTTTTGATT TATTCATTAC	1800
AACACTACAC AATAAAGACT CCAATCCAT ACTAGTATCC ATTTCTTTCA TGTAGTCGAT	1860
GTAAAAATTT ATTATGGCCA TACTTCCATG GCAAAATGTA TCATTATCTA AACTAGCTAC	1920
AATCCCTCT GGAACACTTT GGGGATGATT AACTAATGTC CCAAATCTC CACTACACCA	1980
CTTCAAAGAA TGAATTTTGA TTTTCTCCCT AGGAAGTAGT TGTAATAAATT ATTCTTTATA	2040
TTTTTTAAGT CTTGTCACTT TATAAATATT TTTTAATGTA AAAATTACAC CTGATAGTCC	2100
ATGGCCAAAA CTATATCCAA AATTACTATT ATCTCTCTCG CTTACATCAT TATATAGCGT	2160
ATCACCTAAA CTTAATACTA GCCTTAGAAC ACGTTCCTTC TCTATTCCTC TCCTATAATA	2220
TCTTACCAGT GTATTAAATTA AAGGTAGAAG ACCATTAATA TAGTCAGACT TGTTTGAAAC	2280
ACTTGCAAAA TCAGTCTTTT CAAGCTCAGT TAAACACTC TTTATATAAT TTAAGCATGC	2340
GAGAGTATTT GTATCGTAAT CCTCTATAAT GGATAGAACA ATGAAATATC CTATATCCCC	2400
AGTTAAACCA AATGTGGTCT TAGATAAAGA AACAGATGGC GGAATTGCAG ATAACATTTT	2460
ATTGTACAGT TGAGTATATG ATGATTTATC TTTCAATAAT TTTACATAGT ACATAAACAG	2520
TAATATTTCCA GCTCTACCCC TATACATATC ATTTCCCGTT TGTTCAGAC ACCATTTAGA	2580
ACCTTTAAAA TTAACAGGTA TACTCCAAAT TGGATATTCG TCATAAATAT TATTAATAAC	2640
CAAAGAGTCT GCAATATTTT CTACTTCATT ATGCAGAATA GTAACATAAC TTTCATTTGG	2700
GAGTTTTTTT CTATTAGATA AGTTTAATTT ATATCCTTTT TTTGCTGAT CAAAGCTTGG	2760
AAAATAAATT TCAATGATAT CAAGTTGCTT TTCTAAATTT TCCAAATTAT TATTAGGTAA	2820

1193

ATATTTTCATA AAATAGTCAT ATCCAGAAAA TTGATGTAGG GAAATAAAAT GATTTCCAAA	2880
ATCATCGTAG ATTTTCATTGA TATTTGTATC TGTATAAAAA ATCGGAATAT CTAATAACCT	2940
CATTTGTTCA CATTCGCTTG CTACAATACC TTGATTAGAA AACTTATTGC TCCAGAGATT	3000
TTCCAATGCT TTTTCTCTAT CTAACATTTC TTCATAAAAA TCAGGATGAT ATAAAAAAGA	3060
TAGTACTGAA GCATAGCTAT TTGTGTCTCT AAAAAGTACC CTTGTCTTTA AACCATACAA	3120
GTTTGCTTTT AATAGCATTT TAAATTCTTC TGTTTTATTT AACTCTTCAA ATATCAGATA	3180
AAAATCCCTA AAACCTTTTT TGAAATCTTT TATATACTTA TCAAATTCTA TATCACCATC	3240
CCGAACAGGC AGGTTTTTCC CACCTTCAAA ATCAATT TTC CCAATATCAA ACTTTACCTT	3300
ATCAGTATTT AAATTAATTA AACTTGACC AGGGATCCTC TA	3342

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GAGAAAAGAA TGTTAAAGAA AAATGATATT GTAGAAGTTG AAATTGTTGA TTGACCCAT	60
GAAGGGGCAG GAGTTGCCAA GGTAGATGGT TTGGTCTTTT TTGTAGAGAA TGCTTTACCG	120
AGTGAAAAAA TTCTCATGCG TGTCCTCAAG GTCAATAAAA AGATTGGCTT TGGAAAAGTT	180
GAAAAATACC TTGTCCAGTC ACCACACCGT AATCAAGATC TAGATTTGGC TTACCTGCGT	240
TCAGGAATCG CGGATTTAGG ACACCTTTCT TATCCAGAAC AGCTCAAGTT TAAAACCAAG	300
CAAGTCAAGG ACAGTCTCTA CAAGATTGCT GGAATTGCAG ATGTAGAAGT TGCTGAAACG	360
CTTGGTATGG AACATCCAGT CAAGTATCGC AATAAGGCGC AGGTGCCCCG TCGTCGAGTG	420
AATGGTGTCT TGGAACAGG ATTTTCCCGT AAGAATTCGC ATAACCTCAT GCCCCTTGAA	480
GATTTCTTTA TCCAGGATCC TGTCATTGAC CAAGTCGTAG TAGCTCTTCG AGACCTGCTC	540
CGTCGTTTTG ATTTAAAACC TTATGACGAA AAGGAACAGT CTGGATTGAT TCGGAATCTT	600
GTGGTGCGTC GTGGTCACTA TTCAGGACAA ATCATGGTCG TTTTGGTGAC AACTCGTCCA	660
AAAGTTTTC GTGTTGACCA ATTGATTGAA CAAGTTATCA AGCAGTTCCC AGAGATTGTG	720
TCTGTATGC AAAATATCAA CGACCAGAAT ACCAATGCGA TTTTGGTAA GGAGTGCGC	780
ACTCTTTATG GTCAAGACTA TATTACGGAC CAGATGTTGG GAAATGACTT CCAAATCGCT	840

1194

GGCCCAGCCT	TTTACCAAGT	CAATACTGAA	ATGGCGGAGA	AACTCTATCA	AACAGCCATT	900
GACTTTGCAG	AGTTAAAAAA	AGATGATGTG	ATTATTGATG	CCTATTCTGG	TATTGGAACC	960
ATTGGTTTAT	CAGTCGCCAA	GCATGTCAAA	GAAGTCTACG	GTGTTGAACT	GATTCCAGAA	1020
GCAGTAGAGA	ATAGCCAGAA	GAATGCTTCT	TTGAACAAGA	TTACTAATGC	CCACTATGTC	1080
TGTGACACGG	CTGAAAATGC	CATGAAGAAA	TGGCTCAAGG	AAGGTATTCA	ACCAACCGTT	1140
ATCTTGTTG	ATCCTCCACG	CAAGGGCTTG	ACAGAAAGCT	TTATCAAAGC	AAGCGCCCAA	1200
ACAGGAGCCG	ATCGCATCGC	CTATATCTCC	TGCAATGTCG	CAACCATGGC	GCGTGATATT	1260
AAACTATACC	AAGAGTTGGG	ATATGAATTG	AAGAAAGTCC	AGCCGGTGGA	TCTATTTCTT	1320
CAAAACGCATC	ACGTCGAGAC	GGTAGCACTT	TTGTCCAAAC	TCGATGTCGA	TAAGCACATA	1380
AGTGTGAAA	TTGAGCTGGA	TGAGATGGAT	TTGACAAGTG	CGGAGAGCAA	AGCAACATAT	1440
GCTCAAATCA	AAGAATATGT	TTGGAATAAA	TTTGAATTAA	AAGTTTCGAC	ATTATATATT	1500
GCACAGATAA	AAAAGAAATG	TGGAATAGAA	TTACGAGAAC	ATTACAACAA	GTCTAAAAAG	1560
GATAAACAAA	TTATTCCACA	GTGTACACCT	GAAAAAGAAG	AAGCCATCAT	GGATGCTTTG	1620
AGACACTTCA	AAATGATTTA	ATAGAAAAGA	ATGACAGTAT	ATGACTTTCT	GCATTTATTA	1680
CATTCTACT	TGGTATAGGA	ACAGCTATTA	TTCTTTCTT	GCAAGGTATC	AATTAGAAAA	1740
TAGGCTCAAT	ATAAAGATTG	ATAGGATCAT	TTTTATATTT	AAAGGAGCGT	TGAAATGATT	1800
GATAAAGGCA	ACAAAAAATT	TTAGGATAAA	TTTGCTAAGT	TGTATGCCTC	TTTTATGAAA	1860
AAAGATAAAG	AGGTTTATGA	TAAAGTTTGT	GAATATCTTA	GTCTCATTTT	GAATAAAGAT	1920
ATGGAGGTGC	TTGAACTTGC	TTGTTGGTTT	CGTGTCATAA	CAGTTATAGA	GGCAAATAGT	1980
TATGTAAATA	TAAGGAGTTC	AAGACTTCTA	CCAAAGTTTA	AAACTCAAAA	AATAAATAGT	2040
TGGTGTGCTG	CTTACAATAT	CCATTTTAAT	AATGGATATT	GTAAGCAGCA	CCCCcAtGAA	2100
TTTAAAGATT	CTTTAAAGAG	TCTTATTTTG	TGATGAAAAT	TTAATATGTA	AATCTCAGAC	2160
GATAGAAATT	AAAAACTCTA	TCGTCTTTTT	TATACTCAAA	ATTAGGAGGT	AAAAATGGTA	2220
AGGATAAGAG	GTCCCACTTA	AAACAATTTA	TGGCAAAATA	AGGACGGAAT	AACACAACAA	2280
ATTCTCTAAA	ACAAATCACT	AAATCAATGT	AAGATTGAAT	GAAATCAATA	TTTATGCTAT	2340
AATTAAATAA	ATTTAATGAA	GAAAAAAGA	GGGATATTAT	GGCACTTAAC	TATAAACCAT	2400
TATGGATACA	GTTAGCAAAA	AAAGGACTAA	AGAAAACAGA	TGTAATAGCT	ATGGCAGGAC	2460
TTACAACAAA	TGTTATGGCA	CAAATGGGAA	AGGATAAACC	AATTACATTT	AAGAATTTAG	2520
AAAGAATATG	TAAGGCTTTA	TCTTGCACTC	CTAATGATAT	TATTAGTTTT	GAAGATAATT	2580
TTAGTGACGA	GGAATAGAAA	ATGACTTTAA	GGACAGAAGA	TCAAGTTAGG	GATTATGCAA	2640

1195

GAGAAGTATA GGCTTTAATG AAGTTGAAGA AAACATCAAT CAAGGTACTG GTCAAATAAC	2700
TACTTTTAAT CAATTAGGCT TCAAGGGATA TTCAAATAAG CCAGATGGTT GGTATTTACC	2760
TAAAAATATG AATGATGTAG CAATAATCCT TGAAACAAAA TCAGAAGAAA GAGATATTAG	2820
CAAACAAAT TTTATTGATG AGTTAATGAA AAATATAGAC ATAATTTAAC TAAAAATAAA	2880
AACTAGATCC TTTTGTGAAA AAATTATATT ATTAAATTTG TAACTGTATC TATTGACAAT	2940
GATAATTATT ATCGATACAA TAGACTTGAA ATATGTTTAA GGAGTTTTTA TGAAAaCAAA	3000
TTTTTCTTAA TmGCTATTTT AGCTATGTGT ATAGTTTTTA GCGCTGTTC TTCTAATTC	3060
GTAAAAATG AAGAAAATAC TTCTAAAGAG CATGCGCCTG ATAAAAATAGT TTTAGATCAT	3120
GCTTTCGGTC AACTATATT AGATAAAAAA CCTGAAAGAG TTGCAACTAT TGCTTGGGGA	3180
AATCATGATG TAGCATTAGC TTTAGGAATA GTTCTGTG GATTTTCAAA AGCAAATTAC	3240
GGTGTAAGTG CTGATAAAGG AGTTTACCA TGGACAGAAG AAAAAATCAA AGAACTAAAT	3300
GGTAAAGCTA ACCTATTTGA CGATTTGGAT GGACTTAACT TTGAAGCAAT ATCAAATTCT	3360
AAACCAGATG TTATCTTAGC AGGTTATTCT GGTATAACTA AAGAAGATTA TGACACTCTA	3420
TCAAAAATTG CTCCTGTAGC AGCATACAAA TCTG	3454

(2) INFORMATION FOR SEQ ID NO: 208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3752 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CGGGAGTATA CTTAATATAA TTATAGTCTA AAAATGACTA TCAGAAAAGA GTAAATTTA	60
GATGAATAAG AAAAAATGA TTTTAACAAG TCTAGCCAGC GTCGCTATCT TAGGGGCTGG	120
TTTGTGTACG TCTCAGCCTA CTTTGTGAAG AGCAGAAGAA TCTCCACAAG TTGTGAAAA	180
ATCTTCATTA GAGAAGAAAT ATGAGGAAGC AAAAGCAAAA GCTGATACTG CCAAGAAAGA	240
TTACGAAACG GCTAAAAAGA AAGCAGAAGA CGCTCAGAAA AAGTATGAAG ATGATCAGAA	300
GAGAACTGAG GAGAAAGCTC GAAAAGAAGC AGAAGCATCT CAAAAATTGA ATGATGTGGC	360
GCTTGTGTGTT CAAAATGCAT ATAAAGAGTA CCGAGAAGTT CAAAATCAAC GTAGTAAATA	420
TAAATCTGAC GCTGAATATC AGAAAAAATT AACAGAGGTC GACTCTAAAA TAGAGAAGGC	480
TAGGAAAGAG CAACAGGACT TGCAAAATAA ATTTAATGAA GTAAGAGCAG TTGTAGTTCC	540

1196

TGAACCAAAT	GCGTTGGCTG	AGACTAAGAA	AAAAGCAGAA	GAAGCTAAAG	CAGAAGAAAA	600
AGTAGCTAAG	AGAAAATATG	ATTATGCAAC	TCTAAAGGTA	GCACTAGCCA	AGAAAGAAGT	660
AGAGGCTAAG	GAACCTGAAA	TTGAAAAACT	TCAATATGAA	ATTTCTACTT	TGGAACAAGA	720
AGTTGCTACT	GCTCAACATC	AAGTAGATAA	TTTGAAAAAA	CTTCTTGCTG	GTGCGGATCC	780
TGATGATGGC	ACAGAAGTTA	TAGAAGCTAA	ATTAAAAAAA	GGAGAAGCTG	AGCTAAACGC	840
TAAACAAGCT	GAGTTAGCAA	AAAAACAAAC	AGAACTTGAA	AAACTTCTTG	ACAGCCTTGA	900
TCCTGAAGGT	AAGACTCAGG	ATGAATTAGA	TAAAGAAGCA	GAAGAAGCTG	AGTTGGATAA	960
AAAAGCTGAT	GAACCTCAAA	ATAAAGTTGC	TGATTTAGAA	AAAGAAATTA	GTAACCTTGA	1020
AATATTACTT	GGAGGGGCTG	ATCCTGAAGA	TGATACTGCT	GCTCTTCAAA	ATAAATTAGC	1080
TGCTAAAAAA	GCTGAGTTAG	CAAAAAAACA	AACAGAACTT	GAAAAAATTC	TTGACAGCCT	1140
TGATCCTGAA	GGTAAGACTC	AGGATGAATT	AGATAAAGAA	GCAGAAGAAG	CTGAGTTGGA	1200
TAAAAAAGCT	GATGAACCTC	AAAATAAAGT	TGCTGATTTA	GAAAAAGAAA	TTAGTAACCT	1260
TGAAATATTA	CTTGGAGGGG	CTGATTCTGA	AGATGATACT	GCTGCTCTTC	AAAATAAATT	1320
AGCTACTAAA	AAAGCTGAAT	TGGAAAAAAC	TCAAAAAGAA	TTAGATGCAG	CTCTTAATGA	1380
GTTAGGCCCT	GATGGAGATG	AAGAAGAAAC	TCCAGCGCCG	GCTCCTCAAC	CAGAGCAACC	1440
AGCTCCTGCA	CCAAAACCAG	AGCAACCAGC	TCCAGCTCCA	AAACCAGAGC	AACCAGCTCC	1500
TGCACCAAAA	CCAGAGCAAC	CAGCTCCAGC	TCCAAAACCA	GAGCAACCAG	CTCCAGCTCC	1560
AAAACCAGAG	CAACCAGCTA	AGCCGGAGAA	ACCAGCTGAA	GAGCCTACTC	AACCAGAAAA	1620
ACCAGCCACT	CCAAAAACAG	GCTGGAAACA	AGAAAACGGT	ATGTGGTATT	TCTACAATAC	1680
TGATGGTTCA	ATGGCAATAG	GTTGGCTCCA	AAACAACGGT	TCATGGTACT	ACCTAAACGC	1740
TAACGCGCT	ATGGCAACAG	GTTGGGTGAA	AGATGGAGAT	ACCTGGTACT	ATCTTGAAGC	1800
ATCAGGTGCT	ATGAAAGCAA	GCCAATGGTT	CAAAGTATCA	GATAAATGGT	ACTATGTCAA	1860
CAGCAATGGC	GCTATGGCGA	CAGGCTGGCT	CCAATACAAT	GGCTCATGGT	ACTACCTCAA	1920
CGCTAATGGT	GATATGGCGA	CAGGATGGCT	CCAATACAAC	GGTTCATGGT	ATTACCTCAA	1980
CGCTAATGGT	GATATGGCGA	CAGGATGGGC	TAAAGTCAAC	GGTTCATGGT	ACTACCTAAA	2040
CGCTAACGGT	GCTATGGCTA	CAGGTGGGCG	TAAAGTCAAC	GGTTCATGGT	ACTACCTAAA	2100
CGCTAACGGT	TCAATGGCAA	CAGGTGGGCT	GAAAGATGGA	GATACCTGGT	ACTATCTTGA	2160
AGCATCAGGT	GCTATGAAAG	CAAGCCAATG	GTTCAAAGTA	TCAGATAAAT	GGTACTATGT	2220
CAATGGCTTA	GGTGCCCTTG	CAGTCAACAC	AACTGTAGAT	GGCTATAAAG	TCAATGCCAA	2280
TGGTGAATGG	GTTTAAGCCG	ATTAAATTAA	ATCATGTTAA	GAACATTTGA	CATTTTAATT	2340

1197

TTGAAACAAA GATAAGGTTC GATTGAATAG ATTTATGTTC GTATTCTTTA GGTACCTATC	2400
TTATGATTTC AGGAAATGTC ATTAAAAAAA CGACTCATTT TCTCTAACCT GAAAAATAGA	2460
TTAGAGAAAA TGGGTTGTTT TATCTATTAT AGTTATTTGA ATGAAGmTAA GAAGAAGGTA	2520
TACTCACATC ATTACATAA TCTGTATATT GACTATAAGT TTAAAAAAC AATTTTAAAG	2580
CTCTTCCTTG TCTTCTCTAA CCAAGCGTGT TATAATGAAT ACTGCTCAAG CGACCTTCAA	2640
TCGTGAAGCA CACACGACCT TCAATCGTGA ATAAACGAAT AGATGGGAGA CTTACCATGA	2700
GTGATAACTC TAAAACACGT GTTGTCGTGG GGATGAGTGG TGGTGTGAT TCGTCGGTGA	2760
CGGCTCTTTT GCTCAAGGAG CAGGGCTACG ATGTGATCGG TATCTTCATG AAGAACTGGG	2820
ATGACACAGA TGAAAACGGC GTCTGTACGG CGACCGAAGA TTACAAGGAT GTGGTTGCCG	2880
TGGCAGACCA GATTGGCATT CCCTACTACT CTGTCAATTT TGAAAAAGAG TACTGGGACC	2940
GCGTTTTTGA GTATTTCTTA GCGGAATACC GTGCAGGGCG CACGCCAAAT CCGGACGTTA	3000
TGTGCAACAA GGAAATCAAG TTCAAGGCCT TTTTGGACTA TGCCATAACC TTGGGGGCG	3060
ACTATGTAGC GACTGGGCAT TATGCTCGAG TGGCGCGTGA TGAGGATGGT ACCGTTTACA	3120
TGCTTCGTGG CGTGGACAAT GGCAAGGATC AGACCTATTT CCTCAGCCAA CTTTCGCAAG	3180
AACAACCTCA AAAAACCATG TTCCCACTAG GACATTTTGA AAAGCCTGAA GTACGCAGAC	3240
TAGCAGAAGA AGCAGGCCTT TCGACTGCTA AGAAGAAAGA CTCGACAGGG ATTTGCTTTA	3300
TCGGAGAAAA GAACTTTAAA AACTTTCTCA GCAACTACCT GCCAGCTCAG CCTGGTCGCA	3360
TGATGACTGT GGATGGTCGC GATATGGGCG AGCATGCAGG TCTTATGTAC TATACAATCG	3420
GTCAGCGTGG CGGACTCGGT ATCGGTGGGC AACACGGCGG TGACAATGCC CCTTGGTTCG	3480
TTGTTCGAAA AGATCTAAGC AAGAATATTC TCTATGTAGG ACAAGGATTC TACCATGATT	3540
CGCTCATGTC AACTAGCCTA GAAGCCAGTC AAGTCCACTT TACTCGTGAA ATGCCAGAAG	3600
AGTTTACGCT AGAATGTACG GCTAAATTCC GTTACCGTCA GCCTGACTCT AAGGTGACCG	3660
TTTCATGTCAA AGGAGAAAAG ACAGAGGTCA TCTTTGCGGA ACCACAACGC GCGATTACAC	3720
CAGGACAGGC AGTTGTCTTT TACGATGGCG GG	3752

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TATTTATATT TTTTATCTC TGGCATACTT TGATACCTTT TTAGACTTAA AGTCTTTAAT	60
AGTGCCCTTC CACCTCTTTT TATCTATAAA GATTCTCCTA CATCATAATT CATTTTTTTA	120
TTTAAACCTT TCTGTCCTAG TTTGTCCTTA TCTTCTTCAT ACCATTTTAA GATTGTCACA	180
TAGTGGTTTT GATAGGTCTT ACCACTGCTT TCCATGTATC TGGATAGTTT ATTTATCATT	240
ATATCTGTGT GTGAGTTTAA TTTTCTTTT AGATTTTAT ATTCTTCTTT GCTTAACCTT	300
ACATTTTTGA ATTCTCCATA AAAAATGGGG GTGGACTTTT TATCTATCTC TCCCTCTCTC	360
TCTTTATCTA TCTCTATATC TTTCCATGTA ATTCCAATCT GGAGTACCTC TACTGTCTAT	420
CGGTAATTTA ATTTTGATAT CTGGCAATAC TGTGCTAGAT ATTTGATCTT TATATTCAGT	480
ATTTTTTAAA GCTTGCCTAA TAATTGAAGT TAAATAGAAT GCTACTTCTT TATTCAATTC	540
TTTATTTTTT AATTTTAAAC AATGAATTTT CATATCTAGG CTGCTTTAT ATTTATGATA	600
AAAGACTGCT CCTAAAAATG AAACAGATAT AAAATTTTCA AAAACTCTAT AATTTTTATC	660
ATCTATATCT TCGTAGTAAC CTAAGATACC ATTGTCAATA TTTGTAGCAC TAATTCAGG	720
AGTTTTTCCA TCGAGTAAAT ATCTTTTGG AATAGATGAG CCTGTTGGTA CTTAACTCGA	780
TTTCCCCTTT TTTTCGGTAA TAAATATTTC TTTTATTTT GTTGTCTGAT ATTTTTCCTA	840
CCTGTCCTTT GTAGGATGAG TATTTTCTAG ATTTTCyTGA ATAACTTTTT ACTTGAAGTT	900
TTAGCTTTTG AACTAGTCGT TGTACTTTCT TTTTGTTTAT TATCAGTCCT GATCTTTTTA	960
ATATTGCTGT TATTCTCTAT ATCCATTTT TCATTCATGA TATTCTTTTA CTAATTTTAT	1020
CTTAAATCTT GTGCTGTATT TGCCATTAAA AAAGTACCT CCTTTAGTTA GTTTTTTGGC	1080
CTAACTTTTG AGGGTCAGTT CAAAATTTGC GACTTTTAAA TGAATCCAA TATTCAATTA	1140
TTAAGAGTTA ACATGGTGCT TGCCAATAGG AATCATTAGA GGCGAATTGG AAATAGGGTC	1200
ACGTATAATT TTTGCTTCAA GATTAAAGAT ATCTTTAACT AGTTTATCAT TTAGTATATC	1260
TTCAGGCTTT CCCTCTGCAA CAAGTTTACC TTCTTTAATT GCAAATAGGT AATCAGCGTA	1320
TCTTGCTGTT AGATTTATAT CGTGCAAAAT CATGCAAAAT GTTGTCTTAT ATTTTGGTT	1380
TAGATCAGTC AAGAGGTCTA ATAGTTCTAT TTGATATGAG ATATCCAAGT AAGTAGTTGG	1440
CTCATCTAAA AGTAGGATAC TTGTATCTTG GGCTAGGGCT AGAGCTATCC ATACTCTTTG	1500
CCTTTGACCC CCAGAAAGTT CTTCAACTAG GTTATTTGCT AGATCTTCAA CATTGGCCTT	1560
AACCATTGAT CTGTTTATTA TTTCAAGGTC ATCTTTTCCA AGACTCTTAA AAGGCTTTCT	1620
GTAGGGGAAA CGACCACGGC TTACAAGATC AGCTACTGTT ATTGATTCAG GGATTATTGG	1680
AGATTGAGGT AATATAGCTA TGTGTTTGC TAAATCTTTT TCTTTATAAG AATTAATTGA	1740

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TTTATTATCA	AGCAATACTT	CTCCCTCTAA	TGGCTTTATA	AGTCGAGACA	AGGTTTTAAT	1800
GAGTGTGAT	TTCCCACAAC	CATTTGACCC	AATAATAACT	GATATTTTTT	CTTCAGGTAT	1860
TTTTATATTT	ATATTTTCCA	AGATTATTTT	TTCATCATAA	CCGCAGGTAA	GATTATTTGA	1920
CCACAGACCT	TTCATTATAT	ATTCCTCCTG	TTCATTTTTA	TTAGTAAGTA	TATTAAGTAT	1980
GGTGAACCTA	ACAAGCCAGT	TACAACACCT	ACTGGATATC	TAGCTGGTAA	AATATTTTGA	2040
GAGAATATGT	CTGATAACAA	AACTAGTAAA	ATTCCAACCA	ATCCAGCTAA	TATTGGGCTT	2100
CTTTTCTTGC	CAATATTTAA	GGCTATGGGA	CCAGCTAAAA	AAGATATACA	AGCTATTGGT	2160
CCTGTAAATG	AAGTAGAAAA	AGCAGTTAAA	GATACAGCGC	AAAAAATTAA	AACAAGCCTT	2220
GAAAGCTCGG	GATTTGCTCC	AAGTCCGATT	GCTATTTCTT	CACCAAGTTC	AATAATTTCT	2280
AGTCTTTTAT	TAAAAAATAA	AACTAATATA	GTAGCAATAA	TACTTACTAT	TAGAACAAGA	2340
GGTATGTCAT	CTAACTTTGT	AAAAGATAAA	GAGCCACTGA	GCCATCTCAT	AACTTCTTGT	2400
AATTCATATC	TTGCTACTTT	CAACAATAAA	AATGAGGTGC	CTGCTCTTGT	GACAGCTTGA	2460
AAACCAATAC	CTAATATTAT	CAGTCTTGCT	GCTGAAAAAC	CATCTTTTTT	AGCTAGTAAA	2520
AATAATATTA	AAGATGATGT	TAGTCCACAA	GTTATTGAAA	TAATTCCAGT	AGTTAAACTA	2580
TTTGTTTTTA	ATACCAATAT	GCAAAAGACC	GCTGCAATAG	ATGAAGAAGT	TGTGACACCG	2640
ATTATATCAG	GACTTGCAAG	AGGATTTCTT	AACATAGTTT	GAAAGATAAA	TCCTGCCAAT	2700
CCAAAAGACC	AGCCAGCTAT	AATTCCTGCT	AATAATTTTG	GTAATCTAAT	TTCCATAATC	2760
GAAAAACTAG	CTCCAGGAAC	AGTTTCACTA	TTTAAGACTT	TAATCAAAGT	TGAAAAAGAA	2820
TAACTTTCAT	CTCCGATAAG	TAAAATGAAA	AATGATAGAC	TGATTATTAT	TAATAAAAAT	2880
AGTGAGGAAA	ATAGTGTTAT	TCTATTTTTT	CTTTTTTGAA	TACCTATAAT	TAAATTTTGC	2940
ATTAGTTATT	AACCCCTCTA	TTTTTCATAG	TTACATAAAT	AAGTACTGGA	CCCCGATTA	3000
TTGCAGTAAT	TATCCCTACT	TCAATTTTAC	CTGGTTTACC	TAACATACGG	CCGATTATAT	3060
CACATATAAG	CAAGAGCTCT	GCACCTATAA	AAGATGAAGA	AATGGTCATT	GTGCGTATAT	3120
CTTTGCTTAT	AAATAAGCCA	CAAAAGTGAG	GAACATAAAG	ACCTACGAAG	CCAATAGGTC	3180
CACCAATTGC	AGTAATACTT	GAACATAAAA	GCACACTTGC	AATTATTGCA	AGTGATCTTA	3240
TCCTATTAAC	ATTAACCTCA	AGACCAACAG	CCATTTTCATC	ACCCATAGcT	AAAGCGTTTA	3300
AATCTGATGA	AATAAATATA	GCTATCAAGT	GACCTAAAAT	TATAAAAGGT	AGTAGTGTAG	3360
ATATAGAAGA	TAATGTAGCT	GCTCCAAGGC	TACCTATTTG	CCAAAATCTA	AATTTGTCTA	3420
AGACGTTATT	ATTCGGTAAA	ATTAAAAAAC	TTACAAAAC	GCTTAAAGCC	ATACTAACAC	3480

1200

AAGTTCCTGA TAAGGCAAGT TTTATAGGGG TAAGGCCTGC TTTTCCGTTA CAGCAATCGC	3540
GTATACAAAA ATTGCACTTA CTAAGCCACC AATGATTGCG	3580

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

CCAAATTGCT CCACAATTAT TATGGAGTCG TCGTTTGCCA GATGGGCGTG ATATGTGTGC	60
TCAAGAATGG TTGACAGGCA AGATATTGAC CCCCTATGAT ATGAATCGTA AGCAAATCGT	120
CAATATTTTA ACCCGTCTTC ATCGCTCACG TCCGTTGATG ACACAATTGA GTCGTTTGGG	180
CTATGCCATG GAAACACCTG TAGATTTACT ACAGTCTTGG CAGGAAACGG CTCCAGATGC	240
TTTGCGTAAA AATCATTTTA TCAGTGAAGT GATGGCTGAT TTACGTCAGA CTATTCCAGG	300
ATTTAGAGAG GACCATGCGA CCATTGTCCA TGGAGATGTA CGACATAGTA ATTGGATTGA	360
GACAGATAGT GGCTTGATTT ATTTAGTAGA TTGGGATTCG GTTCGCTTGA CCGATCGCAT	420
GTTTGATGTG GCCCATATGC TCTGCCATTA TATTTCAAGT CATCAGTGGA AGGAATGGTT	480
GACCTACTAC GGTTACAAGT ACAATCAAAC GGTATTAAGT AAATTGTATT GGTATGGTCA	540
ATTGTCTTAT TTGAGTCAGA TTTCCAAGTA TTATATGAAC CAAGATTTAG AAAATGTCAA	600
TCGGGAGATT CATGGTTTGC GTCATTTCCG AGACAAGTAT GGAAAGAGAA GATGAGAGTT	660
AGAAATCGTA AAGGGGCAAC AGAATTACTA GAGGCAAATC CCCAGTATGT GGTCCCTCAAT	720
CCCTTGGAAG CCAAGGCAAA ATGGCGGGAC TTGTTTGCCA ATGATAATCC CATTGATGTG	780
GAAGTTGGAA GTGGAAAGGG TGCCTTTGTT TCAGGTATGG CCAAGCAAAA CCCTGACATC	840
AACTATATCG GGATTGATAT TCAAAAGTCT GTTTTGAGCT ACGCTTTGGA CAAGGTGCTT	900
GAAGTTGGAG TGCCTAACAT CAAGCTCTTG TGGGTAGATG GTTCTGACTT AACTGACTAC	960
TTTGAAGACG GTGAGATTGA TCGCTGTGAT CTGAACTTTT CAGATCCATG GCCGAAAAAA	1020
CGCCATGAAA AGCGTCGTTT GACCTACAAG ACCTTCTTGG ATACCTTCAA ACGTATCTTG	1080
CCTGAAAATG GAGAAATTCA TTTCAAGACG GATAACCGTG GCTTGTTTGA GTACAGTTTA	1140
GTGAGCTTTT CTCAATATGG CATGAAACTC AATGGTGTCT GGTTAGATTT GCATGCCAGT	1200
GATTTTGAAG GCAATGTCAT GACAGAATAC GAGCAAAAAT TCTCAAACAA GGGGCAAGTT	1260
ATCTACCGAG TTGAGGCAGA ATTTTAAGAG ATAACCTAAA ATTAGGCTGT ACAAGTGCTT	1320

1201

TTGCTTTACA TAAGTTGGCA AACGTGCTAT ACTGATAGTA AGAATATGAA AAGTGAGGCG	1380
GGGAAATATC TTCGCCTCTT GCTTATGAGG AGGTGGACGC AATCGCAACA ATCGTAGAAT	1440
TAGTCAGAGA AGTTGTAGAA CCTGTCATAG AAGTCCTTT TGAACTCGTG GATATCGAGT	1500
ATGGAAAGAT TGGCAGTGAC ATGATTCTCA GTATTTTGT AGATAAACCC GAAGAATTAC	1560
CTTGAACGAC ACGGCAGACT TGACAGAAAT TATCAGTCCT GTCCTAGACA CCATCAAGCC	1620
AGATCCCTTC CCAGAACAAAT ATTCCTAGA AATTACCAGT CCAGGTTTGG AACGTCCTTT	1680
GAAAACCAAG GATGCCGTCG CTGGAGCGGT TGGAAAATAC ATCCATGTCG GGCTCTACCA	1740
AGCCATCGAT AAGCAAAAGG TCTTTGAAGG AACCTTGTG GCCTTCGAAG AGGACGAGTT	1800
GACTATGGAA TATATGGACA AGACGCGTAA GAAAACCGTC CAAATTCAT ACAGTTTAGT	1860
ATCAAAAGCA CGTTTAGCAG TTAAATTATA GAAAAGAAA GGATAGCTTT TGAGGATTCA	1920
AAAGTGAAGA AAACATGAGT AAAGAAATGC TAGAGGCC'TT CCGCAT'TTTG GAAGAAGACA	1980
AGGGAATCAA AAAAGAAGAT ATCATCGACG CAGTAGTAGA GTCGCTTCGT TCCGCTTATC	2040
GCAGACGCTA TGGTCAGTCA GACAGCGTAG CTATTGACTT CAACGAAAAA ACAGGTGACT	2100
TTACAGTTTA TACTGTCCGT GAAGTTGTTG ATGAAGTATT TGATAGCCGT TTGGAAATCA	2160
GCTTGAAAGA TGCTCTTGCC ATTAATTTCAG CTTATGAACT TGGAGACAAA ATCAAGTTTG	2220
AAGAAGCACC AGCTGAGTTT GGTGCTGTAG CAGCCCAATC TGCCAAACAA ACCATCATGG	2280
AAAAAATGCG CAAGCAACA CGTGCCATCA CTTACAATAC TTACAAAGAA CATGAGCAAG	2340
AAATCATGTC TGGTACAGTA GAACGCTTTG ACAACCGCTT TATCTATGTC AACCTTGGTA	2400
GCATCGAAGC CCAATTGTCA AAACAAGACC AAATTCCTGG AGAAGTTTTT GCTTCTCATG	2460
ATCGTATCGA AGTTTATGTT TACAAGGTTG AAGACAACCC TCGTGGTGTG AACGTCTTTG	2520
TTAGCCGTAG TCATCCAGAA ATGATCAAAC GTTTAATGGA GCAAGAAATT CCAGAAGTTT	2580
ATGATGGAAC TGTGAAATC ATGAGCGTGG CTCGTGAAGC AGGTGACCGT ACGAAGGTTG	2640
CTGTTCGTAG CCACAATCCA AACGTGGATG CTATCGGTAC AATCGTTGGA CGTGGTGGTG	2700
CTAATATCAA GAAGATTACT AGCAAATTCC ACCCAGCTCG TTACGATGCT AAAAATGACC	2760
GCATGGTACC AATCGAAGAA AATATCGATG TTATCGAGTG GGTAGCAGAT CCAGCTGAAT	2820
TTATCTACAA TGCCATCGCT CCTGCTGAGG TTGACCAAGT TATCTTTGAT GAAAACGACA	2880
GCAAACGTGC CTTGGTGGTT GTTCCAGATA ACAAGCTTTC TCTTGCCATT GGTGTCGTG	2940
GACAAAACGT GCGCTTGGCG GCTCACTTGA CTGGTTACCG TATCGATATC AAGTCTGCTA	3000
GCGAATTGTA AGCCATGGAA GACGCTGCTT CAGTAGAGTT GGAAGTAGAA AACGATACTG	3060

1202

TAGAAGAATA AAAGCTGCTA GAGGAGGGAA AGATGAAAAC AAGAAAAATC CCTTTGCGCA	3120
AGTCTGTTGT GTCTAACGAA GTGATTGATA AGCGTGATTT GCTCCGCATT GTCAAGAACA	3180
AGGAAGGACA AGTCTTTATT GATcCTACGG GCAAGGCCAA TGGCCGCGGC GCTTATATCA	3240
AACTAGACAA TGCAGAAGCC CTAGAGGCGA AAAAGAAGAA GGTCTTTAAC CGCAGCTTTA	3300
GCATGGAAGT GGAAGAAAGC TTTTATGACG AGTTGATCGC TTATGTGGAT CACAAAGTGA	3360
AAAGAAGAGA GTTGGGACTT GAATAAGCAA AAGATAAGTA ATCTCTTGGG GCTTGCTCAG	3420
CGAGCAGGGC GCATCATATC GGGTGAAGAA TTGGTGGTCA AGGCCATTCA AGACGGCAAG	3480
GCCAAGTTGG TCTTTCTAGC TCATGATGCT GGACCCAATC TGACCAAGAA GATTCAAGAT	3540
AAAAGTCATT ATTATCAAGT AGAAATTGTA ACCGTGTTTT CAACACTGGA ATTAAGCATA	3600
GCAGTCGGGA AATCGAGAAA GGTTTTGGCT GTAACAGATG CTGGATTTAC AAAGAAAATG	3660
AGGTCTCTTA TGGAATAGAA GAGGAGGACA TGATTTGTCT AAGAAAAGAT TGTACGAAAT	3720
CGCAAAAGAA CTTGGAAGAG AAAGTAAAGA AGTTGTAGCG CGTGCAAAAG AGTTGGGCTT	3780
GGATGTGAAA AGCCACTCAT CAAGTGTTGA AGAAGCTGTC GCTGCAAAAA TTGCTGCCAG	3840
CTTTAAGCCT GCAGCTGCTC CGAAAGTAGA AGCAAAACCT GCAGCCCCAA AAGTAAGTGC	3900
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GGCAGAGCGA CGCAAGCAAA ATAAGGGCAA TAACCGTGAC CAACAACAAA ACGGAAACCG	4200
TCAGAAAAAC GACGGCCGTA ATGGTGGAAA ACAAGGTCAA AGCAACCGCG ACAATCGTCG	4260
CTTTAATGAC CAAGCTAAGA AGCAGCAAGG TCAGCAAAAA CGTAGAAATG AGCGCCGTCA	4320
GCAAGAGGAT AAACGTTCOA ATCAAGCGGC TCCACGTATT GACTTTAAAG CCCGTGCAGC	4380
AGCCCTAAAA GCAGAGCAAA ATGCAGAGTA CGCTCGTTCA AGTGAGGAAC GCTTCAAGCA	4440
GTATCAGGCT GCTAAAGAAG CCTTGGCTCA AGCTAACAAA CGCAAGGAAC CAGAGGAAAT	4500
CTTTGAAGAA GCGGCTAAGT TAGCTGAACA AGCACAGCAA GTTCAAGCAG TGGTTGAAGT	4560
CGTCCCTGAG AAAAAAGAAC CTGCAGTGGA TACACGTCGT AAAAAACAAG CTCGACCAGA	4620
CAAAAATCGT GACGATTATG ATCATGAAGA AGATGGTCCT AGAAAACAAC AAAAGAATCG	4680
AAGTAGTCAA AATCAAGTGA GAAATCAAAA GAATAGTAAC TGGAATAACA ACAAAAAGAA	4740
CAAAAAGGC AATAACAAGA ACAACCGTAA TCAGACTCCA AAACCTGTTA CGGAGCGTAA	4800
ATTCCATGAA TTGCCAACAG AATTTGAATA TACAGATGGT ATGACCGTTG CGGAAATCGC	4860

1203

AAAACGTATC	AAACGTGAAC	CAGCTGAAAT	TGTTAAGAAA	CTTTTCATGA	TGGGTGTCAT	4920
GGCCACACAA	AACCAATCCT	TGGATGGGGA	AACAATTGAA	CTCCTCATGG	TGGATTACGG	4980
TATCGAAGCC	AAACAAAAGG	TTGAAGTGGA	TAATGCTGAC	ATCGAACGTT	TCTTTGTCGA	5040
AGATGGTTAT	CTCAATGAAG	ATGAATTGGT	TGAGCGTCCA	CCAGTTGTTA	CTATCATGGG	5100
ACACGTTGAC	CACGGTAAAA	CAACCCTTT	GGATACTCTT	CGTAACTCAC	GTGTTGCGAC	5160
AGGTGAAGCA	GGTGGTATTA	CTCAGCATAT	CGGTGCCTAC	CAAATCGTGG	AAAATGGTAA	5220
GAAGATTACC	TTCCCTTGATA	CACCAGGACA	CGCGGCCCTT	ACATCAATGC	GTGCGCGTGG	5280
TGCTTCTGTT	ACCGATATTA	CGATCTTGGT	CGTAGCGGCA	GATGACGGGG	TTATGCCTCA	5340
GACTATTGAA	GCCATCAACC	ACTCAAAAGC	AGCTAACGTT	CCAATCATCG	TAGCTATTAA	5400
CAAGATTGAT	AAACCAGGTG	CTAACCCAGA	ACGCGTTATC	GGTGAATTGG	CAGAGCATGG	5460
TGTGATGTCA	ACTGCTTGGG	GTGGAGATTC	TGAATTTGTT	GAAATTTCCG	CTAAATTCAA	5520
CCAAAATATC	GAAGAATTGT	TGGAAACAGT	CCTTCTTGTG	GCTGAAATCC	AAGAACTCAA	5580
AGCAGACCCA	ACAGTTTCGTG	CGATCGGTAC	GGTTATCGAA	GCGCGCTTGG	ATAAAGGAAA	5640
AGGTGCGGTC	GCAACCCCTC	TTGTACAACA	AGGTACCTTG	AATGTTCAAG	ACCCAATCGT	5700
TGTCGGAAT	ACcTTCGGTC	GTGTCCGTGC	TATGACCAAC	GACCTTGGTC	GTCGTGTAA	5760
AGTTGCTGGA	CCATCAACAC	CAGTCTCTAT	CACAGGTTTG	AACGAAGCAC	CGATGGCGGG	5820
TGACCACTTT	GCCGTTTACG	AGGATGAAAA	ATCTGCGCGT	GCAGCAGGTG	AAGAGCGTGC	5880
CAAACGTGCC	CTCATGAAAC	AACGTCAAGC	TACCCAACGT	GTTAGCCTTG	AAAACCTCTT	5940
TGATACCCTT	AAAGCTGGGG	AACTCAAATC	TGTTAATGTT	ATCATCAAGG	CTGATGTACA	6000
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GACTATCGTC	CACTCAGCGG	TCGGTGCTAT	CAACGAATCA	GACGTGACCC	TTGCCGAAGC	6120
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AGAAGCTGAC	GATGTGGAAG	TCCGTCTTCA	CAGCATTATC	TACAAGGTTA	TCGAAGAGAT	6240
GGAAGAAGCT	ATGAAAGGGA	TGCTTGATCC	AGAATTTGAA	GAAAAAGTTA	TTGGTGAAGC	6300
GGTTATCCGT	GAAACCTTCA	AGGTGTCTAA	AGTGGGAAC	ATCGGTGGAT	TTATGGTTAT	6360
CAACGGTAAG	GTTGCCCGTG	ACTCTAAAGT	CCGTGTTATC	CGTGATGGTG	TCGTTATCTA	6420
TGATGGTGAA	CTCGCAAGCT	TGAAACACTA	TAAAGACGAC	GTGAAAGAAG	TGACAAACGG	6480
TCGTGAAGGT	GGATTGATGA	TCGACGGCTA	CAATGATATT	AAGATGGATG	ATGTGATTGA	6540
GGCGTATGTC	ATGGAAGAAA	TCAAGAGATA	AGATTTTTTG	CTCCTTTCTT	AGGTGGTGAG	6600

1204

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CTGTGATGGG ACTGATAAAT CAGTTCCATC ACTTTCACCA CGGCGAAAGA AGCAGATGAC	6720
TTCAAATGTA ACTTCGTTC AATTTAAACT GAAAAATCAAG AAGTTTAAAA TAGCTAGGTC	6780
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CAGATCGTGT GGGCATGGAA ATCAAGCGTG AAGTCAATGA GATTTTGCAA AAGAAAGTCC	6900
GTGATCCACG TGTCCAAGGT GTGACCATCA TAGATGTTCA GATGCTGGGT GACTTGCTCTG	6960
TTGCCAAGGT TTATTACACC ATTTTGAGTA ACCTTGCTTC GGATAACCAA AAAGCCCCAA	7020
TCGGGCTTGA AAAAGCAACT GGTACCATCA AACGTGAACT TGGTCGCAAT TTGAAATTGT	7080
ACAAAATCCC AGATTTGACC TTCGTCAAAG ACGAGTCCAT CGAGTATGGA AACAAGATTG	7140
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GGAGGAAAAAT AGGTTGAATT TGAAATGGAA AAATATCTT TTATAATAGA TTGAAACTAG	7260
AATAGTACGC CTCTACTTCT AAAATATTGT TAGAAATCGA TTTGACTGTC CTGATCGATT	7320
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AATTAGAAAA TGCTTTTTTT GTAGGAAATA TAATATGATA AGGTGCAAAA AAGAAATAAG	7440
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TCCAAAAGAT ATTCCTACCT TATTGGAACA AGGTCCAACG ACTCTTCTAT CTCAAGAAAT	7620
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TGCAACTATG AAACCAATGG GGGAAAGCTT GCAGAAAGAA TTATCCAAGC TAGTCAACTA	8160
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CCGTGCAAGG TGTAAGAGTG ATGAAAACGA TAAAGAAAGC TGACCATGTC GTTGTGGGTC	8340
TGGGGAAACT TTTTATTGCC GACAAGTTAA TGGATACGGC TCGGTGGCTC ATTAAGCCAG	8400

1205

AGGAGAGAGA ATGAAATTTT TTTGGTCTTC TTGCTATTCT TTTTATCAAA CCGATTATTG	8460
GGATTGTGAA ATTCTTTTGG ATGATCATCT CTTTTCAGT CCAATTGCTG TTTTACAAGA	8520
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TCAAGATCGC TTTGATGCGA CCTTTACGGG CGTGTCAGCC ATCGAGATTT CCCTTATGGA	9240
GCACGAGCTG ATGAACTCGG ATTCGGGCGT CACTTTTGAA GATGTTATGG AACTCTGTGA	9300
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AGAGGAGCCT GTACAGCTAG ATACGGCAGA AGGTCAAGTT CAACAAGTCA TAGATACGCC	9960
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TAGTCAACAG GCTTTTGGTA ATGGCTATCT TTCAGTCGAG CAGGCCAATC TCATCTCAA	10080
TCATCTCCCT ATGGAGATTA CCTTTGTCAA TAAAGAAGAT ATTTTCCAGT ATTACAATGA	10140

1206

CAATACGCCA GCTGATGAGA TGATTTTCAA ACGGACGCCG TCCCAAGTCG GGCGCAATGT	10200
CGAACTCTGC CATCCGCCTA AGTACTTGGA CAAGGTCAAA ACTATCATGA AGGGGCTTCG	10260
TGAGGGAAGC AAAGACAAGT ATGAAATGTG GTTCAAGTCT GAGTCGCGAG GTAAGTTTGT	10320
CCACATCACC TATGCTGCAG TACACGATGA AGACGGAGAA TTCCAAGGAG TGTTGGAGTA	10380
TGTTCAAGAT ATCCAGCCCT ACCGTGAGAT TGATACGGAC TATTTTCGTG GATTAGAATA	10440
AGGAGAAAAA ATGAGTTACG AACAAGAATT TATGAAGGAA TTTGAAGCTT GGTCAATAC	10500
CCAAATCATG ATTAACGACA TGGCGCACAA GGAAAGCCAA AAAGTTTACG AAGAAGACCA	10560
GGACGAGCGT GCCAAAGATG CCATGATTCG CTACGAGAGT CGCTTGGATG CTTATCAGTT	10620
CTTGCTTGGT AAGTTTGAAA ACTTCAAAGT AGGCAAGGGA TTCCATGATT TGCCAGAAGG	10680
CTTGTTTGGT GAGCGAAATT ATTAAACGAG AAAGATTCTT GATTTTTCAC TAAAATCTTG	10740
ATAGAATGTT TATGTTAAAT CCTTGTCAGA GCAGGGATTT TTTATTGAAA GGATTTTATC	10800
ATGTCAAAGA AACTCAATCG TAAAAACAA TTACGAAATG GCCTCCGTCG CGCAGGTGCC	10860
TTTTCAAGTA CGGTGACTAA GGTGTAGAT GAGACAAAAA AAGTCGTGAA GCGTGCAGAA	10920
CAGTCAGCAA GCGCAGCTGG TAAGGCTGTT TCTAAAAAAG TTGAACAAGC AGTAGAAGCT	10980
ACCAAGAGC AAGCTCAAAA AGTAGCTAAT TCTGTAGAAG ATTTTGCAGC AAATTTGGGT	11040
GGACTTCCAC TTGATCGTGC CAAGACTTTC TATGATGAAG GAATCAAGTC TGCTTCAGAT	11100
TTCAAAAAC TGGACTGAAAA AGAACTCCTT GCCTTGAAAG GAATCGGCC AGCTACCATC	11160
AAGAAATGA AAGAAATGG CATCAAGTTC AAGTAATTTT TCTTGAGCCT TGCATTTCCG	11220
AAAAATCTT GCTACAATAG AGCCATTAGA GGTGTTTTGA ATCCCACATT TTACAGAAAG	11280
TGGCGGCGCT GAGAAGTCCA CAAATGTGTC AAAACTGGTT GCTAATGGAT GAAAAATTGA	11340
AATAAAAGTG TCTTTTGCT TTAAAGACGA GAGTTGCG	11378

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CCGCGAGCCA CGGCGAATTT GCTGCGGGTA TTCATCAGTC AGGATCTATG ATCTTTGGTG	60
AACAAGAAAA GGTTCAGTT GTGACCTTTA TGCCAAATGA AGGTCCTGAT GATCTATACG	120
CTAAGTTTAA TAACGCTGTT GCTGCATTTG ACGCAGAAGA TGAGGTTCTA GTTTTGGCTG	180

1207

ACCTTTGGAG TGTTTCTCCA TTAAACCAAG CTAGTCGCGT GATGGGAGAA AATCCTGAGC	240
GTAAGTTTGC CATCATCACA GGACTTAACT TACCGATGTT GATTCAAGCC TACACAGAGC	300
GCCTCATGGA CGCTGCTGCA GGTGTAGAAA AAGTCGCTGC TAATATCATT AAAGAAGCCA	360
AAGATGGCAT CAAAGCTCTT CCAGAAGAGC TAAATCCAGT CGAAGAAGTT GCAAGCGCTG	420
CAGCTGCTCC AGTTGCCCAA ACTGCTATCC CAGAAGGAAC TGTTATCGGA GACGGTAAAT	480
TGAAAATCAA TCTTGCCCGT CTTGACACAC GTCTACTTCA CGGTCAGGTT GCAACTGCTT	540
GGACTCCAGA TTCAAAAGCA AATCGTATCA TCGTTGCTTC AGATAACGTG GCTAAAGACG	600
ACCTTCGTAA AGAATTGATT AAACAAGCAG CTCCAGGTAA TGTCAAGGCT AACGTGGTTC	660
CAATTCAAAA ACTGATTGAG ATTTCAAAAAG ACCCACGTTT TGGAGAAACA CATGCCCTTA	720
TCTTGTTTGA AACACCTCAA GATGCCCTTC GTGCCATCGA AGGCGGCGTG CCAATCAAGA	780
CTCTTAATGT TGGTTCTATG GCTCACTCAA CAGGTAAAAC ATTGGTCAAT ACCGTTTTGT	840
CTATGGACAA AGAAGACGTT GCTACATTTG AAAAAATGCG TGAATTGGGT GTTGAATTTG	900
ATGTCCGTAA AGTACCAAAT GATTCTAAAA AAGATTGTGT TGAATTGATT AACAAAGCCA	960
ATGTCAAATA AGCCATTATT TATGAAAGGA TTTTAAACAT GTCTATTATT TCTATGGTTT	1020
TAGTAGTCGT TGTAGCCTTC TTTGCAGGTC TTGAAGGCAT CCTCGACCAG TTCCAATTTT	1080
ACCAACCACT TGTAGCCTGT ACCCTTATTG GGCTTGTAAC AGGTCACCTG GAAGCAGGGA	1140
TTATCCTCGG TGGATCGCTT CAAATGATTG CCCTTGGTTG GTCAAATATC GGTGCTGCTA	1200
TCGCTCCTGA TGCTGCACTT GCTTCTGTCT GTGCTGCCAT TATCATGGTT CTTGGTGGTG	1260
ACTTTACCAA GACTGGTATC GGTGTTGCCC AAGCGGTTGC TATCCCTCTT GCTGTAGCTG	1320
GACTTTTCTT GACAATGATT GTTCGTACAA TTTCAGTTGG TTTGGTTCAT ACTGCAGATG	1380
CTGCCGCTAA AAAAGGTGAC TTCGGCGCTG TGGAGCGTGC GCATTTTCATC GCGCTACTTT	1440
TCCAAGGACT TCGTATCGCG CTTCTGTCAG CTCTTCTCCT TATGGTACCA ACTGAAACTG	1500
TACAAAGTAT CCTTAGTGCC ATGCCAGACT GGCTCAAAGA TGGTATGGCT ATCGGTGGTG	1560
GTATGGTCGT TGCCGTGGT TACGCCATGG TTATCAACAT GATGGCAACT CGTGAAGTAT	1620
GGCCATTCTT CGCTCTTGGT TTCGTTCTCG CTGCTGTGTC AGATATTACT CTAATCGGAT	1680
TCGGTGCTAT CGGCGTTGCT ATCGCTCTTA TCTACCTTCA CCTTTCTAAA ACTGGTGGA	1740
ATGGTGGCGG AGGAGCCGCA ACTTCTAACG ACCCAATCGG CGATATCCTA GAAGACTACT	1800
AAGATAAGAA AGGACTGAAA ACATCATGAC TGAAAAACTT CAATTAACTA AATCAGATCG	1860
TAAAAAAGTT TGGTGGCGTT CAACCTTCTT ACAAGGTCT TGGAACCTTG AACGGATGCA	1920

1208

AAACTTGGGC TGGGCTTATA CACTCATTCC AGCTATCAAA AAACCTCTATA CTAAAAAAGA	1980
AGATCAAATC GCTGCTCTTG AGCGTCACCT TGAGTTCTTC AACACTCATC CATACTAGC	2040
TGCTCCAGTC ATGGGGGTTA CTCTGCGCT TGAAGAAGAA CGTGCTAACG GTGTGGAAAT	2100
CGATGACGCT GCTATCCAAG GGGTTAAAAT CGGTATGATG GGACCTCTTG CTGGTATCGG	2160
TGACCCAGTA TTCTGGTTTA CAGTACGCCC AATCCTTGGA TCTCTCGGTG CTTCACTTGC	2220
CCTTACTGGC AATATCTTGG GGCCACTCCT CTTCTTTGTT GCATGGAAC TGAATCGTAT	2280
GTCATTCTTG TGGTATGTTT AAGAGATTGG ATACAAGGCT GGATCAGAAA TCACTAAAGA	2340
TATGTCTGGT GGTATCCTTC AAGATATCAC TAAAGGAGCT TCTATCCTTG GGATGTTTAT	2400
TCTTGCTGTC CTTGTTCAAC GCTGGGTAAA TATTAAATTT GCTTTCGATG TTTCTAAAGT	2460
TCAACTAGAT GAAAAGGCTT ATATCCATTG GGATAAATG CCAGAAGGGT CTAAAGGTAT	2520
CCAAGAAGCA TTCGCACAAG TAGGACAAGG ATTGTCTCAA ACTCCTGAAA AAGTTACTAC	2580
TTTCCAACAA AACTTGGATA TGTGATTCC TGGATTATCA GGACTACTCC TTACTTTACT	2640
TTGCATGTAC TTACTTAAGA AAAAAGTATC TCCAATCACT ATTATCCTTG CCCTCTTCGC	2700
AGTGGGTATT GTGGCACATG TTCTTCACAT CATGTAATCA AGCAACTAAA AAGGAACCAG	2760
GTTCTAAAAT CTGATTCCTT TTTTCTATGC TTTTATTGAG CCAAGGCTCC CATTGGATCC	2820
CATGGTGCAA GTACGATTGG TTCTGCTCCA TAGGCAGCTT GTTCTTCTGC TGTCAGCAAT	2880
TCCTTACGAA CAACGATTTG GTATGTGTAT TCGTCCATCC AAGCGTCTGA GGCAACAAAG	2940
TAACCATCTG TACCGACCTT GTCTCCCCAT GAGTTTCAA CCTTCCACTT GGTGATTATA	3000
CCATTTTCGT CCAAGTCAAC ACCTGTCAAG ACCATGGCGT GGGTCATCAA GCTTTCATA	3060
TAGTCCAAAC GTCCAGCCTT GTCTTGAGTA AGTTTAATGT CCATGCTTGA TTCAAAGTCA	3120
TAAACATCTG TCGCAAGGAT GCCAGCTTAC GGTGCTGAG CTGGCCGACA TCAGAACCAA	3180
ACCAAACAGT CTCACCTGCT TGCATTTGGG CAATCGCCAA TTCTTTCAAG CGCTCCATTG	3240
GAACGTTGAT GTAGCGAACT GCACGGCTAC CAACCACATT CCCCACATC TCAACTGTGT	3300
AAGATTTTCC GTAAGGTTTA TCAGCAGTTG GAGCATGAT AACAGAAACG TAGTCTTCTA	3360
AAGGAAGATT GACATATTTC TTGTAAAAT CTTGTGGTGT GATTCCTTTT TCACTTTTGT	3420
AGTTGTTATC TTATCGCGA TAAGCAAAAGT CAAACTTGCG TGGTGGAAGT CCTAATGACA	3480
TAGCAAGAAA GTTAAAGATT TCTTGCAAGA GGTCTTCTTT CTTAGCTTGA ACAGTCGCTT	3540
GATCTGCACC AGAAACAAGC AAGTCACGCA AGATTTGAGC ATCTTGACGA AGCAATTTAT	3600
TAAGGATCGC ATTTAGCTCA CGACTGCTGC TAGATGAAAC AGACTCAGGA TAACTGACT	3660
TAGGCACGAC ACCGTATTTT TCAAAGAGGG AAACGACCAT ATCCCATGA CCGCCATCTT	3720

1209

GTTGAGGTGT TTGGAGTAAG AAGCTAACTT GCGGCTAGTC AATTCTTGGT CTGAAGTCGC	3780
AATGACTTGC TCCAAGAACC AGTTTGATTT CTCATACTTA TCCCAGAAGA AAGTGTGGGC	3840
TTGTGACAAC TCAAAGTTCT CCAATTTGTA TTGCGAGATG AGTTTGTGGC GGAAGGTGTT	3900
GAGAGCCGCA AACATCCAGC AACGACCAGA CGCTTTCTGG TTAGTGACCT TGTCTTGGT	3960
TAAATCCAAT GAGAAAACAG GTGTGTTGTC TACATGGCTT TGGCGACGTT CCAGAGCTGC	4020
AAAAATTCCG TTGTGGCTGG CAGCATTTTC AATCGCTTGG TATTTTACAT TTGCTTCATA	4080
GTTGGCAAAT AGTTTATCAG TAAATGATTC TTGAATCGCG TTCATAGATT CCTCCTTTTA	4140
GTCTACAGTG TATTGG	4156

(2) INFORMATION FOR SEQ ID NO: 212:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3902 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

AAAAACAACA AAATAAAACA AAAACAAAAA TATCGAGGTT TATTTTCAAA ACTTTCGATA	60
TTTTTATTAA GTTATTATTT TGTGTTTCT AGTTTACTTT TTGATGGTTA AGAGTGGTGG	120
AGAATTATAC TCAATGAAAA TCAAAGAGCA AACTAGGAAG CTAGCCGCAG GCTGTACTTG	180
AGTACGGCAA GCGGAAGCTG ACGTGGTTTG AATTTGATTT TCGAAGAGTA TTAGTGCAAA	240
CCGTAGTTGT AGTCATCATC TTGCATGGCT TCAACTTCGC CAAGAAGGTA ACCATTTCCG	300
ACTTGAGAGA AGAAGTCATG GTTGAAGTT CCTGTTGAAA TACCGTTCAT AACGATTGGG	360
TTGACATCTT CAGCTGAATC TGGGAAAAGT GGATCTTGTC CCATGTTTCAT GAGAGCTTTA	420
TTGGCATTTGT AGCGAAGGAA GGTTTTAACC TCTTCAGTCC AACCAACACC GTCATAAAGA	480
CTCTCTGTGT AGCCTTCTTC ATTTTCATAA AGAGTATAGA GTAGGTCGTA CATCCATTCT	540
TTGAGTTTTT CTGCTCTTC TTCAGGTAAT TCATTGAAAC CAAGTTGGAA TTTGTAACCA	600
ATGTAGGTTC CGTGAACAGA CTCGTCACGA ATAATCAATT TAATGATTTC TGCAACGTTG	660
GCAAGTTTGT TGTTACCGAG ATAGTAGAGG GGAGTGAAGA AACCAGAGTA GAAGAGGAAG	720
GTTTCGAGGA AGACGCTGGC AACTTCTTTT TCAAGTGGGC TGCCGTTTAG GTAGATTTCC	780
TTGACAATCT CAGCCTTCTT TTGTAGGTAA GGATTGGTAT TGGTCCATTC GAAAATTCT	840
TCAATCTCAG CCTTAGTATT CAAGGTAGAA AAGATTGATG AGTAAGATT AGCGTGGACA	900

1210

GATTCCATAA ATTGGATGTT ATTGAAGACA GCTTCCTCAT GTGGTGTACG GATGTCTGCG	960
CGAAGGGCTT GAACCCCACT TTCAGATTGC ATAGTGTCAA GAAGGGTTAA ACCACCAAAA	1020
ACTTTTCCGA CCAAGTCTTT CTCTTTGTTA GATAGCTTTC TCCAGTCATC CAAGTCGTTT	1080
GATAAGGGAA TACGTGTATC GAGCCAAAAT TGCTCCGTCA GTTTTTCCTCA AGTTGATTTG	1140
TCGATGACAT CTTGATGGC ATTCCAGTTA ATGGCTTTGT AGTAAGTTTC CATTTAAAAT	1200
CTCTTTCTGT GTTTAGTATT GCGAACTCAC AATTATTTCT ACTTTACCAT AATTCTATAG	1260
GAGTATCGCA CAAAAAGTCG GAAGCCCGAC TTTTAAAATG TTACATAAAT TATGTTATGA	1320
CATAGTAGAT TTGATTTTAT CAGTGCTGCT TAGGGAAAAA TAGTGTTTCT ATGCTAGAAA	1380
CTAAATCACA CAGCTTTCAC ATTGGTTGGC GCCGACTTCT CCACCGTCAT CTGTAAAGGT	1440
ACGGACGTAG TAGATAGACT TGATTCCCTT GTTAAAGGCA TAGTTACGAA GGATGGACAA	1500
GTCACGTGTC GTTTGTTTAT TTTCCCTCTT CCATTCGTAA AGGCCTTTTG GAATGTCACT	1560
GCGCATGAAG AGGGTGAGTG AAAGTCCTTG ATCCACGTGT TCAGTCGCAG CAGCGTAAAC	1620
ATCGATGACT TTACGCATAT CCATATCGTA GGCAGAAGTG TAGTAAGGAA TGGTTTCTGT	1680
AGACAAGCCA GCAGCAGGGT AATAGATTTT ACCAATTTTC TTCTCTTGGC GTTCTTCGAT	1740
ACGTGTCGTA ATCGGGTGGA TAGAAGCAGA AACGTCGTTG ATATAGCTGA TAGAACCATT	1800
TGGCGCTACA GCAAGGCGAT TTTGGTGGTA AAGACCATCT TCTTGAACCT TGTCGCGAAG	1860
TTCAGCCCAA TCAGCAACAC CAGGGATAAA GACATTTTTC AAGAGTTCTT TAACACGGTC	1920
TGATGTTGGA ACAAATTCAC CAGTTACATA CTTGTCAAAG TAACTTCCGT TAGCATAGTC	1980
TGATTTTTC AAGTTGTGGA AGGTAATACC ACGTTCACGT GCAATATTGT TTGACTCTAC	2040
CAAGGTCCAG TAGTTCATAA GCATAAAGTA GATGCTTGTA AATTCAACAG ACTCAGGTGA	2100
ACCATATTCA ATGAGTTGTT GGGCAAGGTA GCTGTGCAGT CCCATGGCAC CGAGACCAA	2160
GGTGTGGGCT TGGCTATTTC CATGGTCAAT CGTTGGTACA GCTACGATAT GTGAACATC	2220
TGTAACGAAA GTAAGGCAC GAACCATAGC ACGGATAGAA CGACCAAAAT CAGGTGAAGT	2280
CATCATGTTA ACCACGTTGG TTGAACCCAG GTTACATGAA ACATCTGTTC CCATTTGAAG	2340
GAATTCTTGA GCATCGTTGA TCAAGCTTGG TTCTTGAAC TGAAGAATCT CAGAACACAA	2400
GTTACTCATG ATAATCTTTC CATCAACAGG ATTTGCACGG TTAGCCGTAT CGATGTTGAC	2460
TACATAAGGA TAGCCAGACT CTTGTTGCAA TTITAGAGATT TCAGTTTCCA AATCCCGCGC	2520
CTTGATTTTT GTCTTGCGAA TATTTGGATT TGCGACCAAT TCATCGTATT TTTCAGTAAT	2580
GTCGATGTAA TTGAATGGCA CACCGTATTC TTTTCTTACA GAGTAAGGGC TGAAGAGGTA	2640
CATTTCTTCA TTTTACGAG CCAATTCGTA GAATTTATCA GGTACTACAA CACCAAGTGA	2700

1211

TAGAGTCTTG ACACGTACTT TTTCATCAGC GTTTTCTTTC TTAGTTGAAA GGAAAGCGAT	2760
GATATCTGGG TGAAAGACGT TGAGGTAGAC AACACCAGCA CCTTGACGTT GCCCCAATTG	2820
GTGGAGTAA GAGAAGCTGT CTTCAAAAAG CTTCATAACA GGAACGACAC CTGAAGCAGC	2880
TCCTTCATAG CCTTTGATAG GTGCACCAGC TTCACGAAGG TTGCTGAGGG TAATTCCCAC	2940
ACCACCACCA ATACGTGAAA GTTGAAGAGC TGAGTTGATA GAACGCCCGA TAGAGTTCAT	3000
ATCATCCGTC ACTTGGATTA GGAAACAAGA TACCAACTCC CCACGACGAG CACGTCCAGC	3060
ATTCAAGAAG GAAGGAGTAG CAGGTTGGTA GCGTTGGTGG ATGATTTTCAT TGGCAATATC	3120
GATTGCAACA GCTTCATTCC CATCAGCGAA ATAAAGGGCA TTGAAGAAGA CACGGTCTTC	3180
CATATTTTCA AGATAGTATT CACCGTCATT AGTCTTTAAG GCATATTGAT TGTAAAATTT	3240
ATAAGCTGCC ATGAATGACT TGAATTGGAA GTTTTGGTCT TTGATAAATT GAGCTAATTC	3300
TTCCAAGAAC TCTGGACGGT ATTTCTTGAT AAAGGCTGTT TCGATGTAGT TGTGTTCAAT	3360
GAGGTAATTG ATTTTGCTTT TGATTGAATC AAAAACCATA GTGTTTGGAA CTACATTTTC	3420
TTTAAAGAAA GCATCCAAGG CTTCTTGTC TTTATGAAGC ATGATTTGTC CATTAACAGG	3480
ACGGTTAATT TCGTTATTAA GACGGAAGTA AGTCACGTCT TCAAGATGTT TTAATCCCAT	3540
AAAATTTCCC TTATCTAATT ACAAAGAAA GGCTTCTAAG TTAGCCCTAA AAGCAGTTTC	3600
TTCTGGATGA TGTAATAAGA TTATGCTAAT TGTTTCAGTT TTCCTGGTTG GAAACCTGAA	3660
AAGACTTCAG TTGGTGTTTG GATAACAGGA GCTGCGCTAA AACCGAGCTC TTAACTTGA	3720
TCGACGTACT CAGGTGCTC ATCAAGATTG ATTTACGAT AAGAGACATT ATTACTGTCC	3780
AAGAAACGCT TGGTCATTTT ACATTGGACA CAATTGTTTT TAGAATAAAC GGTACCATT	3840
GTGTAACCTC TCTTCAAAAT TTAATACTAT CTTAGTATAT CAGAAAATAA AATTTTGTCTG	3900
GG	3902

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TATTGAAGCT ATTGTAGACT ACAAAGATAA GGATTTGCAG TTAGTAGGCG GTGAGACTCA	60
CTGATAACCT AAAAAGGATA GTCAATTATG CTGTTTACT AACTATTAAC TATGCTAAAT	120

1212

CAATTGAGGT TGTTCACATA AAATCTATA TCAGAGAAGC CTGATATAGA GTTTTTCCTT	180
GCTAGTTTTA GGATTTTTTT GTAAAATAGA AAAAGTGAAG AGAGGTATGA AATGAGCAAG	240
AAAGATAAAA AAATCGAAAT TCAAGTAGCG GATGCCAAAG TTAATGTTGG TAAAGACAGT	300
TTTGAAGGTT ATACATTGAC TATCGGTAAA AAAGTTATCG GAGAAATTGC CGAATTAGAC	360
GGACAATTG CCATTATAAA GAATGGGAAT GTCGATAGTT TTTATAAAAA ATTGGAAAAA	420
GCTGTGGAAA TTTTGATTGA AAATTATAAT TTAGCAAAAT AAGTCTTGTT TTTTGAAAT	480
TTTCATGATA TAATAGTCCA TGTGATTGT AGGAGAGATA GCGAAGAGGC TAAACGCGGC	540
GGACTGTAAA TCCGCCCTT CGGGTTCGGG GGTTCGAATC CCTCTCTCTC CATTTTCATTA	600
ATGGGGTATA GCCAAGCGGT AAGGCAAGGG ACTTTGACTC CCTCATGCGT TGGTTCGAAT	660
CCAGCTACCC CAGTCTTAG GTAATAATCA AGATAGAAAG CAAAATATCT TAGGGTATTT	720
TATTTTATA ATTGAAAGAC GTGAATGATA TGAACATGTC CTGCGGGTG CTTAGGAAAA	780
AAATTATAAG TATGTCAAGT TTAAGAAAAA CTTGATTGTT GGAGGATTTT TTAGATGAAC	840
GAATTTGAAG ATTTGCTAAA TAGCGTTAGT CAAGTTGAGA CTGGTGATGT TGTTAGTGCT	900
GAAGTATTGA CAGTTGATGC GACTCAAGCT AACGTTGCAA TCTCTGGAAC TGGTGTGAA	960
GGTGTCTTGA CTCTTCGCGA ATTGACAAAC GATCGTGATG CAGATATCAA TGACTTTGTT	1020
AAAGTAGGAG AAGTATTGGA TGTTCCTGTA CTTCTGCAAG TAGTTGGTAA AGATACTGAT	1080
ACAGTTACAT ACCTTGTATC TAAAAACGC CTTGAAGCTC GCAAAGCATG GGACAACTT	1140
GTTGGTCGCG AAGAAGAAGT TGTTACTGTT AAAGGAACGC GTCCCGTTAA AGGTGGACTT	1200
TCAGTAGAAT TTGAAGGTGT TCGTGGATTT ATCCCAGCTT CAATGTTGGA TACTCGTTTC	1260
GTACGTAACG CTGAGCGTTT TGTAAGTCAA GAATTTGATA CTAAAATCAA AGAAGTTAAC	1320
GCTAAAGAAA ACCGCTTCAT CCTTTCACGT CGTGAAGTTG TTGAAGCAGC TACTGCAGCA	1380
GCTCGCGCTG AAGTATTCGG TAAATTGGCT GTTGGTGATG TTGTAAGTGG TAAAGTTGCT	1440
CGTATCACAA GCTTCGCGC TTTCGTCGAC CTGGTGGTG TTGACGGATT GGTTCACTTG	1500
ACTGAATTGT CACATGAACG TAATGTATCA CCAAATCAG TTGTAAGTGT TGGTGAAGAA	1560
ATTGAAGTGA AAATCCTTGA TCTTAACGAA GAAGAAGGAC GTGTATCACT TTCACTTAAA	1620
GCAACAGTAC CAGGACCATG GGATGGCGTT GAGCAAAAAT TGGCTAAAGG TGATGTAGTA	1680
GAAGGAACAG TTAAACGTTT GACTGACTTC GGTGCATTG TTGAAGTATT GCCAGGTATC	1740
GATGGACTTG TTCACGTATC ACAAATTTCA CACAAACGGA TTGAAAATCC AAAAGAAGCT	1800
CTTAAAGTTG GTCAAGAAGT TCAAGTTAAA GTTCTTGAAG TTAACGCAGA TGCAGAACGC	1860
GTGTCACTTT CTATTAAAGC TCTTGAAGAA CGTCCAGCCC AAGAAGAAGG AAAAAAGAA	1920

1213

GAAAAACGTG CTGCTCGTCC ACGTCGTCCA AGACGTCAAG AAAAGCGTGA TTTCGAACTT	1980
CCAGAAACAC AAACAGGATT TTCAATGGCT GATTTGTTTG GTGATATCGA ACTTTAATCA	2040
AATTGAAAAT TCACAAAATC CTTTGTTTAC TAAACAAGGG ATTTTCTGG CTCTTTGTCA	2100
ACTGTAGTGG GTTGAAGAAA AGCTAAGCTC GAGAAAGGAC AAATTTTGTC CTTTCTTTTT	2160
TGATATTCAG AGCGATAAAA ATCCGTTTTT TGAAGTTTTC AAAGTTCCGA AAACCAAAGG	2220
CATTGCGCTT GATAAGTTTG ATGAGATTAT TGGTCGCTTC CAGTTTGGCG TTAGAATAGT	2280
GTAGTTGAAG GGTGTTGACA AGCTTTTCTT TATCTTTGAG GAAGGTTTTA AAGACAGTCT	2340
GAAAAATAGG ATGAACCTGC TTAAGATTGT CCTCAATAAG TCCGAAAAAT TTCTCCGGTT	2400
CCTTATTCTG AAAGTGAAAC AGCAAGAGTT GATAGAGCTG ATAGTGGTGT TTCAGG	2456

(2) INFORMATION FOR SEQ ID NO: 214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10974 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

AAATAGGATA TAGAGACATC CTTCTGATCT GCTTTTWACA AAGTCCAATT ATATGCGGAT	60
CTATACCTCC ACAATGTCCA TTATTATmCC TAACTATAAT ATGAGCCGAA AACACTATAT	120
CCTTAATGTC TCCATATCCA TCAGGGATAT TAATATTTAT TTTTCCACAA CTATATTGCA	180
TTGTAACCAT TCCCTTAAAC GACGCATTAT GATATTTGAT AGAGAAATTT TTATGAATAA	240
CTCAATAATT TTATAGTAAA TCATGCTTAT ATCTCAAAGA TACCTATTTT ATCTTGCTCTC	300
GACCTTCTCC AAAGAATTGC TATAATACTA TTACAAATCC ATCTGCACTA CACTTCAAAT	360
TTTAGCACTG TATAAAAACG TTCAATACA CTAACCTCAA GAAAACCTCC ACTATTAATT	420
GAAAAAATTG ATAGAGATAA ATTAAAAATC TATATTGAAA CTCATCCCGA TGCTTATTTG	480
ACTGAAATAG CTGCTGAATT CAACTGTCCT CCAACAATA TTCATTACGC TCTAAAGGCT	540
ATGGGATATA GTCTAAAAAA GAGCCGTACC TACTGCGAAC AAGACCCAGA AAAAGTAAAT	600
CGGTTCCCTTA AAGAATTGAA TCACTTAAGC TACCTGACTC CTATTTATAT TTATGAGACA	660
GGGGTTGAGA CCTATTTTTA TCTCGAATAT GATCGAGCCT TGAGCAGGCA GTTAGTCTCT	720
CTGGAAGAAG ATATAATTAT TTGAATTAAAG ATCGAGACAA CGCACACCAG AGATTGCGAT	780
ACTGTTATAG AAGTACTAAT GCCCTTTTTT GTTTCAATAT ACTATGGCTC CGATGACCTA	840

1214					
TAAAGATACG	ATGACGAGTG	ACTTTTTCGA	AGCTTGCTTC	CAAAAATTCT	TACTACCTAC
TTTAGATACA	CCATCCCTTA	TCATTATGGA	CAATGCAAGG	TTTCACAGAA	TGAACATGTG
TAAGGAGCAG	GGCATAGACT	GTTACCACTT	CCTACCTATT	CACCCGAGTA	TAATCCCATT
GAGAAAATAT	GGGCTTACAT	CAAAAACATC	TCAGAATAAT	ATTGTCAAAT	TACGATGCTT
TTCTTGAGGC	ACTTTTGTCC	TATTCTTGTT	TCAGCCGACT	ATACTCCGTT	ATTGGGCAGC
TACGGAACAG	TCGATGGGAC	GATGGGGGGA	CATAAAAAAA	TCCTCCAGTT	TGTTTTTTTA
TAACAGTATA	CTGGAGAATT	GACAATCTCG	GTAGATACCT	CGTTATAGCG	CGGTTACTTA
TTAGGCAGTT	ACAAAACAAC	TGTGAACAGA	AAACATTCCA	GAGTCAGACA	AGACTTTGGA
ATGTTTTGGC	TCTATAATTT	CTGTAGTGGG	TAATCCCACC	CCAGGAATTA	TAGGGTCGTT
TCTTGTAGAA	AAAAAGCCCC	ATATGACCTA	TAATGAAAAG	CGTCTAACCA	ACTCATTAGA
AAGGGTTCAT	ATGGAACAAC	TTAAGAATAC	CACAGATTTG	CTCGGATTGG	AAGACAAAAA
TATCAAAATC	TTGTCTGTTC	TGAAATACCA	AACCCATCTA	GTCGTTCAGG	CAAAGTTGGA
TTCCCCGCT	CCTCCTTGTC	CTCATTGTCA	AGGGAAGATG	ATCAAATACG	ACTTCCAGAA
AGCCTCTAAA	ATTCCGCTTC	TCGACTGTCA	GGGTTTACCC	ACGGTACTGC	ATCTCAAAAA
GCGCCGCTTT	CAGTGCAAGA	ATTGCCTTAA	GGTGGTCGTT	TCTCAAACAT	CCATTGTCAA
GAAAAATTGC	CAGATTTCCA	ACATGGTGAG	ACAAAAAATC	GCTCAGCTCC	TCCTTGAAAA
GCAGTCTATG	ACTGAGATTG	CCCACAGATT	GGCGGTCTCA	ACTTCCACCG	TCATCCGAAA
ACTGAGGGAA	TTTAAGTTTG	AAACCGATTG	GACCAAGTTG	CCAAAAGTTA	TGAGTTGGGA
TGAGTATAGC	TTCAAAAAGA	GCAAAATGAG	CTTCATTGCC	CAAGATTTTG	AGTCCAAATC
CATCCTCGCA	ATTTTAGACG	GGCGAACTCA	TGCGGTGATT	CGAAACCATT	TCCAACGCTA
TCAGAGAGAG	GTTCGGGAGC	TGGTCGAGGT	CATCACCATG	GACATGTACA	GCCCTTATTA
TCGGGCTCGCT	AAGCAACTCT	TTCCAAAGGC	GAAGATTGTT	CTTGACCGCT	TCCACATTGT
CCAACATCTG	AGCCGAGCTA	TGAACCGAGT	ACGAATCCAA	ATCATGAACC	AATTTGACCG
AAAATCCTTG	GAGTATCGGG	CGCTCAAGCG	CTTTTGGAAC	CCTCGCTTTT	TCGTTTCTAG
GCTCGGGCTA	AATCAGTCCA	CTGGACTGAT	TTACTACACC	AGTATAGCTT	CAAGCTCTGT
CAGAAACGAT	TCTATCAGCC	CACGTTTCGA	ATGCACTTAA	CCCATCGGGA	AGTACGAGAT
AAGCTGCTTT	CTTACTCTGA	GGGATTACAG	GTTCACTACG	AACTCTATCA	ACTCCTGCTC
TTTCATTTTC	AAGAGAAGAA	TGCCGACCAT	TTCTTTGGAT	TGATTGAGCA	AGAACTGCCA
ACGGTTCATC	CGCTTTTTC	AACGGTCTTT	TGGACTTTTT	TAAGGGATAG	AGATAAGATT
ATCAACGCAC	TTAAGCTGCC	TTATTCCAAC	GCTAAACTTG	AAGCGACCAA	TAATTTGATT

1215

AAGATTATCA AGCGCAAAGC CTTTGGTTTC CGGAACCTTA ACAATTTTAA AAAACGGATT	2700
TTGATGACTT TGAACATCAA AAAAGAGAGT ACGAATTTTCG TACTCTCCAG ATTGCAGCTT	2760
TTGCGCTACC CACTACACTT GACAAAGAGC CACTCTTTAT TCCATGGTAT CAAAGGCAAG	2820
ACTTGGTTTG GCATTGAGGT CCCAGCCTGC GAAGTTTCTT TGTGTTCCACT CGCTGACGCT	2880
GGCATAGGCA ATCATACCTG CATTGTCTCC GCAGAGTCGC AGAGGGGGGA TGATAACCTT	2940
GACATCTGTG ATTTCCGGCTG CTAGGCGTTC TCTGAGACCT TTATTGGCTG CCACACCACC	3000
TGCCACAACCT AGGATTTTAA CAGGATATTT CTCCAAGCC TTCTTGGTTT TTGCCATGAG	3060
AATGTCCATA ACTGCTGCTT GGAAGGAAGC ACACAAATCT TCTGTAGACA GGCTTTCTCC	3120
CTTTTGCTCG GCATTGTGAT GAAGATTGAT AAAGGCAGAT TTCAAACCTG AGAAGGAGAA	3180
CTCCAGATTA TCTTCCTTAA TCATGGCACG GGGGAAATCA TAAATATCCT GCCCCTGATG	3240
AGCCAGCTCG TCAATCTCAC GACCTGCAGG ATAGGTCAAG CCCATGACAC GGCCGACCTT	3300
ATCATAAGCC TCACCAACCG CATCATCACG GGTTTCCCA ACAATCTTAT AATCTCCTGC	3360
CTCCGAAACA TAAACCAACT CTGTGTGTCC GCCGCTGACC AAGAGGGCTA GCAAGGGAAA	3420
CTCCAAAGGC TCCCACTCT GAGCTGCCAT GAGGTGCCCA GCCATGTGAT TAACAGGAAT	3480
CAGTGGAAGT CCGTGAGCCC AAGCAAAGGC CTTGGCAGCT GACAAACCAA CTAGCAAGGC	3540
TCCGACCAAG CCGGTCCGT AGGTAACCGC AACAGCTGTC ACGTCCTCTT CGGTAATCCC	3600
TGCTTCTGCC AATGCCTCCT CGATACAGGC TGTAATGACC TCGACATGGT GACGACTGGC	3660
TACTTCGGGC ACTACGCCAC CAAAACGTTT GTGACTCTCA ATTTGACTAG CAATGACATT	3720
GGACAAGAGC TCATCGTCGT TTTTCAAGAC GGCGACACTG GTCTCATCAC AGGATGTCTC	3780
AAATGCTAAA ATATATCTAT CCTTCATCTA TTTCTCTCTT CATGATAATG GCGTCCTCGA	3840
CTGGGTCATG GTAGTAGGCC TTTCGCTCAG CGATAACTGT CATCTTTTCT TTCTTGTAAG	3900
ATGCTTGCGC TCGTTGATTT GACTGTCTGA CTTGAGGAA AATTTCCCTG TCTGTCGGCA	3960
ATTGAGCAA CAAGGCTGAC GCAATCCCTT GACCTTGATA AGCTCCTTTG ACAGCGATTT	4020
GCAGGACTTC TGCTTCAAAA AGATTCTCCT GCACAGCTAG AAATCCAATC ACTTCTGCCC	4080
CATCATAAGC CAATGCATAC CAAGTCTGGT CTTGGGACAG ATCTGCTTGG ATTTGCTCCA	4140
GAGTCCAAGG ACTGACTAGG TAAACAGCTG CCATAACAGC GTAGATGGCT TGAGCTAGGT	4200
CAGGCTGTTG TTGAATTCGC TTGATTCTTA TCATAGGCGT TTAATGTAAG ACTCGCCAGA	4260
CTCGGTATGG TTCTTGAGCC AGTTTTCCTC AGCCTCGACT CGTTTGAGGT AATTCGGCAC	4320
AAAATCATGC AAGGAGTCTG CTCCTTGTC CCAGGCCAAA AGAGCTAGAT TAGCTGCATT	4380

1216

GGGCAATGTT	TCTTTGTAAT	CAGTCCTTGG	CAAGTGTTTT	TGAATCTGCT	CAACAAAGGG	4440
GCCAACTTCT	CCGACAAAGG	TTACCTGACT	AGTACCCCTG	ACTTTTCTA	GCACCTCTTC	4500
AAAAGATAGG	TGCGCTTCTG	CCATGACAGG	TTTGGCATTT	TCATAAAATC	CTGCATAAAC	4560
ATTATTGCGA	CGCGCATCCA	TCAAGGGGAC	AAACAAACCT	TCTTGTGAT	GGGGCACCAG	4620
AGCCAAGAGA	CTCGACATAC	CAACCAACTC	GATGTTCAGG	GTGTGAGCTA	AGGTCTTAGC	4680
AGTTGCTACC	GCAATTCGCA	AGCCTGTATA	GCTACCCGGC	CCTTCAGCTA	CCACGATTCCG	4740
GTCCAAATCC	TTGGGTGTCC	AATCCAAACT	TGCCATCAAA	AAATCGATGG	CAGGCATAAG	4800
AGTAATACTG	TGATTTTCT	TAATATTAAT	CGTCGTCTCG	GCAAGAACCT	GCTTATCCTC	4860
TAAAATAGCC	AGAGAAAGAG	CCTTGCTGGA	CGTATCAAAA	GCTAATACTT	TCATAACACA	4920
TTCTATCTT	TTTGTCTGCT	TACTATTATA	CTACAAAAGC	TGGCACATGG	GAATTTTCTT	4980
TGCCCCCAGA	CAAGAGTGCC	CTCACTTAAC	TAAAAATAAT	TTAAAAAAT	GCTCACTTTT	5040
CCTTTTCTTT	TCCGAATATA	AAAGTGAACA	AGAAAAAGG	AGGAAAGTTC	AATGACAAAT	5100
TTTGACATTC	TTGACAATCA	ATTTTATCC	TTATCTGAAA	ATGAATTATC	AGATATTGAT	5160
GGCGGTCTCG	CTCCCTTGGT	TATCTTTGGA	GTAGCAGTAT	CTTGGAAGGC	TATTGCAGGT	5220
GGAACAGCAC	TTATAGGTTT	TGGTTTGGCA	GCTGGTTATT	TTTTAGGAGG	AGATTAATAT	5280
GATGAAAGAT	TTGAACAATT	ATCGTGAAAT	TTCTAATAAG	GAATTGCAAG	AAATCAAGGG	5340
TGGCTTTGGT	GTCGGTGTG	GTATCGCTTT	ATTTATGGCA	GGTATACCA	TTGAAAAGA	5400
CCTTCGTAAA	AAGTTTGTA	AGTCATGCTA	GATAAGAAAC	ACATTTTGTAG	AAGGATAAAT	5460
TTTATTGTCT	TCATCTCTTA	CAGTTTGCTC	AGCATTCTCA	ATGATTTGAA	CATTACTACC	5520
ATCCCTTTAC	CATTGCAATT	ATCTGTTTGT	ATTGTTTTAT	TTTTATGCTT	CAACTCTATT	5580
TTTGATCAGA	ACAATGACTC	CCATAAAAAT	AATAAGCTTT	GAAAATTCCA	TTGTCATGTC	5640
ATGTTAGAAA	AATGCAAAGA	CCACCTCATC	TTGATAGATG	GGGTGGAATT	TTCGTGTCGT	5700
AAATCTACTA	TCTCTACATT	CCCAAACAAA	AAACCCAGC	ATAAGCAGGG	CATCTAAGCA	5760
TTTAATTCAA	AGTAAAATAC	AAACCAAACG	ACATAGGTCA	CGAGGAGGAG	AAAAAGCGAG	5820
TAGAGAGTCA	CAAAGGTCAT	TTCCACAAG	AACTTGTTT	GTCGTGCTTC	CAGTTTGCA	5880
AATAGAAGAT	TCCCCGCATA	AACGCAAGCA	ACAAAAACAA	TAAAAGCTAC	CAAGCGAGCT	5940
CCGATAGCAA	AAGCAAATAA	GTTATACATA	GGGCAACCTC	CTTGACTTAA	AATCTATATG	6000
GAATTATGAC	AAGCAATAAA	TTTCACTTCC	GTTATCAACA	TAATACATTT	TCTTTATTTT	6060
TGAAAACGCT	TACCAAAGAA	ATCGTCCCCT	AACTTCTCG	TTCCGCTT	TTACTAATTT	6120
TTCATTTTGT	GGTATAATTG	AAATAATTGT	AACGAATCAA	GGTCAATCTA	GACACAAAAT	6180

1217

GGAATGAAAT CAAGCAAATA TCTGCTAAAA GTTTGGAATA AGCTGACCTG TAAATAGAAA	6240
GGAACTATAT GATTTACAAA GTTTTTTATC AAGAAACAAA AGAACGTAGC CCACGCCGTG	6300
AAACAACACG CACGCTTTAC CTAGACATCG ATGCCAGCTC AGAACTTGAG GGCCGTATCA	6360
CTGCTCGCCA ACTTGTCGAA GAAAATCGCC CAGAGTACAA TATCGAGTAT ATCGAACTCT	6420
TGTCTGACAA ATTGCTCGAT TACGAAAAAG AAAGTGGCGC CTTGCAAATT ACGGAGTTCT	6480
AATATGGCCT ACACTCTTAA ACCTGAAGAA GTCGGCGTTT TTGCCATCGG TGGTCTAGGA	6540
GAAATCGGGA AAAACACTTA CGGAATTGAA TACCAAGACG AGATTATCAT CGTCGATGCT	6600
GGGATTAAAT TCCCAGAAGA TGACTTGCTT GGTATCGACT ATGTCATTCC TGACTACTCT	6660
TACATCGTGG ACAATATCGA CCGCGTCAAG GCTGTTTTAA TCACACACGG ACACGAGGAC	6720
CACATTGGTG GGATTCGGT CTTACTCAAG CAAGCAAATG TCCCTATTTA TGCTGGACCG	6780
CTTGCCCTGG CTTGATCCG TGGGAACTC GAAGAACAG GCCTCTTGCG CAACGCCAAA	6840
CTTTACGAAA TCAACCACAA CACCGAGTTG ACCTTTAAAA ATCTCAAGGC AACTTTCTTT	6900
AGAACGACTC ACTCTATTCC AGAGCCTTTG GGGATTGTCA TTCATACTCC TCAAGGGAAA	6960
ATCGTCTGTA CGGGTGACTT TAAGTTCGAC TTTACTCCAG TTGGAGAACC TGCGGACTTG	7020
CATCGTATGG CTGCGCTTGG TGAAGAAGGC GTGCTCTGTC TCCTGTCTGA CTCGACAAAT	7080
GCGGAAGTAC CAACCTTTAC CAACTCTGAA AAAGTCGTTG GTCAGTCCAT TATGAAGATT	7140
ATCCAAGGTA TTGAAGGACG TATCATCTTT GCATCCTTTG CCTCAAATAT CTTCCGTCTC	7200
CAGCAGGCAA CAGAAGCTGC TGTTAAGACT GGACGCAAGA TTGCGGTCTT TGGTCTGTCT	7260
ATGGAAAAGG CCATTGTCAA CGGAATCGAT CTTGGCTACA TCAAAGCTCC TAAGGGAACC	7320
TTTATCGAGC CAAATGAAAT CAAAGATTAT CCTGCAGGAG AAGTTCTTAT CCTCTGTACA	7380
GGTAGTCAGG GTGAGCCTAT GGCAGCCCTC TCTCGTATCG CCAACGGAAC CCACCGTCAA	7440
GTACAATTAC AACCAGGTGA TACCGTTATC TTCTCTTCTA GTCCCATCCC TGGAAACACT	7500
ACTAGTGTCA ACAAGCTGAT TAACATCATT TCTGAAGCTG GTGTCGAAGT TATCCACGGT	7560
AAAGTGAACA ATATCCATAC ATCTGGACAC GGTGGTCAGC AAGAGCAAAA ACTCATGCTC	7620
TGCTTGATTA AGCCAAAATA CTTTCATGCCT GTCCACGGTG AATACCGCAT GCAAAAAGTC	7680
CACGCTGGAC TAGCAGTGGA TACTGGTGTT GAGAAGGACA ATATCTTTAT CATGAGCAAT	7740
GGCGATGTGC TTGCCCTTAC TGCTGACTCA GCTCGTATCG CAGGTCATTT CAACGCCCAA	7800
GATATCTATG TCGATGGAAA TCGTATCGGT GAAATTGGCG CAGCTGTCTT CAAAGATCGT	7860
CGCGATCTAT CTGAAGACGG TGTCGTTCTG GCAGTTGCAA CTGTTGACTT CAAATCGCAG	7920

1218

ATGATTCTAT	CTGGTCCAGA	CATCCTCAGC	CGAGGCTTTG	TCTACATGAG	AGAGTCTGGC	7980
GACTTGATTC	GCCAAAGCCA	GCGTATCCTC	TTCAATGCCA	TTCGTATCGC	ACTGAAAAAT	8040
AAGGATGCTA	GCGTGCAATC	TGTCAATGGT	GCCATTGTCA	ACGCTATTCG	CCCCTTCCTC	8100
TATGAAAATA	CCGAACGTGA	ACCGATCATC	ATCCCGATGA	TCCTCACACC	AGATGAAGAA	8160
TAAAGCAAGA	AAACAGCCCC	GTCTCGGAG	CTGTTTTTCT	CTATGCTTTC	TTTGTAGATT	8220
AAAACTCATA	CTCAATGAAA	ATCAAAGAGC	AAACTAGGAA	GCTAGCCGTA	GGTTGCTCAA	8280
AGCACTGCTT	TGAGGTTGTA	GATAGAAGTG	ACGAAGTCAG	TAGCCATACC	TACGGCAAGG	8340
CGACGTTGAC	GCGGTTTGAA	GAGATTTTCG	AAGAGTATCA	ATAAAAAATCG	AAATCAGACT	8400
AGAAGGCTAA	GCGAAAGCAT	AACCTGAGTT	AGCTCCCAT	GTTCGGGAAA	CTATGGGAGG	8460
CTGGAGATGA	ATCAAAGCCA	AGCTTTGAAC	TCATTCGTAA	GAAGCCGACG	ACGTATCATT	8520
TTGATTTTGT	AAGAGTTTGA	GAAATACTAC	GATTTTACC	TTCCAGATAC	ACCATCAAAA	8580
TAGAAATATC	TGCTGGGTTT	ACTCCCGAAA	TACGGCTGGC	TTGGCCGATG	GTTTCTGGAT	8640
TGATGAGTTT	GAACCTCTGA	CGGGCTTCGG	TTGCGATAGA	ATCAATGTCA	TCCCAGTCGA	8700
TATTGGCCGG	AATGCGTTTT	TCTTCCATGC	GTTTCATCTT	GGCAACCTGG	TCCATGGCTT	8760
TGGAAATATA	GCCTTCATAC	TTGATTTCTG	TTTCAATCAA	TTCGATAATC	TTGTATCCAA	8820
AGTCTTCTGC	AGCTGGTCCG	ATGAAGGCCA	CCACATCTTG	GTAAGAAACT	TCTGGACGGC	8880
GAAGGAATTC	CTTGGCTGTC	ACTGCATCGG	TCAAGGGTTT	GAAGCCCATC	TCCTCAACCT	8940
TGGCATTTGGT	TTCTTTGACT	GGCTTGAGTT	TGATACTGTC	TAGGCGCTTC	ATCTCATTAT	9000
CAAATTGATT	TTTCTTGATT	TCAAAACGAG	CCCAGCGTTC	ATCGTCCACA	AGGCCAATCT	9060
CGCGTCCCAT	CTCAGTCAAG	CGCATATCAG	CATTGTTCATG	ACGAAGAATG	AGACGGTATT	9120
CAGCACGACT	GGTCAAGAGA	CGGTAGGGTT	CAATGGTTCC	CTTGGTCACC	AAGTCGTCGA	9180
TCATCACCCC	GATATAACCA	TCACTGCCTG	TCAAAATCAA	TTTCAAGGCTG	CCTTGGATTT	9240
TCAGAGCCGC	ATTGATACCC	GCGATAATCC	CTTGGCCTGC	TGCCTCTTCG	TAACCTGATG	9300
TTCCATTGTG	CTGACCAGCA	GTGAAGAGAC	CTGAGATTTT	CTTGGTTTCC	AAAGTCGCAC	9360
GCAACTGATG	AGGCAAGACC	ATATCATACT	CAATAGCATA	ACCTGTCCGC	ATCATCTCTG	9420
CATTTTCCAA	ACCTTTGATG	GAATGCACCA	AGTCACGCTG	GACATCCTCA	GGCAGACTGG	9480
TTGAAAGTCC	TTGCACATAG	ACTTCCTCAG	TATTGCGCCC	TTCTGGCTCA	AGGAAGAGTT	9540
GGTGACGTTT	CTTGTCCGCA	AAGCGCACAA	TCTTGTCTTC	AATCGACGGA	CAGTAACGAG	9600
GCCCCACTCC	CTTGACCACA	CCTGTAAACA	TAGGCGCACG	GTGGAGGTTG	TTTTGGATAA	9660
TCTCATGACT	GGTACCATTG	GTATAGGTCA	ACCAGCATGG	TACTTGGTCC	TTGACATAAT	9720

1219

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CCTCATCACG TGAAGTGTAT GAGAAATGAT TAGGCACTTC GTCTCCTGGC TGAATTTCTG      9780
TCACATCGTA ATTGATAGAA GAAGCCTTGA CACGTGGAGG GGTTCCTGTC TTGAAACGAC      9840
CGATTTTCGAG ACCCAGTTCC TTGAGATTGT CAGCTAGGTT AATAGAAGCC AAGCTGTGGT      9900
TAGGACCTGA TGAGTACTTG AGGTCTCCGA TGATAATTTC CCCACGGAGA GCAGTCCCTG      9960
TCGTCACAAT AACAGCCTTA GCAGCATATT CTTGATGGGT GGCTGTACGC ACACCGACAA      10020
CCTTGCCATC TTCCACCAA ATCTCATCAA TCATGGTTTG ACGAAGGGTC AGATTTTCTT      10080
GGTTTTCAAC CGTCTTGCGC ATCTCCTTAG AGTAAAGTTC CTTGTACAGC TGCACACGAA      10140
GGGCACGGAC AGCTGGCCCC TTCCCTGTGT TTAGCATCTT CATCTGGATG TAAGTCTTGT      10200
CAATGGTTT GGCCATCTCG CCACCGAGGG CATCGACTTC ACGCACGACA ATCCCCTTGG      10260
CAGAACCACC GATAGAGGGA TTACAAGGCA TGAAAGCCAG CATTTCAATA TTGATGGTCG      10320
CAAGCAGGAC CTTACAGCCC ATACGGCTAG CGGCCAAGGA AGCCTCAACC CCAGCGTGTG      10380
CCGCACCAAT TACAATAATA TCGTATTCTT CAGTAAAATG ATAAGTCATG TTTCTCTCCT      10440
ATTCTCAAG ATGAATGTGT CTTAGTTGGC CTTCCCAATC TGGTAGGGCT GTTTTTAAAA      10500
AGACTGGAAC TAGCTGGATA TTCTGGAGCT TATCCAAGTC AATCCACTCA CAGGGCTGCC      10560
TTTTCTCATC TTCCTGCATG GTCAACGGGG CATCTTCAAG CAAATCCACC AGATAATGAA      10620
ACTCGATATT GTGATAGGAA ACGCCGTCCA CTTCAAAACG ATTTTCAACC ACAAAGCTA      10680
GCTGCCCAGC TTGAGCTTTG ACACCCAGTT CTTCTTCAC TTCACGGACT ACCGCGTCTT      10740
CCGTGCTTTC ATTGACTTGA ATCGCACCTC CAATAGTGTA ATACTTGCCC TTGTCTTTGG      10800
TAACTAGAAG CTTGTGATTT TGGACAATCA AGGCTGTAGC CCGAACACCA AAAACCGTAT      10860
TGTCTACTTT TGTCCGAAAG TCTTGTGAG TCATTCTTGT CCTTCCCTT AAACGACACA      10920
AAAACAGTCA AAATAACAAA GAAGTGCAGG ACAAAAAAGC CTGCAACATC CAGG      10974

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(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

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CCCGTTATGA TTATGGATAG CGCTTTCAAA TTTTAAACT CCTATCCCAT CCTTTTATCT      60
ATATAATAAG TGAAAATATA ATAAGTGTCA AGTAACTGAA GTGAATTTTA TAAAAAATT      120

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1220

ACAAGCCAAA TTTGTAAAGT TTACACTAAG CCGCTAGgCA ATCGTCTATC AGAATATCCG	180
TTTATTGTGC AATAATCCGA GAAAATCTTG CAACGCTTAG AAGTCTATAA AAACATCAAA	240
CATTTATATG ACTTGCGAAT AGCAATCCTG CTAAACCTTT CCACACTCTA TCTATACAAT	300
CAAGATAAAA ACATGTGTAA GCAAATCTGC TACACTTTAC TGGAGGACGC CAAGAATAAG	360
AAAAGCTACG ATAGGCTTGC TATCTGCTAT GTCCGTATTG GGATTTGTAC AGACGATTCT	420
AAACTTATCC AAAAAGGGTT CTCCCTTCTG GAGCTGACCG AGGAAACTTC TATGCTGTCT	480
CATCTCAAAA AAGAAGTAGA GACCCATTAT CAACCAAAGA AATTATAAAA AAAGTCGAGG	540
GAGCTCCTCG ACCTTTTCAT AGAATCGCCG AACGATTTAA CGAGAAAGTA TGACTTTTAC	600
GTTTATCCCA ACTCAATTAT GACATTTTTT TCAAAAGTCA ATATATCTCA CTTTTTCAAC	660
GACAAGAAAG AGGCTGATAA TCTACCAACC TCTTATCTG AACCCATCAC TCCATCACTT	720
TTTAGCTTCA TTCGCTTTCT TAGCGACTGC AATCTGGTAT TCGACTTGGT CATTCCCCTT	780
ACCGGTACAA CCATGAGCAA TTGTAGTCGC TCCTATCTGA TCGGCTATTT CAACCAATTT	840
TTTAGAAATC AGAGGGCGGC TCAAGCAGA TACCAAGAGA TACTTTTGTT CATAATAGGC	900
ATGTGACTGA TGAGCCACTA GCACATAATC TGTAGCAAAT TCGTCCTTAA CATCAATGAC	960
ATAAGATTCT ACTGCCCAA CCTTAAG	987

(2) INFORMATION FOR SEQ ID NO: 216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

CTGGGTCTTG TTCATAGTAG GTGTGGTtCT TTTTTTCGAG TGTAGCCCAT AGCTTTGAGC	60
GCATAGTGGA TGGTAGTTGG ATGACAGCCA AAGTCAGAAG CTATTTCAGT CAAATAAGCA	120
TCTGGATTGT CAGTAAGATA GTTTTAAAGT CTATCTCTAT CAACTTTTCT TGGTTTGTGTT	180
CCTTTTACTT GGTGGTTTAG CTCTCCTGTT TTCTCTTTTA GCTTTAACCA GCCATAAATG	240
GTATTACGTG AGATTTGGA AACGTGTGAT GCTTCTGTTA TACTACCTAT TCGCTCACAA	300
TAAGAGAGAA CTTTTTTACG AAAATCTATT GAATATGCCA TAAGAAGATT ATACCACATT	360
GTGTACTATT TTTGGTTCAT TTTACTATAT TTTATAAGTT ATAGTGTAGC ATTCCAACCTT	420
CAAAGCACTA TAAAGTAAAT TGAACAAGA ACAATACAAA CAATTCTCGT AAACGGATTG	480
CAACCACAAA AAAGCAAGCA TTCACAAGAA TACTTACCTA TCATGGGAGG AACAACCGTT	540

1221

CCTCTTTTTT ATTACTAAAA TTCAAAGAAT TCCAATGCTT TTTTCAAGAG CAAATCCGTA	600
TATTCCTGGAT CTTCTTGGGC TACTTCTATT TCCCGCTGAA CTTTTTCCAA ATCATCTGTA	660
ATCACTCCAT CTACTCCTAA GTGAAGAGAT TTGCTGATAG CTTCTGAATC ATTGACAGTC	720
CAGACATAAA GTTTCGTATC CGTTGTCCAT AGTTTGCTTA CAAAATATTC ATCCAAGGTT	780
GAGTACTCCA TAGTATATCC TGTGCTCTT GTTTTAGGAA AGACAGAATT GTAGGGCATG	840
ATGAAATAAA CTGGTAGTTC GGCATCATAC TGTCTTACTT TTTCGACAAC ATGGTAGTCT	900
AAAGACTGGA TTTGATGTCC ATAAATCTTG AGCTTTGCAG CATAACGGGC TAAAAAGCGG	960
TTCATCATGT CTGGACTATC TTTTTTACTG GTTTTAATTT CAATTAGTAA TTTTGGACCA	1020
AGTTCGTTGG CTCGACTGAG ATAATCTTCA AAGCTTGAAA TTTTAGTCTG GTAGCCATTT	1080
TCAAAAATAT CAATCCCTTT AAGCTCCTCC AAGTTTAAGT CTTGAGGACT TTTATGATA	1140
CCTGCTAGAT TTTTCAAGTT AGCATCATGC ATCATGACAA ACTGCCCATC TTTTGTTC	1200
TGCACGTCGG TCTCCACCAA GTCTGGTTTG AGTTGTGCTG TAGTTTCCAA GGACTCTACT	1260
GTATTTTGAA TCCCATTTGC ATTGGAAACC CCTCGGTGAG AAATAAGTTG AGGTAGATGA	1320
ACCATGGGAG CCTCCAGATA AATATAACCT TCTAAGGCAA AGAAAAGACT GGCACAAGTC	1380
ATGACACCCC ATCGCACGAT GTGATCTTTT TCTCTCCTAG GAAGCATATC CAGCTCCTTT	1440
CCTGTCAAAA ATGAAACAAA TTAAACCAA AAATAAGTCA GAGCCATATA ATAGAGATTT	1500
TTAATCACGA CAAAATTCAA AATACCAAGA ATCAGAGACT CTCTCTGAGT GATATCATCT	1560
ACCAAAGTTT GAGCCAATAA TAAAGGAATC AAAGGAAGAT AATAATAA ATGTGCTTTG	1620
AGCAAGATGT AAAATAAATT CCAAGCATAA AAAGTAACTC TCTTCTTGGT TTTCTCCAAG	1680
CTAAACATCA CTGCTTCTCG AACAGTCAGC TGATCATATA CAATCTTCGG AAGGGCAAAC	1740
ATCAATCTGA CAGAGACATA GAGAAAGATA AGAGATAGAA GTAGGATGCT CAGCCACCAC	1800
ATCCAATATC TATCTTCTAA ATAAGCTTGG ATAAACTCTG GAATGACGAT TTTATTAAGA	1860
TAATAAATCT TCAGCATTTT CCGTATAAAA GGAAACAGCA TAGCTATATA GAAAAAGATA	1920
AACAAGGCTT TAGCGCAAGT TAGCTTTTTC ATAAATCCAA AACTTTCATG GAAAACCTTG	1980
CGGATATACT CAATTAGCCT TCGCTTTTCA TTATAGAGGA GATGACGAGC ACCAATAAAG	2040
AGGAGTCCTA TTTGAAAATA AGCAACCAGA AGGTTAATTA CAATCAAGGC TAAAAAGCT	2100
AGACTAATCA ATGGAGAATG AGTAAGGATG GCTAAGACAT TGTTATAGGA AATAAAAAGA	2160
TAACCTGTCT GATCTAATAA GAAGCTAGCC AACCATGAAT TGAATGGTAC CCACAAATAC	2220
TCCACTATCA TAAAAATCAA GAAAAATAGA AAGAGGATTT TATCAAGATC GAGGTAAATC	2280

1222

TGTTTAAGAC CCAATTTTTT AGGTTTTTCA GGTTCATAG GCACTCCTAG TCAAATAATT	2340
GAGACAAGTC CAAGCCACCA AAAGGATTGT TTGATAAGCT ACTTTCTGTC TCTAACAATT	2400
CCCTAGCTTG ATCCGACTCT AAGAAGGATT CGTAAACACG CGCCGTCATC CGAGCATCCT	2460
CTAAACTATT ATGAGACTGA CCTTGAAATC CAAGAAATGA GGCAACAGTT TGCAATTTGA	2520
GATTGGCAAT ACCATGTAAA TCTGAACTCC GACGTTCAAA AGCTTCATCA TACAAATCCA	2580
CCTTGTAAGT TTGGCTATAG TCTAAACCAT GCTCTGCTAA AATAGGTAAA TCACTTTTAG	2640
CAGCATTTGA G	2651

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CGTTATAATA AACTTGTGAA AAAATTAACA AAGGATATCG TTCCTTGAAA GCTATGGAGG	60
AAAAATATGGC TGATAAAAAA ACTGTGACAC CAGAGGAAAA GAAACTCGTT GCTGAAAAAC	120
ACGTAGATGA GTTGGTTCAA AAAGCTCTAG TTGCCCTTGA AGAAATGCGT AAATTGGATC	180
AAGAACAAGT TGAATACATC GTTGCCAAAG CATCAGTAGC AGCTTTGGAT GCCCACGGAG	240
AATTGGCTTT ACATGCCTTT GAAGAAACAG GACGTGGTGT ATTTGAAGAC AAAGCAACTA	300
AGAACTTGTT TGCCTGTGAA CACGTAGTAA ACAACATGCG CCACACTAAG ACAGTTGGCG	360
TTATCGAAGA AGACGATGTA ACAGGATTGA CTCTTATTGC TGAACCAGTT GGTGTTGTTT	420
GTGGTATTAC TCCAACAACA AACCCAACAT CAACAGCAAT CTTCAAATCA TTGATTTTCAT	480
TGAAGACACG TAACCCAATC GTCTTTGCCT TCCATCCATC AGCACAAGAA TCATCTGCTC	540
ATGCAGCTCG TATCGTCCGC GATGCAGCTA TCGCAGCTGG TGCTCCTGAA AACTGTGTGC	600
AATGGATTAC TCAACCATCT ATGGAAGCAA CAAGTGCCCT TATGAACCAC GAAGGTGTTG	660
CGACAATCCT TGCAACAGGT GGTAATGCCA TGGTTAAGGC GGCTTATTCA TGTGGTAAAC	720
CAGCTCTTGG GGTAGGTGCC GGAAACGTTT CAGCTTATGT TGAAAAATCA GCAAACATTC	780
GTCAAGCAGC ACACGATATC GTCATGTCTA AATCATTGTA TAACGGTATG GTCTGTGCAT	840
CTGAACAAGC AGTTATCATT GATAAAGAAA TTTACGATGA ATTTGTAGCA GAGTTCAAAT	900
CTTACCACAC TTACTTTGTA AACAAAAAAG AAAAAGCTCT TCTTGAAGAG TTCTGCTTCG	960
GCGTCAAAGC AAACAGCAAA AACTGTGCTG GTGCAAAATT GAACGCTGAC ATCGTTGGTA	1020

1223

AACCAGCAAC TTGGATTGCA GAACAAGCAG GATTTACAGT TCCAGAAGGA ACAAACATTC	1080
TTGCTGCAGA ATGTAAAGAA GTTGGCGAAA ATGAGCCATT GACTCGTGAA AAATTGTCAC	1140
CAGTTATTGC AGTTTTGAAA TCTGAAAGCC GTGAAGATGG TATTACTAAG GCTCGTCAAA	1200
TGGTTGAATT TAACGGTCTT GGACACTCAG CAGCTATCCA CACAGCTGAC GAAGAATTGA	1260
CTAAAGAATT TGGTAAAGCT GTTAAAGCTA TTCGTGTTAT CTGTAACTCA CTTCTACTTT	1320
TTGGTGGTAT CGGGGACGTT TACAATGCCT TCTTGCCATC ATTGACACTT GGATGTGGTT	1380
CTTACGGACG CAACTCAGTT GGGGATAACG TTAGTGCCAT TAACCTCTTG AATATCAAAA	1440
AAGTCGGAAG ACGGAGAAAT AACATGCAAT GGATGAAACT TCCTTCAAAA ACATACTTTG	1500
AACGTGATTC AATTCAATAC CTTCAAAAAT GTCGTGACGT TGAACGTGTC ATGATCGTTA	1560
CTGACCATGC CATGGTAGAG CTTGGTTTCC TTGATCGTAT CATCGAACAA CTGGACCTTC	1620
GTGCAATAA GGTGTTTAC CAAATCTTTG CGGATGTAGA ACCGGATCCA GATATCACAA	1680
CTGTAAACCG TGGTACTGAG ATTATGCGTG CCTTCAAACC AGATACCATC ATCGCACTCG	1740
GTGGTGGGTC TCCAATGGAT GCTGCCAAAG TAATGTGGCT CTTCTACGAG CAACCAGAAG	1800
TGGACTTCCG TGACCTTGTC CAAAAATTCA TGGATATCCG TAAACGTGCC TTCAAGTTCC	1860
CATTGCTTGG TAAGAAGACT AAATTCATCG CGATTCCAAC TACATCTGGT ACAGGATCTG	1920
AAGTAACACC ATTTGCCGTT ATCTCTGATA AAGCAAACAA CCGTAAATAC CCAATCGCTG	1980
ACTACTCATT GACACCAACT GTGGCAATCG TAGATCCTGC TTTGGTATTG ACAGTTCCAG	2040
GATTTGTTGC TGCTGATACT GGTATGGACG TATTGACTCA CGCGACAGAA GCATACGTAT	2100
CACAAATGGC TAGTGACTAC ACTGATGGTT TAGCACTTCA AGCCATTAAA TTGGTCTTTG	2160
AAAATCTCGA AAGCTCAGTT AAGAATGCAG ACTTCCACTC ACGTGAGAAA ATGCATAACG	2220
CTTCAACAAT CGCTGGTATG GCCTTTGCCA ATGCCTTCCT AGGTATTTCT CACTCAATGG	2280
CCCATAAGAT TGGTGCGCAA TTCCACACAA TCCACGGTCG TACAAATGCT ATCTTGCTTC	2340
CATACGTTAT CCGTTACAAC GTTACACGTC CAGCTAAGAC AGCAACATGG CCTAAGTACA	2400
ACTACTACCG TGCAGATGAA AAATACCAAG ATATCGCACG CATGCTTGA CTTCCAGCTT	2460
CTACTCCAGA AGAAGGGGTT GAATCTTACG CAAAAGCTGT CTACGAACTC GGTGAACGTA	2520
TTGGGATCCA AATGAATTTT AGAGACCAAG GAATTGACGA AAAAGAATGG AAAGAACATT	2580
CTCGTAAATT AGCCTTCCTG GCTTATGAAG ACCAATGTTC ACCAGCTAAC CCACGTCTTC	2640
CAATGGTAGA CCATATGCAA GAAATCATCG AAGATGCATA CTATGGCTAC AAAGAAAGAC	2700
CAGGACGCCG TAAATAATTG TTTATCAGTC TAGAAGCAAG AAAAAACTC AATTTGAGGG	2760

1224

AAAGATCCAG TAATTTTCT ATGATAAAAG GCATCCTATC AAGGTTTTTG AACACCTGAT	2820
AGGATGCCTT TTTATGATAT TGAGGCCTTT TTGCCCTTTT TGAAAACTA GAATAGAAAC	2880
AAAATATATA ATAGATTGAA ACTAGAATAG TACATATCTG CTTCTAAAAC ATTGTTAGAA	2940
TTCGATTTGA CTGTCCTGAT CGATTTGTCC TGTCTTATT TCATTTTGAT ATATAAAAAA	3000
TATAGTATAG TAGACTGAAT CTAAAATAGT ACGAAACAAT TGCTAAAACA TTTATAGAAA	3060
TTAATTTTAC TTTTCTGATA GAGTTGTTCA CATCTTATTT CAATTCACCTA TAGTTTAATT	3120
TAAGAGTAGT ATTTACTAAG GCCCAATTAA AATCAAAGAG CAAACTAGAA AACGAGTGCC	3180
ATTCAGCTCA AAACACTGAT TTGAGATTGC AGATAAGACT AGCCCCCTCA TTAACAGATT	3240
TACGATAAAA CGATGACAAG GTGTGTTGCT TTTTGATTTC TAAAGAGTAT AATGATAGAT	3300
CTCTATAAAA TAAGTGCAGG GGAATGAGC TTTTATAGTC CTTTCGTTTT AAAATACTAT	3360
CTCAGATATT CTTATATCGA CAAGAAGTTT TTGAGTCATT CCCTCATCAT ACATATTAAA	3420
TAAATAGTGG CTCATTCAAT TTTTCACTAG AATAATAAGC TAGTATAGTA AACTGAAATA	3480
AGATATAAAC AAATAAATTG GAGCTTAACA TCCATTTCCT GCAATTTTTT AGAAACTACA	3540
GTGGACTATT CTAGATTCAA CATATTATAA AAACCTAGAGT AAAAGAAAAG GATTGGATCT	3600
TGTGTAATGC AGGATCCAAT CCTTCAATC ATTTTGTCCA ACTTTTGAG GTTCTACAA	3660
TGTAGTCGTC ATTAATAAAG ACAGATGGGA ATGACAGTGT TCCTATTTAT TTTGATAGAG	3720
ATCGATGAAT TCTTTAGATA GCAACTGAAT AATCTCTGTT GAAGCCATTT GGTCTTCTGC	3780
ATGCATAAAT AGCAAGGAGA ATCTATTTT TTCTCCAGTA GCTTCTTTTT GTATGAGATT	3840
AGAGTGAATC TTGTGCGCTT CTAATAAGGA GTCTTCCGCT TCTTCAACTT TAATTTTCGC	3900
TTCTTTTAAA TTTCTGCCT TAGCTAGTTG GATGGCTTCA ATAAAGGATG ATTTGGCTGC	3960
TCCACTATTG GCAATGAGCT GAAAACAGAT ATATTCCATT TCTTCTGTCA TCTTATTTCT	4020
CCTATCCATG CAAGTGCTTG TTCCAGAACT TTTGCTCCAT TCATCATTC GTATCCCGC	4080
ATATCAATGG TATCTACAGG GATATTTTCT GCAATTTCTT TCACAGCAAG TAACTCATAA	4140
CGAATTTGTG GCCCAATTAG AATGACATCT GCTTCATGGA TATCTTTTTT AGCTTCTGTC	4200
ATTGATTTTG CTTGGATAGA GATTTCAATC CCACGTTTCA TCGCACTTTG TTGCATTTTT	4260
TTAACAAGCA TACTTGTCGA CATTCCTGCA TTACATACTA ATAAAATTG TTTCATAATC	4320
TTAACCTTCC ATTTCTTGTT CAACAACCTT GTCATTAACT TTGATAAATG GAAATGTATAG	4380
AAGAAGTCCA AGTGCAAAGA TGATGAATTG AACTAGAACT GCTCTCACGT CCCCTGCTGT	4440
TGCTAACCCT GCATTTAAGA ATACTGGTGT AGTCCAAGGA ACTTGTATAA ATGCAGGACT	4500
CATGAATTCT GTAAGTGTG CTAAGTAGCT GATTAAAATA CCAAGGACTG GAACTGTGAT	4560

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AAATGGAATA GCTAATGAAA TGTATATAAC GATTGGGTAA CCGAATAATA CTGGTTCATT	4620
GATATTGAAG ATACCAGGTC CAAAAGATAA TTTAGCCACG TTTTGTAGAGA CAGCATTGCG	4680
ACTCACTAAG AATGTTGCTA TTAATAAACA TAATGTAGAT CCACTACCAC CCATTAAAGC	4740
GAATGTTTGT ATTTGTGATA GGTTGATGAT GTGTGGAATG GCTTGTCCAT TATTTGCTGC	4800
AGTGATGTTT TCAGTAATGT TAATTAATAG TAATGGTCT AGGATGGCAC TGTAATAAAC	4860
TGCTTGGTGA ATACCAAATA GCCATAACAT ATTTCTTAA GAGTAAATAA TAATGACCCC	4920
GATTAAGCTT GTACCAATAT GACGAATTGG TTCTGGAATA AAGATTGTAA TGATTGAGAT	4980
TAAGTTCATT CCAGTTATAT TGAATAATAA TGCTGAAACA ACCCCAAATA AGGAGATGAC	5040
GGTCATGACT GGAAGTAATA CGCTAAATGA TCTACTAACA GCTGGTGGAA TATTTTCACC	5100
AAGGTTTATT TGTAAGCTT TAACGTTTGA TAATCAATG AATAATTCTG TTGCAATAAT	5160
CGTACGATAA CCCCAGCGAA CATTGCGCCT GTACCTGTGT TGTGGAATGA AAGAACACCT	5220
GAAATGTTTA CCGCATCTTT TGCTCCGTCA GGAAGTACAG AAAGTGTATT TGGCATCATC	5280
ACAATTAAAG AAAGTAATGA TAGCATTGAT GCTGCTAACG GGTTCGAA ATCTCTGTTT	5340
TTAGCTAAGA AATAACCAAC CATTACAGCA ATAATCATACT CTGAAATACT TAAAGTACCG	5400
TTTGCAATTG TTATTCCCCA ATATTGGAAT CTTGTTAATG TATCCCTTG GAAATCCAC	5460
TTAAATACCG TGTGTTCAA AAGAAGGATT AAACCTGCCA AAATATATAA TGGCATTACT	5520
GTTACGAATG CATCTCTTAG GGTTCCTTAA TGAATTTGGT TCCCTAGTTT ACCAGCAAAG	5580
GATGGCAAAA AAATTTTTTT GGGGGGGGG GTTATTAAAC CCCCCTTTT AAAAAAA	5638

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

CCGGAAGCTG TTGCCCTTGG AACTCCAAAT GAAGAAACAG CCTTGTCTT GAACTATTTT	60
GGTGTGGAAG CACCACGTGT TATCACTTCT GCCAAAGCAG AGGGGGCAGA GCAAGTTATC	120
TTGACTGACC ACAATGAATT CCAACAATCT GTATCAGATA TCGCTGAAGT AGAAGTTTAC	180
GGTGTGTAG ACCACCACCG TGTGGCTAAC TTTGAACTG CAAGCCCACT TTACATGCGT	240
TTGGAGCCAG TTGGATCAGC GTCTTCAATC GTTTACCGTA TGTCAAAGA ACATGGTGTA	300

1226

GCTGTGCCTA AAGAGATTGC AGGTTTGATG CTTTCAGGTT TGATTTCAGA TACCCCTTCTT	360
TTGAAATCAC CAACAACACA CCCAACAGAT AAAATCATTG CTCCTGAATT GGCTGAATTG	420
GCTGGTGTGA ACTTGGAAGA ATATGGTTTG GCAATGTTGA AAGCTGGTAC CAACTTGGCT	480
AGCAAATCTG CTGAAGAATT GATTGATATC GATGCTAAGA CTTTGTAACT CAACGGAAAT	540
AATGTCCGTG TTGCCCAAGT GAACACAGTT GACATCGCTG AAGTTTGTGA ACGCCAAGCA	600
GAAATTGAAAG CTGCAATGCA AGCTGCCAAC GAATCAAACG GCTACTCTGA CTTTGTCTTG	660
ATGATTACAG ATATCGTCAA CTCAACTCA GAAATCTTGG CTCTGGGTGC CAATATGGAC	720
AAGGTCGAAG CGGCTTTCAA CTTCAACTT GAAAACAATC ATGCCTTCCT TGCTGGTGCC	780
GTTTCACGTA AGAAACAAGT GGTACCTCAA TTGACTGAAA GCTTTAATGC GTAAGATTTT	840
GGGTGTGAGC TCAAAATCGG AAAGTCTAGT TTGCCCTTATA TCGCAAGGAG TTTCGGCTCC	900
TTTTTCTAG GAGTGAAGTA TGTTAGAAAA TGGCGATTG ATTTTGTGA GAGATGGGTC	960
AGACATGGGA CAGGCCATCC AGACTTCCAC AGGTAATAT AGCCATGTTG CCATTTATTT	1020
GGATGGGATG ATTTATCATG CTAGTGACA GGCTGGTGT GTCTGTCAAG AACCAGCAGA	1080
CTTCTTTGAG TCCAATCAT TATACGACCT CTATGTTTAC CCAGAAATGG ATATCCAGTC	1140
GGTGAAGGAA AGAGCTTGCA AACATCTTGG AGCACCTAC AATGCTTCTT TCTATCCAGA	1200
TGCAGCTGGT TTTTACTGCT CCCAGTATAT AGCAGAAATC CTACCTATTT TTGAACTAT	1260
TCCTATGAAA TTTGGAGwTG GGGAGCAGGA GATTAGTGAT TTTTGGAGGG AGTATTACAT	1320
AGAACTAGGT CTGCCCTGTC CTCTGAACCA AGCTGGTACC AATCCTAGTC AGTTGGCAGC	1380
ATCGCCTCTG TTACAATGTA AAGAAAGGAA TCTTCATGAT TCAGATTTTT AATCCATCTC	1440
GTTTGACGAG ACAGCCATTT TTGGAGAATT GATCCGCTAT CTGGATCAGT ATGAGGATGT	1500
GATTCTACGG GAAATTAAGG CTCAATTTCC AGATGTTGCA GTTGATAAAC TCATGGAAGA	1560
GTATATAAAG GCAGGCTTGA TTCTACGTGA AAATAAGCGC TATTACCTCA ATTTTCCTAC	1620
GCTTGAATCA CTTGATAGTC TTGAACTGGA TCAAGAGATT TTTGTCAGAG AAGCTAGTCC	1680
GGTCTATCAA GCCTTGTGAG AGCAGAGTTT TGAGACGGAA TTGCGCAATC AAATCAATGC	1740
AGCTATTTTA GTTGAAAAGA CGGACTTTGC GCGCATTTAA ATGACCCTGT CCAATTATTT	1800
TTACAAGGTC AAACAGCAGT ATCCTTTGAC AGAAAAACAG CAGGAGCTCT ATGACATTTT	1860
AGGAGATGTT AATCCTGAGT ATGCCCTCAA GTATATGACG GCTTTTTTGT TGAAATTTCT	1920
CAAAAAAGAC CAGCTTATGC AGAAATGCCG TGATATCTTT GTGGACAGTT AGGTTGTCTT	1980
AGGCTATATT GTGCAAAATG AAGATGGAAA GTATGAGTTG GCTATCGATT TTGATAAGGA	2040
GAGGTTAACT TTCTACTTAG CGTGATTCTT TGTTTCTGAG TACATTGTTT GACTTTCCTT	2100

1227

AGTATTCGGT ATAAACTATA TGTAACCGGT AACACATATC GGAATAAACT AAAGGAGACA	2160
ATCATATGTC ACTTGAAAAC AAATTGGAAC AAGCAACAGG CGCTGTCAAA GAAGGTTTGTG	2220
GTAAAGTTAC TGGAGACAGC AAGACAGAAC TTGAAGGAGC TGTGAAAAA ACAGTTGCTA	2280
AGGCAAAAAGA CGTTGTAGAA GACGCAAAAG GTGCTGTAGA AGGTGCCGTT GAAGGTTTGA	2340
AAAACGTTTT TACTAAAGAA TAGGAAAAAA TCAAGGGTTT CATTTTCCCT TGATTTTTTC	2400
TATTCTTATA AATAATTTTC TGCACGCGT GTATCTCCTG GGTAGGATTC TTTCTTGCCC	2460
TGGATGATTT GGTAAACAATC GGCTCCCTTA CCCGCAATAA TAACTGCATC TAATTCGTGA	2520
TTTGTGATAG CCATTGCCGC CTTGATGGCT TCTTGGCGAT CCGCAATCTT TTCAACAGGA	2580
TGATTGATGT AGCTACTAAT TTCATCTGCA ATGGCCATTG GGTCTTCATA GTTAGGGTCA	2640
TCAGCAGTCA GAAAGACTTG AATCTCAGG TGTGATTGA GGAGGAGGCC AAAGTCCTTA	2700
CGACGACTTT CTCCCTTGTT TCCTGTTGAT CCCAGAACCA GAGCAATCTT TCCGGTTTGA	2760
TGAGTTTCAA CCACATTGAT GAGTTTTTTC AGACTATCCC CATTTGTGGC ATAGTCGATG	2820
AAGACCTTGG CTCCATTTTT CTGAGTGAGG ACTTCCATAC GACCAGGAAC GCGGGTTGCA	2880
GCGATGCCTT TTTTGATGTC CTCAAGACTT GCTCCGAGAC GGAGACAAGC AAGTCCAGCA	2940
GCAACTGCAT TTTCTTGTT GAAGTTGCCA ATGAGTTGAA TATCATAATC TCCAGCGAGT	3000
TTACCCGTAG CTGAAAAGCT AAAGGCTTTG GAATCTCGA TTTGGTTATC AAATTGGCTA	3060
CCATAGAAAT CATGGTCTTG ATCTTCAACC TGTTCTTTCA AGACTGAGAA GTGGTCCATG	3120
TCACTGTTAA TGATGACTGC TCGGCTCTTT TCCATCAAGA GACGCTGTG GTAGAAATAG	3180
TCTTCAAAGC TAGGGTGTTT AATCGGGCCG ATATGGTCTG GGCTGATATT TAGGAAAAC	3240
CCCACATCAA AGGTTAGACC ATAGACACGT TTGACCAGAT AGGCTTGACT GGAGACTTCC	3300
ATGATGAGGT GGGTACGGTC ATTTTGACA GCCTGATTCA TCATGTCAA GAGGTCAATA	3360
CTCTCAGGGG TTGTCAACGC TGAATTAAAG AAAGTCTCGC CATCAAGAGT TGTGTTTCATG	3420
GTCGACAACA TAGCAGGTCT ATGCCCTTGA GATAAGATGT TATAGGCGAA ATAGGCTGCT	3480
GTTGTCTTAC CCTTAGTACC AGTAAAGGCA AGGAGTTTGA GTTTTTCCTG TGGATTACCA	3540
TAGAACTCCA TGGCAATCAA ACTCATGGCT TTCTTTATAT CGTTCACAA GATGACAGGG	3600
ATACCGACTT CGTAGTCCTT TTCAGCTACA TACCAAGCTA ATCCTTGTGT TATAGCAGAA	3660
AGAAGGTATT CTTTTTAAA GGCAGCGCCT TTTGCGAAAA AAAGAGTGTC TTCTGTTACT	3720
TTTCGGCTGT CGTAGCTGAT GCTATCAAAA ATAACTTTGC TGTAGTTGTA GTGGTAATGA	3780
CCTTGGTCAA TAATTTTCGCG AAAAAGGCCA TCTTCTTTA AAATATCTAA TACGGTTTCA	3840

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ATCTTAATCA TACTTTCTAT TGTAACCGA AAGTCGTAAA TTTACAAGTA ACAAGGAAAA	3900
GTTTATAATG GAAGATAAGG AGTTTTTCCT AGTTATCAAA ATTGAATGAG GAATCTATGT	3960
CGCACGAAAA CAATCACCAG CAGGCCCGA TGTTACGGGG GACTGCTTGG CTAACGGCTA	4020
GTAACTTTAT CAGTCGCCTA CTCGGGGCTG TTTACATTAT CCCTTGGTAC ATCTGGATGG	4080
GGGCTTATGC AGCTAAGGCA AATGGTCTCT TTACCATGGG TTACAATATC TATGCTTGGT	4140
TCTTGTTGGT TTCAACAGCG GGGATTCCAG TTGCGGTGGC CAAGCAAGTT GCCAAGTATA	4200
ATACCATGCG AGAAGAAGAG CATAGCTTTG CCCTGATTCG GAGCTTCTTA GGCTTTATGA	4260
CAGGACTAGG CCTGGTTTTT GCTTTAGTCT TGTATGTCTT TGCTCCTTGG CTAGCAGACT	4320
TGTCTGGCGT GGGCAAAGAC TTGATCCCAA TCATGCAAAG CTTGGCTTGG GGAGTCTTGA	4380
TTTTCCCGTC TATGAGTGTT ATCCGAGGAT TTTTCCAAGG GATGAATAAC CTCAAACCCT	4440
ATGCCATGAG CCAAATTGCT GAGCAGGTCA TTCGTGTTAT CTGGATGCTC CTAGCAACCT	4500
TTATCATTAT GAAGCTCGGT TCAGGAGATT ATCTAGCAGC CGTTACCCAA TCAACCTTTG	4560
CTGCCTTTGT CGGTATGGTA GCCAGTTTGT CAGTCTTGAT TTATTTCCCTT GCCCAAGAAG	4620
GTTCACTCAA AAGAATCTTT GAAACAGGAG ATAAGATTAA CAGTAAGCGT CTCTTGTTTG	4680
ATACCATTAA GGAAGCCATT CCTTTTATCC TGACAGGGTC TGCCATCCAG CTCTTCAGA	4740
TTTTG	4745

(2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CCTGATTGAC CTTATAATAA GGAACAAAAC ACAATGCACT ACCTTTTCAA CAAAAGAGTT	60
GCTGCTTGAT TAAAACCATC ACACCAGTTA TACCATTTTG CTTCATACCC ATCTTGAGCT	120
AGGATACGAT CTTCTAAATC AAAAACAGAG TAAATCTTTC TTTCTCGCA AGCTTGCGCA	180
TAGAGATGAT ATAGTTCATC ACCACCATCT CTATCCCACT CAGCAGAAAT CGTATCCCGA	240
CCTGCCAATA AAGCCTGATA AGCCCTGTGA TGCCCATCTG TAATCAGCAA ACAATCTCCA	300
AAGGCAAGAA TACTGATTGG ATCGACTTGG ATTGTTTCTG CCGACTGGTA AAGCATCTGA	360
ATATCTTGCA ACTTCTTTTC TGATAAATAT AGTTGAGTCA GATGAAGATC TGCTATATTG	420
ACTTTCATTT CTTTCTCCTC AAGGGAATTC GATACTCACT TCTGTTTGCC TTAAATCGC	480

1229

CATTGGAAGC GGAgCTTGTC ATAAAAGGGA AACTCGATAA ACAGGACTCC CAAGCCCACA	540
CAGAGACTGG CAAGGACGTC TGATGGGTAA TGAAGTCCCA GATAGACTCT TGATACCAGC	600
ACACTGACTA GGTAAGGCC AAGGACGATT TGTACGATTT TTCTCCAGAC CTGATCTTTA	660
ATCCGCTGAC TAAGAATAAC AATCAAAGTC CCTACCATCA GCGTTACAGC TAGAGAATGC	720
CCACTTGGGA AGGAAAATCC CTTCTCCTCC ACCAGATGTA AAATAGCTGG TCGTGGGCGC	780
TGGTAGATAT TTTTAAAGGT CACGATTAAA AGACCTGCCA AAGCCAGATT TCCCAGCATG	840
AAGAACTTT CTATCTTCCA TCGCTTACGA TAAAAGACAA AAGCTGTAAT GACAACCCAA	900
GTGATAATCA CTGGGATATC AATCAGACGT GTGAGGGCTC GAAAAAGAAT AGTCAAATAA	960
TCTGGTAAGT CTCCTCGAAT GGCAGTCTGA ATCGATTGGT CAAAATTGAC CAACATTTCA	1020
GGGTAAAATT TGACCATGTA GCCAAGAATA ACGAAAAGTA AAAGGGCAAA ACTGCCCTTC	1080
ATTAAAAATG TTTGTTTATC TCTCATAATG TTTTAAGGTT GGTTCAGA GAACATACAA	1140
CAACCAGAAT GAAACGGAAA AGATAACACC TTCAATCAAG TTAAGGTA ATACCATGGT	1200
CATTAGGTAG TTGGAAAGTC CCAAAATTTT TCCAATATCA AAGTTAGCAA ACTTAGCGTA	1260
CAAAGGAACA GCATAACAT AGTTGAGAAC CAACATGGCC AAGGTTAAAC CAATAGTTCC	1320
AGCTAGAGAG CCTAGTAGGA AACGAAGGT TGTCCGTTC TTTTCCAAA TCAAAGCAAA	1380
TACGATGACA AAAACTCCCA AAGCTACGAT ATTCATCGGC AAACCAATGT AAGTATTCAC	1440
TCCTTGCTG TTAAGAAGCA ATTTCAAGAG TGAGCGAAGC AAGAGCACTC CTAGAGmCsC	1500
AGGCAAAATCC ATGACCACCA GACCCACAAG GACTGGCAAG ATACTAAATT CGATCTTGAG	1560
GAAAGATGCC GCTGGTAAAA GCGGAAAGTC AAAGTACATC AGCACAAATG AGATGGCTGA	1620
TAGAATTGCA ATGGTCGAAA GTCGACGTGT GTTTGTCATA ACAGGTTCCCT CCAATTTTCT	1680
ATAAATCAG AAGAAGTTGG AAAGGATTCC TCTATCTATT CTCACTTTT ATATCCCAA	1740
AGTTCCTCT TACTCTATTA AAGAAAAACA AAGCAAGTGG TTACAATCCG GCTATAAATC	1800
TATCAAAACA GACAAGGCTA TTCTTTCGTC TTCTCCCATC CAGACTATAC TGTCGGTTGT	1860
GGAATCTCAC CACATCACGT TGCGCTCACG GACTTCTTTA	1900

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4692 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

GGTTTTCCAG CAGGAGCTTC TCCTTTATCA GAATGACCAT CCCATCTGCT CACGATAGAT	60
GAATAATGAT ATTTTTTACC ATGATAGTAA TTTGAAAAAG CCTAACCACC TCCTGAACCT	120
TCTCCATATG TCCATACTCC TCCATCTGGA TATTATACAG CAGCTGATGC AGCTCCCAAT	180
AATGTAAAC TTGAAATAAG AGCTAGAGCA AGTAATCTAT GTTTTTTCGT TTTCATTTTA	240
TTTTTCTTT CAAAAAAGC ACACCTTGAG CAACAATGCA ACAAATAAA TCCTCCTCTC	300
TCTTTTATTG AAACCGCTTT CTTATGTGAT AAGAATAACT TTTTATtAT TGTTGTCAA	360
GGAAAAATC GAATTTTTTA GATATTTTAC TATATTACCT CTGTGAATAA TATTATATAG	420
TAGTTTTATT TCAAAATAAT ATGCAACCAG TACTAACCAA ATATAAAATA GATGCCATTA	480
ACGAATTTTA TTCAAGTTTT TCCCATTCAT ACTATACAAG TAAAAGAGAT GGTGTTAACT	540
AAAAAGCAAT TCAAACTATT GTAAATTC TAGCAAAAAG AGAGCCGAAA CTCTCTTTTT	600
TATCTCTTT TACTTTTTTT GACTGGCATG AGTGTGATGT CTCTAACACT AAAGTAAGCT	660
AGGATCAACA TGGCTATTGC TAGGAATATT TCTGTTGGTA ATTGAAAAAT TTTCAGAAAA	720
GATAGAACCA ATAAAAACAA GAGTGCCACT AAAATACATA CCATAGCGAC GATATTGACA	780
GTCCCTTTAA TGCTTTCTGG TGTCGCAAAT ACATAGAGTA GGAGCAGTAA AATTCCTAGG	840
ACTAAATAGA CCATCTTTCT CTCTTTCTAG CTCTTATTCA GCTGATTTTT TCTTCTTGTT	900
AGCTTTCTCA CGCTCTGCTT TGTTAAGGAT TTGTTTACGC AAACGGATAG ACTCAGGCGT	960
TACTTCCATG TACTCATCGT CGTTCAAGAA CTCAAGAGAC TCTTCAAGTG TCAAGATACG	1020
AGGCGTCTTG ATAACAGCTG TTTGGTCCTT AGTAGCTGAA CGAACGTTGG TCATTTGTTT	1080
TGCCTTCGTG ATGTTAACTG TCAAGTCATT TTCACGAGAG TTTTCACCGA TGATCATTC	1140
TTCATAAACC TCAGTACCTG GGTGACAAA GATCGTACCA CGTTCCTCGA TAGACATGAT	1200
TGAGTAAGTT GTAGCCTTAC CAGCATCGAT AGAAACAAGG GCACCACGGT GACGTCCACC	1260
AATTTCCCTT GGAATCAATG GCAAGTATTG GTCGAAGGTA TGGTTCATGA TACCGTAACC	1320
ACGAGTCATT GATAAGAACT CAGTTGAGTA TCCAATCAAA CCACGCGCTG GAACAAGGAA	1380
GACCAAACGA GTTTGACCAT TACCAGTTGA AATCATATCC AACATTTAC CTTTACGTTT	1440
AGAAAGGCTT TGGATAACAG ACCCTTGGTA TTCTTCTGGA GTGTCGATTT GTACACGTTT	1500
AAATGGTTCA CATTTAATAC CGTCGATTTT TTTTACGATA ACTTCTGGAC GAGATACTTG	1560
AAGTTCATAG CCCTCACGAC GCATTGTTTC GATAAGGATT GACAAGTGCA ATTCTCCACG	1620
TCCTGAAACA GTCCATTTAT CTGGTGAATC AGTTGGGTCA ACACGAAGGG AAACGTCTGT	1680
TTGCAATTCT GCCTGCAAGC GTTCTTCCAC CTTACGAGAA GTTACCCATT TACCTTCTTT	1740

1231

ACCAGCAAAT GGTGAGTTGT TGACCAAGAA AGTCATTTGA AGAGTTGGCT CATCGATGTG	1800
TAGGATTGGA AGAGCTTCTA CTGCATCTGT CGGAGTGATG GTTTCACCGA CAAAGATGTC	1860
TTCCATACCT GAAACGGCAA TCAAGTCACC CGCTTTGGCT TCTTGGATTT CACGACGTTT	1920
CAAACCAAAG AAACCGAAGA GTTTTGTAAC ACGGAAGTTT TTAGTTGTAC CGTCAAGTTT	1980
AGAAAGGGTA ACTTGGTCCC CAACCTTAAC TGTACCACGG AAGACACGAC CGATACCGAT	2040
ACGTCCAACG AAGTCATTGT AGTCCAAAAG TGACACTTGG AACTGCAAAG GCTCATCTGA	2100
GTTATCTACT GGAGCTGGGA TATGGTCGAT AATCGTGTCA AAGATTGGTG CCATAGTCGC	2160
TTCTTGGTCA GCTGGATCAT CTGACAATGA AGAAGTCCG TTGATCGCTG AAGCATAAAC	2220
CACTGGGAAA TCAAGCTGGT CGTCATCTGC ACCAAGCTCG ATGAAAAGTT CCAAGACTTC	2280
ATCCACTACT TCTGCTGGAC GAGCTGATGG CTTATCGATT TTGTTAACAA CCACGATTGG	2340
GACAAGGTCT TGTTCGAAGG CTTTTTCAA TACGAAACGA GTTGTGGGCA TGGTTCCTTC	2400
ATAGGCATCT ACGACCAAGA CAACACCGTC AACCATTTTC ATGATACGCT CAACTTCTCC	2460
ACCAAAGTCC GCGTGTCTG GTGTGTCCAT AATGTTGATA CGAGTTCCTG TGTAAAGCAAC	2520
GGCAGTATTT TTAGCAAGGA TGGTAATTCC ACGCTCTTTT TCGATATCGT TTGAGTCCAT	2580
AGCACGCTCT GCCAATTCAG TCCGTGCATC AAGCGTTTCT GATTGTTTCA ATAATTCGTC	2640
AACCAGGGTT GTTTTACCGT GGTCAACGTG GCGGATAATC GCAATGTTAC GGATATCTTC	2700
TCTTAATTTT GTCATGATTT CCTCTATAAT ATTCAAAATT TATTTTCTAA CTGAACGATT	2760
ATACCATAAT TTCAAATAAA TAACATAACT CAAGCAAGTG TAAATGTTTT CACTCTGCTT	2820
TTCTTTTCAC GTCAAGCCTT TTCAAAGCGA GCGACTTATG ATAAGATAGG CACAGTATGC	2880
GTTTAGATAA TTTATTAGCT CAAGAAAAAA TCAGCCGAAA GGCCATGAAG CAAGCACTCC	2940
TCAGAGGGGA AATTCTAGTC GATGGTTGCC CAGCCCGCTC CCTAGCTCAA AATATCGATA	3000
CAGGACTACA AGAACTCCTT TTTCAGGATC GAATCATTCA AGGCTATGAA CACACCTATC	3060
TTATGCTTCA TAAACCTGCT GGTGCCGTTA CAGCCAACAA AGACAAGGAA CTTCCGACCG	3120
TCATGGACCT GCTTCCATCT AACATCCAGT CTGACAAGCT CTATGCCGTT GGCCGACTGG	3180
ACCGAGATAC AACGGGACTC CTCCTCTTGA CCGATAACGG TCCCTTGGGC TTTCAGCTCC	3240
TCCATCCCCA ATATCATGTC GATAAGACTT ACCAAGTTGA GGTAAATGGA CTTCTAACAC	3300
CTGACCATAT CCAAACCTTT CAAAAAGGAA TTGTCTTTTT AGATGACACT GTCTGTAAAC	3360
CCGCAAAACT AGAGATTCTA TCTGCAAGTC sCTCCCTCAG TCAAGCCTCT ATCACCATTT	3420
CAGAAGGAAA ATTTCATCAA ATCAAGAAAA TGTTCCTCTC GGTTGGTGTT AAGGTGACTA	3480

1232

GCCTCAAAAG AATCCAATTT GGGGACTTCA CATTGAACCC AGATTTAGCA GAAGGTAAC	3540
ACCGCCCTTT GAACCAAAAA GAGTTACAAA TCATTAAAAA CTATTTAGAG ATGAGTCGAT	3600
AAAACAAAAA AAGCTTTAAA ACTAAAGCTT TTTTCTTTTA TTTACCGAAA AATTAAGGCG	3660
ATTGTACAAA TCCAGTTAAC TACAGAAATC ACAATTCCTA AGATATTAAG AATCTTTTCT	3720
ATTTTATAGT CTAATGTGA CTCTTTTGG TATGAAATAG CCAAGACCAA TCCTATGATA	3780
CCCAAAATCA GGCCTACAAT TGGAAATAAC AAACCAAGAA TAATCGACAA GATACCCACA	3840
AAAAGTGAT TTTTCTTCTT TTCTTTTATG TTCTAAGAAC TCCTTAAATT TTATACAAAT	3900
TAATTATACT ATAAACAAT AGCTTCATCC TATCATTCGA CTAATTGGA AATAAGGTTA	3960
GCTAGTCTTC ACTTCCCTT TCCAAGAATC CAAGCCATAA GAAAGGATAT AAATCTCAGA	4020
AAAACCTTGT TTTTCAAGT AAAGAGCTGC ATTTGTAAC CGTTGCGCAC GTTGGTTTTC	4080
GTAGAGAAGG ACAGGTTTAT CTTTACGAAG GGCTGCAAGA CTAGTTTCA ACTGACTTGA	4140
AGGAATATTG CGTGCACCAA GGATATGTTT TCTGTGGAAT TCTGTGGGT CGCGCAAATC	4200
AATCAATTGA CCCGTACGAA TCAAGGCTTC AAACCTCCTCA TTGTCCACAA TTTTAGCCGC	4260
ACGGCGAATA CGAAGATAGT TAAAGCCCAT CCACGCCAAC ATTGCTAGTA TAAGTGCCCA	4320
CAAAATCCAA GTAACCATTA GTTCTTTTCT CCATTTTCT CAATATAATC CAATCTACC	4380
TTGTGCTCTC TCGGAAGAAC TGCTTCTGCC TCTAGATAGT CTAATTTATC CATCAACCCT	4440
GCATCGTAAA TCCGAGATAG TTCCAACCTC ATCAGTTCAA TATCATATAA GCGTTTCCC	4500
ATGTAACAA TAATACCAA TCGTTTGAGG AATTGCTGCA CATCATAGAA TGTTTTCATA	4560
AGACTCATTC TAGCAAAATT TTGTGTTTTT TTCAAGAAGA GACTCACACA ATGCTCCTTA	4620
TTTTCTTATC TTCTTTAGCG ATTCTAAGGC AAGTATGGTA CAATAAAAAC ATGGGGATTC	4680
AACAATTACA TT	4692

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 706 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

GCTAAAAAGC TGATAATCTT CGACTCCTGT ATATGATGTG TCTTTTCATG TAAGACACGC	60
GCCGCCAGAA TCATGGCAAG AGCTGCAAGA CTGGCAAGTA AGAAGCCGAT AAGATAGGCA	120
AAAAGATAAG TGAATTTGAC AAAGAAAGTC AAAAGAACTA GGAAACCAAA GCCTCCTCCA	180

1233

AAAAC TACCA AAGTC TTTTCG TAAAT CCCAG ATTTT ATCCA ACTGC TTGAC GAGGG AAGTC	240
GTCTG AC GAA CGCCT ACAAT AGTTG CTAAC ATACT TCCTA AAAAG AATGG ATAGAC ATGA	300
GTTAA ACTGG AGAAAT AAAC AGAGGA ATAA GAGGT CACTA GAAAA CTACC AATAAA CATG	360
GAGAAG AAAC TGATCA AGAA GGCAAC AGCA GATAAG AGAA AGACCAT CCC CTTCA ACTGA	420
CCATT TGATT TAGCT TGT TT GGATA AGAAC CAAACT GCCA ATCCCC AAAAG AATATA GTAG	480
TGAAC CTCAA CTGCC AAAC CCAATT ATGA ACAAAC AAAT GAGGA ATGAA CTGAG ATTCA	540
TAAC TCCAC CTGTT AGGAG TTCAT AGAAG TTGGT CATAA AGCCT AAGAC GCCCG CAATC	600
TGGCC ACCAA TTCCAG CAAC ATAGT CTTGG CGAAC CAAGA AAGTAAA AGG CATGG TCACC	660
AAGACC ATCA AAACC ACAGG TGGCA CAATC TCGATA AAAAG CGTCT T	706

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CAGCTGATGG GCAATATCAG TCATAGAAAT TTTTCAATT AACTTTTGAG CAATTTTTTG	60
GTTGATGATA CGAGGGATTT GGTGATTTTT CTTTACCAGG GGAGTCTCAG CAACCATCAT	120
TTTTGAACAG TGATAGCACT TGAAACGGCG TTTTCTAAGG AGAATTCTAG AAGGCATACC	180
AGTTGTTTCG AGGTAAGGGA TCTTAGACGG TTTTGTAAAG TCATATTCTT TCATTAGACT	240
TCCACAATCA GGGCAAGATG GAGCCTCATA ATCCAGCTTA GCGATAATTT CTTTGTGGGT	300
ATCCATATTG ATGATATCTA GAATCTTGAT GTTTGGGTCT TTAATATCGA GCAGTTTGTG	360
GATAAAATGT AATTGTTCCA TATGATTCTT TCTAATGAGT TGTTTTGTCT CTTTTCATTA	420
TAGGTCATAT GGGACTTTTT TTCTACACAA AAATAAGCTC CATAATATCC ATAGGGGATT	480
TACCCACTAC AAATATTATA GAGCCCGAAA ATATGGGAAA ACTGATCCTT GTTCTGCTT	540
TTGTCTATAG AAGAATAATA AAGATTATCT TCTTCAAAT CTCCGATATT CTCTAAAGTT	600
TTGTGCAAGT TGCACAGAAC TTGTTTATTT TTTTGGTCAT CTTGCCATAG AAATATAAAG	660
CGTTTTCATA TATAATATAA TTATCAAAAG ACAAAGGAG TTCACCTCAT GGTAGAATTG	720
AATCTTAAAA ATATTTACAA AAAATATCCA AACAGCGAAC ACTATTCACT TGAAGATTTC	780
AACTTGAACA TCAAAGATAA AGAATTTATC GTTTTCGTAG GACCTTCAGG ATGTGGTAAA	840

1234

TCAACTACAC	TCCGTATGAT	TGCTGGTCTT	GAAGACATTA	CAGAAGGTAC	TGCATCTATC	900
GATGGCGTAG	TTGTCAACGA	CGTAGCTCCA	AAAGACCGTG	ATATCGCCAT	GGTATTCCAA	960
AACTACGCTC	TTTACCCACA	CATGACTGTT	TATGACAACA	TGGCTTTCGG	TTTGAAATTG	1020
CGTAAATACA	GCAAAGAAGA	CATTAACAAA	CGTGTTC AAG	AAGCAGCTGA	AATACTTGGA	1080
TTGAAAGAAT	TCTTGGAACG	TAAACCAGCT	GACCTTTCAG	GTGGTCAACG	TCAACGTGTT	1140
GCCATGGGGC	GTGCGATTGT	CCGTGATGCG	AAAGTATTCT	TGATGGACGA	ACCTTTGTCA	1200
AACTTG GATG	CCAAACTTCG	TGTATCAATG	CGTGCTGAAA	TCGCTAAAAT	TCACCGTCGT	1260
ATCGGAGCTA	CAACTATCTA	TGTAAC TCAC	GACCAAACAG	AAGCGATGAC	ACTTGCAGAC	1320
CGTATCGTTA	TTATGTCAGC	TACTAAGAAC	CCTGCTGGTA	CAGGTACTAT	CGGACGTGTA	1380
GAACAAATCG	GTA CTCTCA	AGAAGTTTAC	AAAAATCCAG	TTAACAAATT	CGTTGCAGGA	1440
TTTCATCGGAA	GCCCAGCTAT	GAAC TTCATC	ACCGTGAAAT	TGGTTGGTAG	CGAAATTGTT	1500
TCTGACGGTT	TCCGTTTGAA	AGTGCCAGAA	GGAGCATTGA	AAGTTCTTCG	TGAAAAAGGC	1560
TACGAAGGAA	AAGAATTGAT	CTTTGGTATC	CGTCCAGAAG	ACGTGAATGC	AGAACCTGCT	1620
TTCTTGAAA	CATTCCCAGA	CTGTGTTGTA	AAAGCGACTA	TCTCTGTATC	AGAACTGCTT	1680
GGTTCAGAAAT	CTCACCTTTA	CTGTCAAGTT	GGTAAAGACG	AGTTTGTTCG	AAAAGTTGAT	1740
GCTCGTGACT	ACTTGCAAAC	AGGTGCAACA	GTTGAGCTTG	GATTTGACTT	GAACAAAGCA	1800
CAC TTCTTCG	ATGTAGAAAC	TGAAAAAACA	ATCTACTAAA	ATAAATAAAA	TTCAAAGCAC	1860
TACAAGAAAA	GATATCTCTT	TATCAATTGT	AGTGGAGAGA	TATCAGTTAA	TCTAGGGAGA	1920
GAAACAAAAT	GCTTCTCTCC	TTTTTGCTAG	AGAAGTCATA	TTATGCATCT	ATATTGTGAT	1980
GCTCTTTAAT	ACTCTTCGAA	AATCTCTTCA	AACCACGTCA	ACGTGCGCTT	GCCGTACGTA	2040
TGATTACTGA	TTTCGTCAGT	TTTATCTGCA	ACCTCAAAGA	TGTACTTTGA	GCAGCTTACG	2100
GCTAGTTTCC	TAGTTTGCTC	TTTGATTTC	ATTGAGTATT	ATTTGTGGGT	ACCATCTACA	2160
AGTGAAGCTA	TATGCGTAAA	CTACGTGAGC	AATTGAATTC	GAAC TAGAGA	GGTAATAATA	2220
AATTTATGCT	ATAGTTATGG	TGACTTGTAT	GCTTTTGATT	CTAGTTTATC	AAATAATAGA	2280
TTAGAATTGT	CAGATAATAT	CATTTTGTGT	TATAATGAAG	AAAAACAGA	GGTGTTCAAA	2340
TGTCAGAAGC	AGGTCATAAG	TTTTTAGCAA	AATGGGGGAA	AAAACGCTTA	CGTCCAGGTG	2400
GAAAGCGTGC	CACAGATTGG	TTAATTGCAG	AAGGAGGATT	TTCAAAAGAA	AAGAGAATAC	2460
TAGAGGTTGC	GTGTAATAGG	GGA ACTACAG	CAATTGAGTT	GGCACAGCGT	TTTGGTTGCA	2520
AGATAACTGC	TGTTGATATG	GATGCTCAAG	CTTTAGAAGT	GGCTAAAAAA	TCTGCTGGAA	2580
CGGCAGGTGT	TGCTCATTTA	ATCAGTTT TG	AAAGAGCAAA	TGCAATGAAA	CTTCCTTATC	2640

1235

AAGATGCTAG TTTTGATATT GTTATAAATG AAGCTATGCT GACTATGCAA GCCGATCAAG	2700
CTAAGAAAAA ATGTGTAATG GAATATCTAA GGGTATTAAA ACCTGGAGGT CTTCTCTTGA	2760
CACATGATGT GCTTCTTAAG GAAGCTAAAG AGTCTATCAG ACAGGAATTA TCACAAGCAA	2820
TTCATGTAAA TGAGGTCCT TTAAGTCAAG ATGGTTGGGA ACAGGTGATG ATAGAATCAG	2880
GTTATTGTGA TGTGAAAGCA TTGACTGGTG AAATGACATT AATGAAATTA TCGGGTATGA	2940
TTTATGACGA AGGTTTGCTA GGAACCTTGA AAATTTGTGT AAATGCTTGT AAAAAGGAGA	3000
ATAGAAAGCA GTTTTTAACT ATGTATAAAA TGTTTGCTAA GAATAACAG AAATTGGGCT	3060
TTATTGCGAT GGCTAGTTAT AAATCGTCAA AACGTTAGAT AATTATTGAA GTTAACTTTT	3120
CCTTTTTTCT TTCTTAAAAA ATATGCTATA ATAGAGAGTA AAAAAGTTTG AAAGAAAGAA	3180
AAAGATGAAT TTTAAAGATT ACATTGCAAC AATTGAAAAT TATCCAAAGG GTACCG	3236

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

CCTGACTTTT CAAATTGGTT AGTTTGCCAC ACTTGGTTTA TATGGTCGTG GAAAGCATGG	60
CTATTACTTC TCAAAGGGCG ATTTCTCACC CCATGAAAAG TGTCTATTTT TGTTTAGGTT	120
TGTAAGTTAA TTCATTGTCA CATATTACTC TTAACTGAT TGAGTGAGTA CCGCTTATAT	180
TTGATGCCAA ACGCCTTAAA AGTGTTACCC TCAAGTCCTT TTAGAATACG GCTATAATTC	240
CGCTCATTGT AAAGTATCTT AAGCTCATCA CTATCTAGGT TGGTATTAAA AATGGTATTT	300
TCACGATTGT TTAGCACGTC AAAGAGTAAA TCCTGCTCCC AGTCACTCTT AGGCTTAATA	360
ACAGCATTTT TTGCTCCTAA ATCATCAATA ATTAAGTAAT CAACAGACTT CATGAGTTCA	420
GTAGCTTCAA ACTCTGTAAG TGTTGCACCT TTACCATAAT TCCACCCCTC TTTAATTGT	480
TTGATCATTT CGGTTAGGCT TACAAAAAGC ACACTCTTAG GTTCTCCTTT TGTCTTATAC	540
CCCTCATTTA TACCTTTGGC AATAGCAACT GATAAAAGTG TTTTTCCTT CCCTGTACCT	600
CCTGTGATAA GCGTATTTCC CCTCATGCCA TCAAGATATT TTTGTACCTG ACCTTTTGCA	660
AATTCTAAAA ATCGCTTTTC TTCTGATGTT ACAGCATTAA AATCATCAA AGTTTTAGTT	720
TTAAACTCAT CTGCTACATA GCTCTTATTG CTCATCAACA CATTATAAGT TTGCATATAT	780

1236

AGTTTAGCAT TCAAATTATC AGCAATCGCA TCTTCTTCAT CTTGCTTTTT CTGTTCTTCT	840
TGGCATTGTT CACAATAGGG TGGGATACAG CGAACTTCTT TTATTGCCTC TCCGTTCTCA	900
TTCCACCCCA CTA CTACTACATG TCTTTCTCCT TTGATTTGTG TTAGCTGTAT TTCATGCTTA	960
GGACACAATT CGTCTAGTTT AAATGTCTCA ATATTTCCTA AACTAGATTG TAATGATTTT	1020
ATTTTCTGAC CTCCTAAAAT GGT'TTTTCTT GTGT'TGGTAT CCAATCTTCA TAGCTGGTAG	1080
GCTCTAGTTG ATTGGTTTGC TGT'TTTT'TAG CCTCACGCGC TGCCCTGCTA TTTCTAACAA	1140
GTTCCACCGT CAATAAATTG TCCTGTTTCC AACGGTTAAG GATTACCTTG ATGTATGCAA	1200
AGTTTGCTTT ACCCTGACTG ACAGCCTCTT TTAACGCCTC ATGGATAAGC TCTGGGCTAA	1260
AATCTTCTAG CATATACTGC AATTCTTGAA TCTGTAACGG TGACAATGCT TTACCTGTCT	1320
CAGCTCGCTT CATATTCAAC AAGTCGTCTA TTTCCACACT GGTTACTTTT TTATTTACAA	1380
AATCAGAAAT CAGTTGAAAA ATGTTTGGAC TTTGTAGCTG GATTTCAGCC ATTACCTCAT	1440
CAAATTCTGC TTGTGTCATG TTGTCTAAAT CTAGTGTATG TGCATTGCCT CCTCAAAGTT	1500
CTCTATAAGA CAACTTTTAT TTGCTTTCTG AGTTCCATT TTAGAGTTAA AAAGAATATC	1560
TTTTAAGGTT ACAGTAGCCT CTAAATACTC CTTTTCAGCA TGCTCTATAT ACGCCTGTTG	1620
CTCTGCTTCG TTCTCAAAAA AGTGCTTAGC TTGGCGTTTA AAGAATGCTT TTCGCATAGC	1680
GTCCATTTC A AAATACCAG GGGCGAAAAA CAT'TCCCGTA GTGCTTTTAG AGACCGCTTC	1740
GATTTTATGG CTTTCATTCA ATTCAGGAAG TTCAATCCAA AGTAAACGGG ACAACTCATC	1800
TTTGATGGAT TTTGTCTGAC TTTCCAATAA AGAAAGGATT CTTAGGCCAT TTTCTTCGCT	1860
AA'TTCTCGC ATTTCTGCGC TAAT'TCTGTC TATACGTCTA GTTAAATTCT CATATGTTGT	1920
TTCTGTATG TTTTACCTC TGT'TCTTTG TTGGTGTGAT TTTT'TAGCTT ATTTT'TTAC	1980
TTCTAAACAT CAT'TGTCTTA ATTTCTGAT AACTCATTTT CAATTCATC ATAGCTATTG	2040
CCATATCCTC AAATGCCTGG TACTGCTCCA ACTCCTCACT AGTCAAGCTA TCGATACCGT	2100
TATAGCCCCC ACGCTCTTCT CTAACTGCT TAGCGTTCAT GTCTGTTACT GCCTTTAGTA	2160
GCAAGTTGTT CATGGTGCTA TCGCGGTGCT TTGGTGCATT AGGCCATGTT TCTATACTGT	2220
CATGCAAGGT TTTTCTTTTC GGT'TTTTCTA GCGCCCTCTG CAGACGAATT TCAGAAAGTT	2280
CCTCACGCAT TTCAAAGAAT GCTTTGACTA GGT'TTAGTTT GAATTGCCGT ACTGTTTCGG	2340
TATTCTTTAA ATAAGTGATC AGAAAAGTAG CCTGTTGCTC GTTCAGAATA TAGGATTTT	2400
TAGGTTGTCC TCTAGTATCT AATT'TATGGA TTTTAAATCC AAGTATTCCC AACTCTTCAA	2460
AGTCAGCCTT ATTTTCTCTT ATTAAGCGCG TGATAGTGTG GTGTGTACT TCAGCACATT	2520
CAGCGATGAT CTCGCTTGTG GTGTACGGCT CTTTCTTACC GTCCATGTAA ACTAGTTCCA	2580

1237

TTACGGTTCT ACCTCCTGTA TAAATCTGGT TAGCTTACTT TTAAATTGCC TCCTCTAGCC	2640
TCTTTTTHAG CCTCTAAAAC GGCTTTGGCT AGTGGTTAAT ATTATTTACC ACTTGTCCTCT	2700
ATAAACGTGT TAGAGGCCTT TATAACGACT TGTATCGCTG TATCGATATC CTCCGTGGAA	2760
TAGTAGATTT ATTTTCTAAT ATCATTCAAG ACTTGTTTAA CCCATTTCTT GAAAGAAATA	2820
AAATTACATC TTCTTTATCC TTGGCATCTG CTTTGTCTGA GACAAATTAG AATGTCAATA	2880
CTTGG	2885

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

TATCAATCCT TTCCATTAT AGGAGCAACA GAGTGGGAGT AGTCATCTAA GGAATAATTT	60
ATGTATTTTT ACGAGTCAGT ATCTGGGAT ACTGGTTTTT ACTTTTCTAG ACTTTTGAC	120
TACTTGTTAA AACTGGGATA ATTTTCGACT GTTTAACAGT TATTATGCAA AGTCTAAAAG	180
ATTAGAATTG TCAAAACAAT CCGTCTAGGC TTGATTTTAT CCTTTATTTA CTATAAAATG	240
AGAAGGAAAA ATGTCAAAC TTTATATTGC AAATAGGAGA AATCATGACA AAAACATTAA	300
AACGTCCTGA GGTTTTATCA CCTGCAGGGA CTTTAGAGAA GCTAAAGGTA GCTGTTCACT	360
ATGGAGCAGA TGCTGTCTTT ATCGGTGGTC AGGCCTATGG TCTTCGTAGC CGTGCGGGAA	420
ACTTTACTTT CGAACAGATG GAAGAAGGCG TGCAGTTTGC GGCCAAGTAT GGTGCCAAGG	480
TCTATGTAGC GGCTAATATG GTTATGCACG AAGGAAATGA AGCTGGTGCT GGTGAGTGGT	540
TCCGTAAACT GCGTGATATC GGGATTGCAG CAGTTATCGT ATCTGACCCA GCCTTGATTA	600
TGATTGCAGT GACTGAAGCA CCAGGCCTTG AAATCCACCT TTCTACCCAA GCCAGTGCCA	660
CTAACTATGA AACCCTTGAG TTCTGGAAAG AGCTAGGCTT GACTCGTGTC GTTTTAGCGC	720
GTGAGGTTTC AATGGAAGAA TTAGCTGAGA TCCGCAAACG TACAGATGTT GAAATTGAAG	780
CCTTTGTCCA TGGAGCTATG TGATTTTCAT ACTCTGGACG TTGTACTCTT TCAAACCACA	840
TGAGTATGCG TGATGCCAAC CGTGGTGGAT GTTCTCAGTC ATGCCGTTGG AAATACGACC	900
TTTACGATAT GCCATTTGGG AAAGAACGTA AGAGTTTGCA GGGTGAGATT CCAGAAGAAT	960
TTTCAATGTC AGCCGTTGAY ATGTCTATGA TTGACCACAT TCcAGATATG ATTGAAAATG	1020

1238						
GTGTGGACAG	TCTAAAAATC	GAAGGACGTA	TGrAGTCTAT	TCACTAyGTA	TCAACAGTAA	1080
CCAACTGC	CAAGGCGGCT	GTGGATGCCT	ATCTTGAAAG	TCCTGAAAAG	TTTGAAGCTA	1140
TCAAACAAGA	CTTGGTGGAC	GAGATGTGGA	AGGTTGCCCA	ACGTGAACTG	GCTACAGGAT	1200
TTTACTATGG	TACACCATCT	GAAAATGAGC	AGTTGTTTGG	TGCTCGTCGT	AAAATCCCTG	1260
AGTACAAGTT	TGTCGCTGAA	GTGGTTTCTT	ATGATGATGC	GGCACAACAA	GCAACTATTC	1320
GTCAACGAAA	CGTCATTAA	GAAGGGGACC	AAGTTGAGTT	TTATGGTCCA	GGTTTCCGTC	1380
ATTTTGAAAC	CTATATTGAA	GATTTGCATG	ATGCTAAAGG	CAATAAAATC	GACCGCGCTC	1440
CAAATCCAAT	GGAAC TATTG	ACTATTAAAG	TCCCACAACC	TGTTC AATCA	GGAGACATGG	1500
TTCGAGCTCT	TAAAGAGGGG	CTTATCAATC	TTTATAAGGA	AGATGGAACC	AGCGTCACAG	1560
TTCGTGCTTA	ATGTAGTTGT	TTAGTTTTAA	AAACTATGC	AAAGCTCCAT	ATACAACACT	1620
TAAACGAGAT	TAAAGAATGG	CGAAATCCCT	TGATGCGCAA	GAGATTAGCT	GTCTTTTTTA	1680
TTTTTTAAGT	GATAAAGTCG	GAGTTTAGGC	ATCAAAGCCT	ATCAAATTAA	ACAAAGAAGC	1740
GATGTCTTAG	ATATTTTGAA	AAAAATTAAT	AAGCAGAAAA	CTCTCTATTA	TTTTGTTGTA	1800
GAGAGTTTTT	TGTTAATAAA	ATTTCACAAA	ATGACATTTA	TATATTGCAT	TAAGTTAGAT	1860
ATATGATATA	ATATTGTTAA	AAAGAGGCGC	AACTTTTTTA	AATTAATGAG	AATCAAAGAG	1920
AAAACCAATA	ATATTAATGG	AGGAATAAAA	AATGTAAGTA	AGCATTATGG	TCATTCAATC	1980
ATTCTCAAAG	ATATAAATTT	TGCACTTAAC	AAGGGTGAAA	TTGTTGGTCT	AGCAGGGAGA	2040
AATGGAGTTG	GTAAGAGTAC	GTTGATGAAA	ATTCTTGTTC	AGAATAATCA	ACCGACTTCA	2100
GGTAATATTA	TAAGCAGTGA	TAATGTTGGG	TATTTAATCG	AAGAACCAAA	ATTATTTTTTA	2160
TCTAAAACAG	GTTTAGAGAA	TTTAAAATAT	TTGTCAAAT T	TATATGGTGT	TGACTACAAT	2220
CAAGAAAGAT	TTAGATGTTT	GATCCAAGAG	TTAGATTTGA	CTCAGTCTAT	TAATAAAAAA	2280
GTAAAGACCT	ATTCTTTGGG	TACAAAACAA	AAATTAGCTT	TGCTTCTAAC	TCTCGTTACG	2340
GAACCTGATA	TATTGATTTT	AGATGAACCG	ACTAATGGTT	TAGATATTGA	ATCATCACAA	2400
ATAGTTT TAG	CGGT TCTAAA	AAAATTAGCT	TTACATGAAA	ATGTGGGAAT	TTTAATATCG	2460
AGTCATAAAT	TAGAAGACAT	TGAAGAAATT	TGTGAGAGAG	TTCTTTTCTT	GGAGAACGGG	2520
CTTTTGACAT	TTCAAAAAGT	AGGAAAAGAT	AGTCATAATT	TCTTGTTTGA	GATAGCTTTT	2580
TCATCAGCTA	CAGATAGAGA	CATTTTCATT	ACCAAACAAG	AATTTTGGGA	TATTGTTTAG	2640
GAAGAGGGAT	TGAGAATTAC	TATGTCTGGG	AATATTCAAA	ATAGTGAGCT	TTTTAAATTT	2700
TTTAACGAAA	ACTCTATTAA	AGTAGTTGAT	TTTGAAACTA	AAAAAGAGAC	GCTTAAAGAT	2760
ATTTACCTAA	ATCGTTCAAA	ATAAAGGAAG	GTTATAATCA	TGAAATTAAA	TAAACAGAAG	2820

1239

AATCGGATGA TTTACGTCTT GTCTAATTTT CTATATGCTA TCTCAGTTTC CATTATTTAT	2880
GCTTTGAATG GCATTGTGTT ACTAGTCATA GTAAGTAAAT TGGGTATTCC AGGTGATTTA	2940
GGATTAAATT TTATAGTAGC TATTGTAGTC AATACAATTT TGTTAGTCCT GTTTTATTTT	3000
CTATTATCTT ACATTTTCTA TTTATACAAA TTGAAAAGTG GCTTGGTATw TGGTATTTTA	3060
GTAGCTTTAC TACTCTTTAT CTCTAATATA TTAAATACGA TGATGATGAA TACTAGTAAT	3120
GATTTGTTTA TCAAAGCAAT TGAA	3144

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TACGGTATTA TTTTAAAGGA GAAAGAATCA TGAAAATCAA AAAATGGCTT GGTCTAGCAG	60
CCCTTGCTAC AGTCGCAGGT TTGGCTCTTG CAGCTTGCGG AAAGTCAGAA AAGAAAGCAG	120
ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG CGGTTCTGAA GAAAAACGTT	180
GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC CTTGGAATTT ACAGAGTTCA	240
CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA AGTAGATTTG AACGCTTTCC	300
AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG AAAAGACCTT GTAGCGATTG	360
CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT GAATGGAAGT GCCAACAAGT	420
ACACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC TGTACCGAAT GACGCTACAA	480
ACGAAAGCCG TCGCCTTTAT TTGCTTCAAT CAGCTGGCTT GATTAAATTG GATGTTTCTG	540
GAAGTGTCTT TGCAACAGTT GCCAACATCA AAGAAAATCC AAAGAACTTG AAAATCACTG	600
AATTGGACGC TAGCCAAACA GCTCGTTCAT TGTCATCAGT TGACGCTGCC GTTGTAACA	660
ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC ACTTTTCAAA GAACAAGCTG	720
ATGAAAACCTC AAAACAATGG TACAACATCA TTGTTGCAAA AAAAGATTGG GAAACATCAC	780
CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA CACAGATGAC GTGAAAAAAG	840
TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG GTAATAAGAA ACAGGGAGGT	900
GGGAGAGAAA ATTCCACCTC TTGCTTTTGT ATAGAGTATA GATTGTAAAG AAGACTATTC	960
GTTCATAGAA AGGTAGAGAG AATATGGTTT TTCCTAGCGA ACAAGAACAG ATTGAAAAAT	1020

1240

TTGAAAAGGA TCATGTAGCC CAGCATTATT TTGAGGTTTT GCGTACCTTG ATTTCTAAGA	1080
AATCAGTCTT TGCCCAGCAG GTTGGACTCA AGGAAGTCGC AAATTATCTG GGTGAGATTT	1140
TCAAGCGTGT TGGAGCTGAA GTGGAGATTG ATGAGAGCTA TACAGCGCCC TTTGTCATGG	1200
CACATTTCAA GAGTTCGCGT CCAGATGCCA AGACCTTGAT TTTCTATAAC CACTATGACA	1260
CTGTGCCAGC GGATGGGGAT CAGGTCTGGA CAGAGGATCC kTTTACGCTT TCGGTCCGCA	1320
ATGGCTTCAT GTATGGGCGT GGGGTTGATG ACGACAAGGG TCATATCACA GCTCGCTTGA	1380
GTGCTTTGAG AAAATATATG CAGCACCATG ATGATTTACC TGTC AATATC AGCTTTATCA	1440
TGGAGGGAGC GGAGGAATCG GCTTCAACAG ACCTAGATAA GTATTTGGAA AAGCATGCAG	1500
ACAAACTCCG TGGGGCGGAT TTGTTGGTCT GGAACAAGG GACCAAAAAT GCCTTGGAAC	1560
AGCTGGAAT TTCTGGTGGC AATAAGGGGA TTGTGACCTT TGATGCCAAG GTAAAAAGCG	1620
CTGATGTGGA TATCCACTCG AGTTATGGTG GTGTTGTGGA ATCAGCTCCT TGGTATCTCC	1680
TCCAAGCCTT ACAGTCTCTT CGTGCTGCGG ATGGCCGTAT CTTGGTTGAA GGCTTGTACG	1740
AAGAAGTACA AGAGCCCAAT GAACGAGAAA TGGCCTTGCT AGAAACTTAT GGTCAACGAA	1800
ACCCAGAGGA AGTTAGTCGG ATTTATGGAT TGGAGTTGCC TCTCTTACAG GAGGAGCGGA	1860
TGGCCTTTCT AAAACGTTTC TTTTTCGATC CAGCGCTTAA TATCGAAGGA ATCCAGTCTG	1920
GTTATCAAGG TCAGGGTGTT AAGACTATTT TACCTGCAGA AGCCAGTGCC AAGCTAGAGG	1980
TTCTGCTGGT TCCGGGCCA GAACCGCATG ATGTTCTGGA AAAAATTCGG AACAGCTAG	2040
ACAAAAATGG CTTTGATAAG GTAGAATTAT ACTATACCTT GGGAGAGATG AGCTATCGAA	2100
GCGATATGAG CGCACCAGCC ATCTCTCAATG TGATCGAGTT GGCCAAGAAA TTCTATCCAC	2160
AGGGCGTTTC AGTCTTGCCG ACGACAGCGG GGACAGGACC TATGCATACG GTCTTTGATG	2220
CCCTAGAGGT ACCAATGGTT GCATTGGGTC TAGGAAATGC CAATAGCCGA GACCACGGTG	2280
GAGATGAAAA TGTGCGAATC GCTGATTATT ACACCCATAT CGAATTAGTA GAGGAGCTGA	2340
TTAGAAGCTA TGAGTAGAGA TATTATCAAG TTAGATCAGA TCGATGTGAC TTTTCACCA	2400
AAGAAGAGAA CCATCACAGC GGTAAAGGAT GTGACCATT CACATCCAAGA AGGGGATATC	2460
TACGGAATCG TTGGATATTC TGGAGCAGGA AAATCAACCC TTGTACGGGT GATTAATCTC	2520
TTGCAAAAAC CATCTGCAGG GAAAATTACC ATTGACGACG ATGTGATTTT TGACGGCAAG	2580
GTGACCTTGA CGGCAGAGCA GTTGCGTCGT AAACGTCAAG ATATCGGAAT GATTTTCCAG	2640
CATTTTAACC TGATGAGCCA AAAGACAGCA GAGGAGAATG TAGCCTTTGC CCTTAAACAC	2700
TCTGAACTCA GCAAGGAAGA AAAGAAGGCT AAAGTAGCTA AGTTGTTGGA CTGCGTTGGT	2760
TTGGCAGATC GTGCTGAAAA CTACCCTTCA CAACTATCTG GAGGGCAAAA ACAGCGTGCTG	2820

1241

GCAATTGCGC GTGCCTTGGC CAATGATCCA AAAATCTTGA TTTCAGACGA GTCAACTTCT	2880
GCCCTTGATC CGAAGACAAC CAAGCAGATT TTGGCCTTGT TGCAAGATTT GAACCAAAAA	2940
TTAGGCTTGA CTGTTGTCTT GATTACGCAT GAAATGCAGA TTGTCAAAGA CATTGCCAAC	3000
CGTGTTGCAG TTATGCAGGA TGGGCATTGT ATTGAAGAGG GTAGTGTGCT TGAAATCTTC	3060
TCAAACCCTA AACAACTTT GACTCAAGAC TTTATCTCAA CAGCTACAGG TATTGACGAA	3120
GCCATGGTCA AAATCGAGAA GCAAGAAATC GTGGAACACT TGTCTGAAAA CAGTCTCTTG	3180
GTGCAACTCA AGTACGCTGG AGCTTCAACA GACGAGCCAC TTTTGAATGA ATTGTACAAG	3240
CATTACCAAG TAATGGCTAA TATTCTCTAT GGAATATCG AAATTCTCGA TGGTACTCCT	3300
GTTGGAGAAT TGGTGGTGGT TTTGTCAGGT GAAAAAGCAG CGTTGGCAGG TGCCCAAGAA	3360
GCCATTCGTC AAGCAGGTGT ACAACTAAAA GTATTGAAGG GAGTACAGTA AGATGGAATC	3420
ATTGATTCAA ACCTATTTAC CAAATGTCTA TAAGATGGGT TGGGCTGGTC AGGCAGGCTG	3480
GGGAACGGCT ATCTACTTAA CTCTTTATAT GACAGTTCTT TCCTTCATTA TCGGAGGCTT	3540
CTTGGGGCTA GTGGCAGGTC TCTTCTCGT CTTGACAGCG CCAGGTGGTG TCTTGAGAA	3600
TAAAGTCGTA TTCTGGATTT TAGACAAAAT TACCTCAATT TTTCGTGCGG TTCCCTTTAT	3660
CATCCTCTTG GCAATCTTGT CACCACTTTC TCACTTGATT GTTAAACAA GTATCGGGCC	3720
AAATGCAGCC CTGTCCAC TTTCTTTTGC AGTCTTTGCC TTCTGG	3766

(2) INFORMATION FOR SEQ ID NO: 226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

TGTTGCTGAG TTAATCGGTA CGTTCATGTT TGTATTCGTC GGGACAGGAG CTGTTGTTTT	60
TGGAAATGGT CTGATGGCC TTGGTCACCT TGAATCGCC TTGCGCTTGT GTTTGGCAAT	120
CGTGGTGGCA GCCTACTCAA TCGGAAGTGT TTCAGGTGCT CACTTGAACC CGGCTGTTTC	180
GATTGCTATG TTTGTAAACA AACGTTTGTC ATCTTCAGAA CTTGTAAACT ACATCCTTGG	240
TCAGGTGTT GGAGCTTCA TCGCTTCTGG CGCTGTCTTC TTCCTCTTGG CTAACCTCAGG	300
TATGTCAACT GCTAGTCTTG GTGAAAATGC CTTGGCAAAC GGTGTCACTG TCTTTGGTGG	360
TTTCTTGTTT GAAGTCATCG CAACTTTCTT GTTGTATTG GTTATCATGA CTGTGACTTC	420

1242

AGAAAGCAAG GGCAATGGCG CGATTGCTGG TTTGGTAATC GGTTCGTCAT TGATGGCGAT	480
GATTCTTGTC GGATTGAAGA TTAAGTGGACT TTCAGTAAAC CCAGCTCGTA GCTTGGCACC	540
AGCTGTCTTG GTAGGCGGCG CAACTTCAA CAAGTTTGGA TTTTCATCCT TGCACCAATC	600
GCTGGTGGAG TTCTTGACGC CCTTGTGCA AAAAATTTCC TTGGAACAGA AGAATAATTG	660
AAACTCAAAA AGCCTTGCTC CTCATCTTGA GGAACAGGGC TTTTTCGTAT GATACTCTTC	720
GAAAATCTCT TCAAACCACG TCAGCTTCAT CTTGCCGTAG TATGGTTACT GACTTCGTCA	780
GTTCTATCCA CAACCTCAAA ACAGTGTGTTT GATCTGACTT CGTCAGTTCT ATCTGCAACC	840
TCAAAACAGT GTTTTAAGCT GACTTCGTCA GTTCTATCTG CAACCTCAAA ACAGTGTGTTT	900
AAGCTGACTT CGTCAGTTCT ATCTGCAACC TCAAAACAGT GTTTTAAGCT GACTTCGTCA	960
GTTCTATCTG CAACCTCAAA ACAGTGTGTTT AAGCTGACTT CGTCAGTTCT ATCCACAACC	1020
TCAAAACAGT GTTTTGATCT GACTTCGTCA GTTCTATCCA CAACCTCAAA ACAGTGTGTTT	1080
GATCTGACTT CGTCAGTTCT ATCCACAACC TCAAAACAGT GCTTTGAGCA ACCTGCGGCT	1140
AACTTCCTAG TTTGCTCTTT GATTTTCATT GAGTATGACT TTAGCGGTG TCAATTTTCT	1200
CTGGATAAAG GTCGTGTTGG AAGAGGCGTT GTTCTGCCAA GCCCTCATAC TTAGTTCCTT	1260
GCTTACCGTA GTTGTAAGTAG GGGTCGATTG AAATGCCACC GCGCGGAGTG AATTTTCCCC	1320
AGACTTCTAA ATAGCGAGGG TCTAGCAAGT TGACCAAGTC TTTCCCGATG GTGTTGATAC	1380
AGTTTTCGTG GAAATCTCCG TGGTTTCGGT AGCTAAATAG ATATAGTTG AGGGATTTTG	1440
ACTCGACACA GAGCTTGTC GGAATGTAGG AAATATGAAT CGTCGCAAAG TCTGGCTGAG	1500
CAGTGATTTG TCCCAGCAGA GACATATCGA GGATATGGTG ACGAATGCCC TGTTCCTTAG	1560
CGATTTCTCT AGTAATTTGA ATTTGAGGT GATGACGTTG GCCGTAGGCA AAGGTGACAG	1620
CTTCGACTGT TTCATAGTGT TGCATGACCC AGAAAAGGCA GGTGTTGAA TCTTGACCAC	1680
CACTAAAGAC GACCAAGGCT AATTGACGTT TCATAGTACT CCTTCCAAA TGGGAAATGT	1740
TCAGAGCAG CAAAAGCTC CCATTAGGGA GCTAAAAAAT ACCAAATCGA GGTTTTTTTA	1800
GCGATGGCAT ATCCCAAACA TCGTAATATT CTACTTATAT AGTAAAATGA AATAAGAACA	1860
GGACAAATCG ATCAGGACAG TCAAATCGAT TTCTAACAAT GTTTTAGAAG TAGAGGTGTA	1920
CTATTCTAGT TTCAATCTAC TATAGTCTAG CATATTTTTC GAAAAATGGC AAAGGGCAAG	1980
AAAAAAGAGA CCAAAGAAAG TACTTGGTCT CTCGTTTGAT TAGCTCAATT CAGCAATGAT	2040
GGCCTTGATT TGTTCGCTG TGTGAACACC TGCAACTTGT TTGACAACCT GGCCGTCTTT	2100
TTTGAAGAGA AGAGTTGGAA TAGACATGAT TCCAAAAGCA CGAGCTGTGT TTGGATTTTC	2160
ATCAACGTCC ATTTTAACGA TTTTCAAGAC ATCTTCTGAA AGTTCTTCAG ACAATTTGTC	2220

1243

CAAGATTGGA CCTTGCATAC GACATGGACC ACACCAAGTT GCCCAGAAGT CTACTAAGAC	2280
CAAACCGTCT TTTGTTTCTT GTTCGAATGT TGCATCTGTA ATTGCTTTTG CCATTGTATT	2340
TCTCCTTTTT TTAGTTATAT TGGCTTAAAT CTTGTTTCAT GAGATAGAAG AAGATATCTC	2400
CATAAGTCCC ATGGTAGTCC AAATTATGAC CCTTGTAAGT TAATTTTGG ACAGGGTAGT	2460
AkkCTGCGAC GCCGATAAGG CAAGCTTGT GCGAACGTTT AAAGTCTTCA TAAGACTCGG	2520

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

ACTCAGTTAG ATTTTGT TTTT CAAAAACAAC GAAGAAAAAG ACCATGTTGC TCTACTTGGA	60
AGAATTGGCT CCGAACGTGT TTATCGATAT ATTAATAAAA AATATTTAGA TTTACCGGAA	120
ACATTCGAAA ATTATAATGT TTTTGTACCA GAAGCTAATG GAAGTGGTGC CTTAGGTGAA	180
GTCTTATCAA CACCCCTAAT CGGGGAACCC CTAATCGGGC ATACAGATAC TTTTTTATCT	240
ATTGGTAATT TTTAAACAAA ATTTGAAGCC GATGCTTGTA TTAAATTTAT TAAAACTAAA	300
TTCGCTAGAG TATTATTAGG TGTTTTGAAA GTTACTCAGC ATAATTCACG CAAAACCTGG	360
TATTACGTCC CCCTCCAAGA CTTTACGGTC AATTCGGACA TTGATTGGAC ACAATCAGTG	420
ACTGATATTG ACCGCCAGCT TGATCAAAAA TATGACTTTT CCCCTGAAGA AATGCGCTTT	480
ATTGAGAATC ATGTAAGGGA GATGGATTAG AAAAGTATTT TTATTTGACA AATAGTGCTC	540
AATGATCTAA AATGACTATA TAGGATTAGG TCAGGAAGCA TACGATGCCC TGACCCTTTT	600
TGTACTTATG AGATGAGAAA GTCATTTGTT AGATAAATTG ACTCGTTAGC AAACGTTCAA	660
AAAAGGAAAA CTTATGCCAG TAGAAATTAA AACCCTAAA GAAATTCATC CTAAAATCTA	720
TGCCTACACC ACACCGACAG TAACCAGTAA TGAAGGCTGG ATTAAGATTG GGTATACAGA	780
ACGTGATGTC ACACAACGTA TCAAGGAGCA AACGCATACA GCTCATATAG CTACAGATGT	840
CTTATGGACT GGTGATGCAG CTTATACAGA AGAGCCTGAT AAGGGGAAAA CTTTCAAGGA	900
CCATGATTTT CACCATTTC TTTCTTTCCA TGATGTAGAA CGTCGTCCCA AGACGGAATG	960
GTTCTATTTT AATGGAACTC CTGAAAAATC AAAAAATCTT TTTGATAAGT TTGTTTCAGCA	1020
TGATTTGTCT GGTTATCAGC CTGGAAAAGG ACAGGACTAT ACTCTGCGAC AAGAGCAAGA	1080

1244

AGAAGCAGTT GCTAAGACAT TAGCTTATTT CCAAGAACAT GCTGGAGGCA AGTTTCTCTG	1140
GAATGCCAAG CCACGCTTTG GTAAAACCTT GTCTACCTAT GACCTAGCTC GACGGATGGA	1200
AGCTGTCAAT GTCCTAATTG TAACAAACCG CCCTGCCATT GCTAACTCAT GGTATGATGA	1260
TTTTGAAACA TTCATAGCAG GTCAAACGAC TTACAAGTTT GTTCTGAAT CAGATAGCCT	1320
TAAGAGTCGT CCAATCTTGT CACGACAAGA ATTTCTTGGT ATTTTAGCTG ACGATGTAAG	1380
ACAACTTGCT TTTATCAGTC TCCAAGACTT GAAAGGATCT GTTTATTTAG GTGGAGAGCA	1440
CGATAAACTC AAATGGGTAA CTGATCTGCA TTGGGACTTG TTGGTTATTG ACGAGGCTCA	1500
TGAAGGAGTT GATACCTTCA AGACTGACCA AGCCTTTAAT AAGATTCGAC GAAATTTTAC	1560
TCTGCATTTG TCAGGTACAT CATTTAAAGC ATTTGGCTAA GGAGATTTTA CAGAGGAACA	1620
AATCTACAAC TGGTCTTATG CTGATGAGCA GGCTGCTAAG TATTCGTGGT CTCTGAGCA	1680
AGAAGAGGAA AATCCTTATG AAAGCTTGCC TCAGTTGAAT CTCTTTACCT ATCAAATGTC	1740
TCAGATGATT GCGGAAAAGT TAGAAAAAGG CGCTCAGATC GATGGTGAAA ATATTGACTA	1800
TGTTTTTGAC TTAAGTGAAT TTTTCGCTAC AGATGATAAA GGGAAATTTA TTCATGAGCA	1860
TGATGTCAGA AATTGGTTAG ATACTCTATC AAGCAATGAA AAATATCCAT TTTCAACCAA	1920
AGAACTCCGT AATGAACTCA AGCATACTTT TTGGCTTTTA GAACGTGTCG CTTCGGCCAA	1980
AGCATTAATA GCCCTACTAG AAGAACACCC AATCTATGAA AACTATGAGA TCGTTCTAGC	2040
TGCTGGTGAC GGACGTATGT CCGAAGAAGA CGATAAAGTC AACTCAAAT CCTTGACTT	2100
GGTTAGAAAA GCGATAGCAG AGAATGACAA AACCATTACC CTATCCGTTG GTCAGCTGAC	2160
GACAGGTGTC ACTATCCCTG AATGGACAGG TGTATTGATG TTATCAAATT TGAAATCACC	2220
AGCTCTTTAT ATGCAGGCCG CCTTCCGTGC TCAAAATCCT TACTCATGGA GCGATAACAA	2280
AGGAAATCAC TTTGCAAAAG AAAGAGCCTA TGTATTTGAC TTTGCGCCGG AAAGAACCTT	2340
GATTCTCTTT GATGAGTTTG CCAACAACCT ATTGCTTGTA ACTGCAGCTG GTAGAGGAAC	2400
TTCAGCTACA CGCGAAGAAA ATATTAGAGA ATTATTAAAC TTCTTTCCAA TTATTGCCAA	2460
AGACCGTGCT GGTAAAGATG TTGAAATGA TGCAAAGGCA GTTCTAACCA CTCCTCGCCA	2520
GATAAAAGCT AGAGAAGTTC TTAAACGAGG TTTTATGTCC AATCTCTTAT TTGATAATAT	2580
TAGTGGTATT TTCCAAGCAA GTCAAACAGT TTTAGATATT TTAAATGAGC TGCCAGTTGA	2640
AAAGGAAGGG AAGGTACAAG ATAGTTCTGA TTTATTAGAT TTTTCAGATG TTACAGTCGA	2700
TGATGAGGGA AATGCAGTAG TAGACCATGA AATGTAGTT AATCAGCAAA TGCGACTTTT	2760
TGGTGAAAAA GTTTATGGAC TTGGTGAATC TGTGCTGAG TTAGTCACAA AAGATGAGGA	2820
ACGAACCTCA AAACAGCTGG TCAATGACTT GAGTAAGACC GTTCTTCAG TGATTGTAGA	2880

1245

GGAATTGAAA GCAGATTATT CTCTAAAAAC AAGGGAAACT GAGCAAATTA AGAAACAAAT	2940
TACAGCAACA CTTGAGAATG AAATTCGAAA AAATGATATC GAAAGAAAAA TTTCTGAAGC	3000
TCATATCAAG CAAGAGTTGC AACAGCAGCT CAAAGAAGCA AATGATAAAG CGCAAAAAGA	3060
TAAGATTCAA GAAGATTTGG AAAAACGTTT AGAAGAAAAT AAACTCATTC ATAAAGAAAA	3120
ACTAGAACAA ACAC'TCAAAA AAGAAGTGG AAAAAATGCCT GAGAAATTTA TCGAACAGGT	3180
TGAGATAAAA CGTGTGGAAC AGTTGAAACA ATCAGCTCAA GATGAAATTC GTGACCATTT	3240
ACGAGGGTTT GCAAGAACAA TTCCAAGTTT TATTATGGCT TACGGTGATC AAAC'TCTAAC	3300
ACTTGATAAT TTTGATGCCT TTGTTCTCTGA ACATGTTTTT TATGAAGTAA CAGGGATTAC	3360
GATTGATCAG TTTAGATATT TGCGAGATGG TGGGCAGGAT TTTGCAGGGC ATCTCTTTGA	3420
TAAAGCAACA TTTGACGAAG CTATTCAAGA ATTTCTTCGC AAGAAAAAGG AGTTGGCGGA	3480
TTATTTTAAA GATCAAAAAG AAGACATTTT TGACTATATT CCACCGCAGA AGACCAACCA	3540
AATTTTCACT CCTAACGAG TGGTGAAGG GATGGTAGAT GATTTGGAAA AGGAAAATCC	3600
AGGGATTTTT GATGATCCAT CTAAGACTTT TATTGATTTA TATATGAAGT CAGGCCTCTA	3660
TATTGCAGAA CTTGTGAAGC GGTATATAA TAGCAATGGC TTGAAAGAGG CCTTTCCAAA	3720
TCCTGAAGAA CGCTTAAAAC ATATTTTGGA AAAGCAAGTT TATGGATTTG CTCCGTCTGA	3780
GATTATCTAT AACATTTCCA CTAATTTTAT ATTTGGCAAT CTTTCTAAAG ATATCAGTAG	3840
GAAGAATTTT GTTTTAGCAG ATACCATTCC AGCGGCTAAA GAAGGGAGCA TTCAAAAGTT	3900
GGTTGATTCC TATTTTGAAA ATAATTAAAA AGAAGGCCGA GTCAAAATTC TTTGAAATCA	3960
GAAAAAACGC ATAATATTGA GTGCTTTTGT ACTGCCCCC AAAAGTTAGA CAGAAAAAT	4020
CTAACTTTTG GGGGCAGTT CAGACAATCC TTGGTATTAT GCGTTTTATT GTGGGAAGAT	4080
GTATAATGGA TTGAAATAAG ATATGAACAA ATCAATTAGG AATTTAAAGC ATTTTATAAC	4140
AACGTTT TAG AGTAATGGG GGCTATTTCA ACTTCAACCT ACTATAATAC AGAAAAAAC	4200
AACTCCCTGA TAATTCAAGG AGTTGTCTAT AGTTAAATTA GTTTT'TAGAA GCTTCTTGGA	4260
ATTCTGGGTT TTTCCATGCT TCGTCAATGA TAGCTTGTA TTTCTTAGCA GATGCTTGCA	4320
TTTTTTGAGT TTCTGCGTCG TTCAATGGGA TATTTACTGG ACGAACGATA CCATGTGCAC	4380
CAACAACAGC TGGTTGACCG ATAAAGACAT TCTCAACTCC GTATTGACCT TCTTGGAATA	4440
CTGAAAGTGG AAGTACTGCG TTTTCATCGT CAAGGATTGC TTTAGTGATA CGAGCAAGGG	4500
CTACTGCGAT ACCGTAGTAT GTTGACCTT TTTTGTGAT GATTGTGTAG GCTGCATCAC	4560
GAACACCTTC GAACAATTCA ATCAATTCAG CTTCTTGAAC ATTTTGAGTG TCTTTAAGGA	4620

1246

ATCTCTCAAG GTTACACCA GCGATGTTAG CGTGTGACCA AACAGCGAAC TCAGAGTCAC	4680
CGTGTTCCACC CATGATGTAG GCGTGCACTG AACGAGCATC CACATCCAAT TTTTCAGCAA	4740
GTGCTTGACG GAAACGAGCT GAGTCAAGTG AAGTACCTGA ACCGATAACG CGTTCCTTTAG	4800
GGAAACCAGA GAATTTCCAA GTTGAGTAAG TCAAAACGTC AACTGGGTTA GCAGCAACAA	4860
GGAAGATACC TTTGAAACCA GATTCAACAA CTTGAGTTAC GATTGATTG TTGATAGCAA	4920
GGTTTTTACC TACAAGGTCA AGACGAGTTT CACCTGGTTT TTGAGGTGCA CCTGCAGTGA	4980
TCACAACAAG GTCAGCGTCT GCACAGTCAG AGTATTGAGC TGCATAGATT TTTTtagGTG	5040
AAGTGAAGGC AAGGGCGTGA CTAAGGTCAA GCGCATCACC AACAGCTTTT TCATGCAATT	5100
GTGGAATTTC GATAATTCCA AGCTCTTGTG CAATTCCTTG GTTAACAAGT GCAAAAGCGT	5160
AAGATGAACC TACAGCACCA TCACCGACAA GGATAACTTT TTTGTGTTGT TTAGTTGAAG	5220
TCATTGTTTT AAACATCTCC TTAATTTTAT TAGGGGATTT TCCCTAGACA ACTTCATT	5278

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

ATAAGGAATC TCTAAAAAAT TTTAAGGAGA ATCTAGCAAA TGGATTTTAC ATGGGCACTG	60
AAGTATGCCA CTGAATTTTT GGGAACTGCC ATTTTGATCA TTCTTGGGAA TGGTGCACTT	120
GCCAACGTTG AACTTAAAGG TACGAAAGGT CACCAAAGTG GCTGGATCGT CATCGCTGTT	180
GGTTATGGTA TGGGGGTTAT GATCCCAGCC TTGATGTTTG GTAACGTATC TGGGAATCAC	240
ATCAACCCTG CTTTCACTCT AGGGCTTGCA GTTAGCGGTC TTTTCCCTTG GGCACAAGTG	300
GTACCTTACA TTATCGCGCA AGTCTTGGGG GCTATCTTTG GCCAAGCCTT AGTTGTGGCA	360
ACATACCGTC CATTCTACTT GAAAACGTAA AACCCAAATA ACATCTTGGG AACTTTCTCA	420
ACTATTTCAA GTATTGACCA TGGTACAAAA GAAAGTCGCT ATGCAGCAAC TGTCAATGGT	480
TTGATTAATG AGTTTGTTGG TTCATTGTGT TTGTTCTTTG CAGCTCTTGG TTTGACTAAA	540
AACCTCTTTG GTGCTGAAGT GCTTCAATTC ATGAAACAAA AGGCAACAGA AGCAGGACAA	600
ACAGTTGATT TTTCTGACTT GGCTATTAAA GCACAGGTGG CTCCACACAC TGCTTCAGGA	660
CTTCTGTGG CTCACTGGC ACTTGGATTC CTCGTTATGG CTTTGGTAAC ATCACTTGGA	720
GGACCTACAG GACCTGCCTT GAACCCAGCC CGTGACTTGG GACCACGTCT CCTTCATGCT	780

1247

TTCCTTCCCA AATCAGTTCT TGGTGAGCAT AAAGGCGATT CAAAATGGTG GTATTCTTGG	840
GTACCAGTAG TAGCACCTAT CGCAGCAGCA ATTGCGGCAG TAGCTGTATT CAAATTCCTT	900
TATCTCTAAG AAATAGCTCC TTTAACATTT GAGTGAGCAC CATCTATAAG TAAGAGAGGA	960
TCAGACTGGk TCTCTCTTTT kGATTTTtaG GGAAATGAAA GAacTCTAAA CAAACTCCTC	1020
TCCAGCAGTG GTTTAGAAGT CTCAGTGGGC TATTCCAGCT TCAATGGACT ATAGTAGGTT	1080
GCAGTTGAAA TAATAGACCC TTGTTTCTAA AACATTGTGA GAAATTGGTT TGAATTCTCC	1140
AATCAAATTG TGCAGTTTTC ATTCTACTAT ATATTATCGG AATATTATCG GAGATGGGTT	1200
CCCTATCTTG TAAGTCTGCT TTATAGTGGG TTGAAGTTGG AATAGTCCTC CCTTCTTTCT	1260
CAAACATTGT GAGGAATTGA TTTACCTTCC TCAACAAAAT GTTCAGTTTC TATTTCATTT	1320
TACTATAAAA TAAGCGATTA GGGGGGCTAT TCTTCGACCT ACATTGACTC TGCTGAGTCC	1380
TATGATTGTT ATCGTTTTAT CTGCAATTTT ATACTCAATG AAAATCAAAG GGCAAACATA	1440
GAAGCTAGCC GCAGGTGTT CAAAACACAG TTTTGAGGTT GTATAGTAGA TTGAAACTAG	1500
AATAGTACAC ATCTACTTCT AAAACATTGT TAGAAATCGA TTTGACTGTC CTGAACGATT	1560
TGCCCTATTC TTGTTTCATT TTAATATATA AACCAGAGAC TGTTTACATT TTCAGCAAGT	1620
GAGTGGATGG ATAATGCTGA AAACCTCTTG AAGGATAAGT CTATTTAGTA CTTTCTATTA	1680
ATTAGTTAAA TTTTACCAA GAATAATTCA CAAAACGTT GTAAAACACT TGCAATTTAG	1740
CTGAAATTTG ATAAAATAGT AAGGAAAGTT AGACTGTATT GCCTACTGTC TATCTATAAA	1800
ATATATTTTA TTGGAGGCTT TTAATCAAAT GGCAAAAGAA AAATACGATC GTAGTAAACC	1860
ACACGTAAC ATTGGTACTA TCGGACACGT TGACCACGGT AAAACTACCC TAACTGCAGC	1920
TATCACAACCT GTTTTGGCAC G	1941

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATTTGAAGAA ATTGAAGAAA TCGTAGCCCC TACAGATGGT GAATTTTGG GGAAGTTTT	60
ACTTGGAACCT GGGGTAGTTC TCTTAATTGG AGTAGCCTGT TGTTAAAAAG ATAGGGAGTG	120
ATAATCATGC AAGATAACTT TTTATTTGAG GAAATTGAAG AAATTCAGT ACCAGTTAAT	180

1248

GATTTTTCAG CTGGACTTGC AACAGGTATC GGATTTGGTT TAGCAATCCT TGCTCTTGCT	240
GGTTGTTGAA GTTTGTTTCAT TTACTAACAT CAAGCTTTTT CAATTTTCATT TTAGACAGTC	300
ATTTAAATTT TCCGTATTAG TCTTGCAGCA AGAGATTAAT AGAATTAGTC ATTATTTTAT	360
TGATTGCGGA CTGAGGGACT AGAGTATGTT TTACTTAACC CCTCTTTTAT TTATTAAAGG	420
TTAGGTTTGT TATGAGAATT GTTGATAAGA TTAAGATATT ACCTACTCCT TATGAGGGAC	480
ACTATCATTT ATATATACCA TCCAGTAAGA AACATGTATT AGTTGGGAAA CAGGAAAAAA	540
ATGGTTAGAG CAACTAATAG GTCAAGAATT TACCATATCG GACTTATTAG TGTTAGTAGG	600
GAAGAAATAT TTTTAAAATA TCTTGGGACT TTAATATAAC ATTATCTGAA AAATTAAACT	660
ATAAAAGATT TAATAAGAAT TTTGAAAAAA TCCTATCTTG TTGTCATTAT ATTTGCAACG	720
ATACATGAAA TTAGTCATGC AATAATTGCT AATAA	755

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CCAGAAAAAC CGTAGTGAG CTCGTGGAAC AGTGGAATTG ATTTTCCAAA AAGAATACAA	60
TAAATTTTCA AGTATCTCAA AGAGGGAGGC ATAAGATGTC AGATGCATTT ACAGATGTAG	120
CCAAGATGAA AAAAATCAAA GAAGAAATCA AGGCACATGA GGGACAAGTC GTAGAAATGA	180
CTTTGGAGAA TGGTCGTAAG CGCCAAAAAA ATAGATTGGG TAAGCTAATT GAAGTTTATC	240
CATCTCTATT TATTGTGGAG TTTGGGGATG TGAAGGAGA TAAACAAGTT AATGTTTACG	300
TTGAATCCTT TACTTACTCA GATATTCTTA CAGAAAAGAA TTTGATTCAT TATCTTGACT	360
AAAGTGAGAA ATTTTCTCAC TTTTCTTTT TTCTCCGAAT AATTAGGTG AAGGCAATCA	420
TCGCTTTATA TTATTTTTC AAGAGGAAGA ATGAAAATTT TACCGTTTAT AGCAAGAGGA	480
ACAAGTTATT ACTTGAAGAT GTCAGTTAAA AAGCTTGTTT CTTTTTTAGT AGTAGGATTG	540
ATGCTAGCAG CTGGTGATAG TGTCTATGCC TATTCCAGAG GAAATGGATC GATTGCGCGT	600
GGGGATGATT ATCCTGCTTA TTATAAAAAT GGGAGCCAGG AGATTGATCA GTGGCGCATG	660
TATTCTCGTC AGTGTACTTC TTTTGTAGCC TTTCTTTTGA GTAATGTCAA TGGTTTGTAA	720
ATTCCGGCAG CTTATGAAA TGCGAATGAA TGGGGACATC GTGCTCGTCG GGAAGGTTAT	780
CGTGTAGATA ATACACCGAC GATTGGTTCC ATTACTTGGT CTACTGCAGG AACTTATGGT	840

1249

CATGTTGCCT GGGTGTCAAA TGTAATGGGA GATCAGATTG AGATTGAGGA ATATAACTAT	900
GGTTATACAG AATCCTATAA TAAACGAGTT ATAAAAGCAA ACACGATGAC AGGATTTATT	960
CATTTTAAAG ATTTGGATGG TGGCAGTGTT GGAATAGTC AATCCTCAAC TTCAACAGGC	1020
GGAATCATT ATTTTAAGAC CAAGTCTGCT ATTAAACTG AACCTCTAGC TAGCGGAACT	1080
GTGATTGATT ACTATTATCC TGGGGAGAAG GTTCATTATG ATCAGATACT TGAAAAAGAC	1140
GGCTATAAGT GGTGAGTTA TACTGCCTAT AATGGAAGCT ATCGTTATGT TCAATTGGAG	1200
GCTGTGAATA AAAATCCTCT AGGTAAtTCT GTTCTTTCTT CAACAGGTGG AACTCATTAT	1260
TTTAAGACCA AGTCTGCTAT CAAACTGAA CCCCTAGTTA GTGCAACTGT GATTGATTAC	1320
TATTATCCTG GAGAGAAGGT TCATTATGAT CAAATTCTCG AAAAAGACGG CTACAAGTGG	1380
TTGAGTTATA CGGCTTATAA CGGAAGTCGT CGCTATATAC AGCTAGAGGG AGTGACTTCT	1440
TCACAAAATT ATCAGAATCA ATCAGGAAAC ATCTCTAGCT ATG	1483

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1027 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CCCGGAAAC AAGTTAAAGT TGAAGTTGGT CAAGCAGTTT ACGTTGAAAA ATTGAACGTT	60
GAAGCTGGTC AAGAAGTTAC TTTTAACGAA TTGTCTTGT TGGTGGTGAA AACACTGTTG	120
TCGGAACTCC ACTTGTGCT GGAGCTACTG TAGTTGGAAC TGTTGAAAAA CAAGGAAAC	180
AAAAGAAAGT GGTACTTAC AAGTACAAAC CTAAAAAAGG TAGCCACCGT AAACAAGGTC	240
ACCGTCAACC ATATACAAA GTTGTCATCA ACGCAATCAA CGCTTAATTT TAAGGAGAAC	300
ACATGATACA GGCAGTCTTT GAGAGAGCCG AAGATGGCGA GCTGAGGAGT GCGGAAATTA	360
CTGGACACGC CGAGAGTGGC GAATACGGCT TAGATGTCGT GTGTGCATCG GTTTCTACGC	420
TTGCCATTAA CTTTATCAAT TCTATTGAGA AATTGTCAGG CTATGAACCA ATCCTAGAAT	480
TAAACGAAGA TGAAGGTGGC TATCTGATGG TTGAAATACC AAAAGATCTT CCTTCACACC	540
AGAGAGAAAT GACCCAGTTA TTCCTTGAAT CATTTTCTT AGGTATGGCA AACTTATCGG	600
AGAACTATTC TGAGTTCGTC CAAACCAGAG TTATCACAGA AAATAACAC GGAGGAAAC	660
ATTATGTTAA AAATGACTCT TAACAACCTG CAACTTTTCG CCCACAAAAA AGGTGGAGGT	720

1250

TCTACATCAA	ACGGACGTGA	TTCACAAGCA	AAACGTCTTG	GAGCTAAAGC	AGCTGACGGA	780
CAAACGTGTA	CAGGTGGATC	AATCCTTTAC	CGTCAACGTG	GTACACACAT	CTATCCAGGT	840
GTAAACGTTG	GTCGTGGTGG	AGATGATACT	TTGTTCGCTA	AAGTTGAAGG	CGTAGTACGC	900
TTTGAACGTA	AAGGACGCGA	TAAAAACAA	GTGCTGTTT	ACCCAATCGC	TAAATAAAAA	960
GGTCCATTGA	ACCTTTTATC	CCGAACCTTG	AAATGTAGAG	GTGAGGAAGC	TAGAAACAGC	1020
TTAAAAAT						1027

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1990 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CGGTTCAAAT	GGTGCAGGTA	AATCTACGTT	AATTAATTCT	ATTGTAGGTT	TTCAAGAGAT	60
TTATTTAGGA	GAAATAGAGT	ATTGTGATAA	AGATTTGATA	GTTAGTTCTC	AACCTTTTGC	120
TCATTTAGGC	TTTACTCCTC	AAACCACAGT	AATTGATTTT	TATACTACTG	TGAAGGACAA	180
TGTAATATTG	GGGCTGAACC	TTGCTGGAAA	GTTTGGGAAA	AATGCTGAGA	AGTTGTGTCA	240
AATAGCCTTA	GAAATTGTTG	GGTTAGCTGA	TAAAAAAAAT	AATTTGGTAG	AAACATTGTC	300
AGGTGGACAA	CTGCAACGCG	TCCAGATTGC	TAGAGCAATA	GCTCATAATC	CAGATTTTTA	360
TATTTTAGAT	GAACCTACCG	TTGGTTTAGA	TACTGAATCT	GCCGAAAAAT	TTTAAATGTA	420
TTTAAAAGAT	AAGAGTTTGG	AAGGAAAAAC	TATTATCATA	TCTTCACATG	ACATAAATCT	480
ACTCGAAAAG	TTTTGTAAAA	AAATACTTTT	TTTACAAAAT	GGCTCCATAT	CATTTTTTTG	540
TGATATGCGT	GACTTTGTAG	ATAATTCAAC	TATCAAATTA	AATTTTTTCAA	TGCAGAATAG	600
AATTTCTAGA	TATCAAATTG	AATTTTTAGA	AAATTTTAGA	TTTAAAGTTC	ACATCGAAGA	660
TAATGATAGT	TTTACAATAG	AAGTCCCTAT	AGAAGAAAAG	ATCTTAGATG	TTATCAATGA	720
GGTAGGAAAA	GCATGTGAAA	TTAAAACTT	TTCAACAAGT	AAATTAACCT	TACAAGAAAG	780
TTATTTGCAA	AGAATAGGAG	GAGAAAAATG	AAGGCTGATC	AATTAAGGCA	CAAATCGGAC	840
TTAGGTTTAA	GAGGTCTAGC	GATTATTGCT	AAAAATGAGA	TTATTGCTTT	TTTTAGAAGT	900
AAAGGTTTAA	TTATTCTCTCA	GTTTCTACAA	CCAATCTTAT	ATGTTGTTTT	TATAATAATA	960
GGATTAAATT	CTTCGATAAA	GAACATTGAG	TTTAATGATA	TAAAAACCTC	TTATGCAGAA	1020
TATACAATCA	TTGGTGTTAT	AGCTTTATTG	ATAATCGGGC	AGATGACTCA	AGTTATTTAT	1080

1251

AGGGTGACAA TAGATAAAAA ATATGGGCTA CTTGCTCTTA AGTTATGCAG TGGAGTTCGT	1140
CCTTTATATT ATATTTTAGG GATGAGTATC TATTCTATAT TAGGGTTGAT AGTCAAGAA	1200
ATTATTATAT ATATAATTAC GTTAGCGTTT GAGATAAATA TCGCAATGGA TAGATTTTTT	1260
TATACAGTTT TGTATCTAT TGTGTTTTTA TTATTTGGG ACTCCCTTGC AATTTACTT	1320
ACAATGTTTA TCAATGATTA CAGAAGACGT GATATTGTAA TACGTTTGT ACTAACACCG	1380
CTTGTTTTTA CAGCTCCTGT TTTCTACTTA ATAGATTCTG CTCCTAGTAT TGTGAGATGG	1440
ATTGGTCAGT TAAATCCCTT AACTTATCAA TTAATATTT TGAGAACTT TTATTTTAA	1500
AATTCAACAA CTTTGAATT AGTTTCTTA TTGTTAACAT CATTACTTGT CCTTATATCT	1560
GTATCTTTTA TTATACCAA GATAAAATTG ATACTGATAG AAAGATAAAA GTTGGGTCAT	1620
CCAACTTTTT TGTGCTCTCC CGAAAACCAC TAGCTATGCT AGTGGTTCCA TAGAGCTTTT	1680
AGCGTGGTAA CAAAAAGAAC CTCCTAAAAT GATAAGATAG AAGTGGTTTC TCCGCCACTA	1740
CAACATATCA TACAGGAGGT ACCTCATGAG AGAGGATAAT CAAAGTTTAT CACATACCAC	1800
ATGGAATTGT AAATATCATA TTGTTTTTGC ACCCAAATAT CGTCGTCAAA TCATTTATGG	1860
CAGATACAAA GCTAGTATCG GAAGAATCAT ACGTGACTTA TGTGAGCGTA AGGGTGTAAT	1920
AATCCATGAA GCGAATGCTT GTTCAGACCA TATTCACATG CTTATCAGTA TTCCTCCGAA	1980
ACTTAGTGTT	1990

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GAACATATATT GCATATATTT C'TAGCAATGA TCATGGCGAA TCTTGGTCTG CACCAACTTT	60
ATTACCTCCT ATAATGGGAC TTAATCGGAA TGCGCCATAT TTAGGTCCTG GACGTGGAAT	120
CATTGAAAGC TCAACTGGAC GTATTCTTAT TCCGTCTTAC ACTGGTAAAG AGTCTGCGTT	180
CATTTATAGT GACGATAATG GAGCATCTTG GAAAGTTAAA GTAGTGCCAC TTCCTTCTAG	240
TTGGTCAGCA GAAGCACAAT TTGTAGAATT GAGTCCAGGA GTAATTCAAG CATATATGCG	300
TACAAATAAT GGTAATAATT CATATTTAAC AAGTAAAGAC GCAGGTACTA CTTGGAGTGC	360
ACCGGAATAT TTGAAATTG TTTCAAATCC AAGTTATGGA ACACAATTAT CAATCATCAA	420

1252

TTATAGCCAA TTGATTGATG GTAAAAAGGC TGTCAATTTTA AGTACTCCAA ACTCCACAAA	480
TGGTCGTAAA CACGGACAAA TTTGGATTGG TCTAATTAAT GATGATAATA CAATTGATTG	540
GCGTTATCAT CACGACGTTG ATTATAGTAA CTATGGATAC TCATATTCAA CATTGACAGA	600
GTTACCAAAT CATGAAATTG GATTGATGTT TGA AAAAATTT GATTCATGGT CTCGTAATGA	660
ACTTCATATG AAAAATGTTG TACCATATAT AACATTTAAG ATTGAAGATC TGA AAAAGAA	720
TTAAAGCTGA AATTTGAAAA TATATAAAAA GAGGATAAAA ATTATGGTAA ATTACGGTAT	780
TGTTGGAGCT GGATATTTTG GAGCTGATTT AGCTCGCTCA ATGAACAAAA TTGAAGATGC	840
AAAAGTGGTT GCGGTATTTG ACCCAAATCA TGGAGAAGAA GTTGCTCAAG AGTTGGGATC	900
AGATGTTTTGT GCAAGTTTAG ATGAACTTGT AGCACGTGAA GATATTGATT GTGTGATCGT	960
AGCTTCACCT AGCTACCTTC ACCGTGAACC AGTTGTGAAA GCTGCTCAAC ATGGCAAACA	1020
CGTATTTTGT GAAAAGCCAA TTGCATTGTC TTAGAAGAT TGTAAGCCA TGGTTGACGC	1080
ATGTAAAGAA AATAATGTCA TCTTTATGGC TGGTCACATC ATGAACTTCT TTAACGGTGT	1140
ACACCATGCT AAAGAATTGA TTA CTCAAGG TAAATCGGT AAAGTTCTTT ATTGCCATGC	1200
TGCTCGTACA GGTGGGAAG AACAACAACC AACTGTATCA TGAAGAAAAC TTCGTCTCA	1260
ATCTGGAGGA CATTTGTACC ACCATATTCA TGAATTAGAT TGCATTCAGT TTATCATGGG	1320
AGGACTTCCT GAAAAGCGA CAATGGTAGG AGGCAATGTA TATCATAAAG GTGAAAACCT	1380
TGGTGATGAA GATGATATGC TCATTGTAAA CTAGAATAC TCTGATGATC GTTATGCTGT	1440
TTTGGAATAT GGAATGCTT TCCGTTGGGG TGAACACTAC GTCTTGATTC AAGGAACTGA	1500
AGGAGCTATC AAAGTTGACT GTTCAATAC TGGCGGTACT CTTGCTGTTA AAGGTGAAGG	1560
AGAATCACAC TTCTTAGTTC ATGAAACTCA AGAGGAAGAT GATGATCGTA CAGCTATCTA	1620
TACCGGTCGT GGTATGGATG GAGCAATTGC GTACGGTAAA CCAGGAGTAC GTTGCCCAT	1680
ATGGTTGCAA ACATGTATTG ATAAAGAAAT GGAATATCTA CATGACATCA TTAAAGGTGG	1740
AGAAATTACA GAAGAATTG AAAAAGTTCT CAATGGTGTA GCTGCTTTAG AATCAATC	1800
TACCGCTGAT GCATGTACTT TATCAGTTAA AGAAGATCGA AAAGTAAGTC TTTCAGAAAT	1860
CACAAATGCT TAACTTTTGT AAAACAGAAT AGTAAATCTT TGTCAATTATA TAATTTCTAA	1920
AGTTCTGTGA TACAATCAT TGAATAAAGA AATAGAGATG GGAAGTGGAT AATGCCCAGT	1980
CCCATTTTTT ATCAAAAAGT AATGAGATCA AAAATGTGGG AGTGTTGAAA TGAAGATTAT	2040
AGGTATCGAT ATTTGGCGGA CAACAATTAA GGCAGATTTA TACGATGAGT TTGGAACGAG	2100
TTTGAATCAT TTCAAAGAGA TAGAAACAAT TATTGACTAT GATTTGGGAA CGAATCAGAT	2160
ATTAAATCAG GTCTGTGATT TAATTGGTGA GTATACTTTA AATCATTCAA TTGATGGTGT	2220

1253

TGGGATTTC	ACTGCTGGAG	TTGTTAATGC	TAATACTGGA	GAAATCATCT	ATGCAGGCTA	2280
TACAATACCA	GGGTATATCG	GAGTAAACTT	TACTGCCGAA	ATAGAAAAAC	GTTTTGGGTT	2340
GTATACTTTT	GTGAAAAATG	ATGTTAATTG	TGCTGCATTA	GGTGAATTGT	GGAAGGGACA	2400
AGCCAAAGAT	AAGAAAAATG	TAGTAATGGT	TACTATTGGA	ACAGGTATAG	GAGGCAGTAT	2460
TATTGTCAAC	GGACAAATTG	TTAACGGATT	TAACTATACT	GCTGGTGAAG	TAGGTTATAT	2520
TCCTGTAGGT	AATTCGGATT	GGCAAAGTAA	AGCCTCAACA	ACCGCATTGA	TTCATTTATA	2580
TCAAAAAAAG	AGCTTGAAAA	CTAATCAAAC	TGGACGTACT	TTCTTCACTG	ATTTAAGATC	2640
TGGAGATAAA	GTGCTGAAG	AACTTTTGA	AATTTTGTGA	GAAAATCTAA	CAAAAGGTTT	2700
ATTAACGATT	TCTTATCTAC	TTAATCCAGA	AATTCCTCATA	TTAGGAGGTG	GGATTCTGGA	2760
TAGTAAGGAT	ATTTTGTGTAC	CTGAAATCA	AAGTCTCTTA	GCTAAAAATG	CAATGGATAA	2820
TAGGTTTTTA	CCTAAAAATC	TTGTGGCAGC	TACATTAGGA	AATGAAGCTG	GTCGTATAGG	2880
AGCTGTAAAA	AATTTCTTAG	ATAGAATTTC	TAATAAATAG	TATGTAAGAT	AAGGAGGTGT	2940
CACAATGACT	AACTCTGTAT	TTTCGACAAT	GCAAGATATT	GAGAATGTTG	CAACCGATAT	3000
TATAAAATCA	TATGATAATG	AGATTTATAC	TTATAAAGCT	GTTTCCCAAG	AAGAATTGGA	3060
AAAAGTAGAA	AAAAGTTATG	ATGAAAAAAG	TCACGAAGAA	TTAGTTTCAA	TAGAAAGCAA	3120
TTTAGAAATG	AAACAACAGA	ACCTTATTGA	TGAGGTTAAT	AAAACAATCA	AGGAAAATGA	3180
TGCAAATATT	CAGTATATTT	CATCAAGTAG	GAGAGGAGAA	TTTGTAGAAA	AAATTATTGG	3240
TAGGGTGGTA	GAAAAATATG	GCCATTAGTC	AGATGAAAAG	AATCTCTCTA	CTATTTTCTA	3300
AAAGTAGTCT	TGATGATGTT	TTAAAACTA	TTCAAGAACT	AGAGTCAGTG	CAGTTCCGTG	3360
ATTTAAAGGT	TCAGGATAAC	TGGTCAGAAG	CTCTAGAAAA	AGATGAAGTT	GTATTTCCAA	3420
CTATTCAAAT	TTTTCATACT	TCTAATTCCA	ATCATGGGGT	TATTGAGGGA	AATGATGCCT	3480
TGACTTATTT	GATGAATCAA	CAACAACATT	TAGAAGCAAC	TGTAGAGAAA	TTACAAGAAT	3540
ACCTACCGAA	AGAAAACACG	TTTAAATTAT	TGCAGCAACC	TCCGATAACT	ACCTCTTATG	3600
AAGAATTAGA	GAAATTTGGT	AAAGCTAATG	TTGCTGAGGG	TGTTCTTAAA	AAAGTGAATC	3660
ATCAAATTAA	CAGAGTTCAT	GAATTAGAAA	GACACATTCA	AAGTAATAAT	GAGGAAATAG	3720
AGCGATTAAT	AAAGTGGGAA	AAATTAGAAA	TTGTTCTCTG	GAATTTAGAA	CAATTTTCTT	3780
TCTGTAAAGG	AAAAGTCGGA	ACAATTCCAA	GGACTGAAGA	TAATCGCTTA	TACAATAGTC	3840
TTTTAGAAAA	CAATATTGAA	GTTCAGAAA	TATTTTCTAA	TGATAGAGAG	TACGGTGTG	3900
TTGTTTTCTA	TCAGTCTAGT	TACTCTATAG	ATTTTGATGA	ATACTTATTT	GAACCATTTG	3960

1254

ATTATCTAG AAAGGAATTA CCGAAGCAGC GAGTAGTAGA TTTAGATCAA GAAAACATGC	4020
AGTTAATAAC TGAAAAAGAG AATATTATCG CATCGTTGCA AGATTCAAAG AAATATTTGA	4080
TAGATTTACA ATGGCAAATA GACTATATTT TATCTATCTA TGCTCGTCAA ATCTCTAAGA	4140
ATAACTTTTT GTGCACTCCG CATCTAGTTG CATTAGAAGG ATGGATAGAA GAAACTCGTA	4200
TTTTATATTT TATAAAAGTT ATGGATGAGC ATTTTGGACA TTCTATTTAT ATTTATGAAT	4260
CGGAAACATT GACGGATAAT CAAGATGAAA TACCTATCAA ATTAACGAAT CATTCTTTAA	4320
TTGAACCATT TGAATTATTG ACAGAAATGT ATGCTCTGCC CAAATATTAT GAGAAAGATC	4380
CTACACCTGT ATTAGACCA TTTTACTTTA CATTTTTTTG AATGATGGTT GCTGATTTAG	4440
GCTATGTTTT ACTATTGTTT TTAGGAACAA TGTTAGCATT AAAAATTTTT CATCTACCTT	4500
CAGCAACTAA GAGATTTTAA AAATCTTTA ATATATTAGG GGTAGCCGTT GCAATTTGGG	4560
GTGGAATCTA TGGCTCATTT TTTGGATATG AGTTGCCATT TCATCTGATA TCTACAACCT	4620
CTGATGTCAT GACTATATTA GTAGTGCAG TTGTGTTTG GTTTATTACA GTATTTGCAG	4680
GTTTGTTAGC TTCAGGACTA CAAAAAGTAA GAATGAATAA ATATGCAGAA GCATATAATT	4740
CAGGATTTGC GTGGTGTGTT ATTCTG	4766

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

CCTTTTAGAA AAAATTAAAG AATACGACAC CATTATCATT CATCGTCATA TGAAACCAGA	60
CCCTGATGCC TTGGGAAGTC AGGTGGGATT GAAAGCCTTG CTGGAACATC ATTTCCAGA	120
AAAAACCATC AAAGCCGTCG GTTTTGATGA ACCAACTCTT ACTTGGATGG CTGAGATGGA	180
TCTTGTTGAA GATAGAGCCT ACCAAGGCGC ACTTGTCATC GTCTGTGATA CAGCTAATAC	240
TGCTCGTATC GATGATAAGC GCTATAGTCA AGGTGATTTT CTCATTAAGA TTGACCACCA	300
TCCAAATGAT GATGTATACG GTGACCTGTC TTGGGTCGAT ACTAGTTCAA GTAGCGCTAg	360
aGaTGATTAC CCTATTTGCC CAAACAACCC AACTAGCCTT GGCAGATCGC GATGCTGAGT	420
TGCTCTTTGC AGGAATTGTC GGTGATACAG GTCGCTTCCT CTACCCTTCT ACCACTGCAC	480
GGACTCTTCG CCTGGCTGCT TATTTGAGAG AACATAACTT TGACTTTGCG GCTCTCACTC	540
GCAAAATGGA CACTATGAGC TACAAAATTG CTAACTGCA AGGCTACATC TACGACCATC	600

1255

TGGAAGTGA	TGAAAATGGT	GCTGCTCGCG	TTATCCTGAG	TCAGAAAATC	TTGAAACAAT	660
ACAATATAAC	CGATGCTGAA	ACTGCGGCCA	TTGTAGGTGC	ACCTGGACGC	ATTGACAGAG	720
TGAGTCTCTG	GGGAATTTT	GTCGAACAGG	CTGATGGCCA	CTACCGAGTT	CGCTTACGCA	780
GTAAAGTCCA	TCCTATCAAT	GAAATTGCCA	AGGAGCATGA	TGGTGGAGGC	CACCCCTCTAG	840
CAAGTGGTGC	TAATTCCTAT	AGCCTAGAAG	AAAACGAAAT	CATCTACCAA	AAGTTAGAAG	900
ACTTGCTTAA	AAACTGATAA	AATACTTGCC	AAACTTTTCA	GAATCTGATA	GACTAGTATA	960
GTAACAATCT	ATGGCTCGCA	AAGAGACCAT	GGCAGAAAAG	AAATATTGCA	AAATGAAAAT	1020
AGATATCCAT	CCAGAATATC	GCCCAGTTGT	CTTCATGGAC	ACAACACTCTG	GTTACCAATT	1080
CCTTAGCGGT	TCAACAAAAC	GCTCTAACGA	AACAGTTGAG	TTCGAAGGCG	AAACTTACCC	1140
ATTGATCCGT	GTGGAAATTT	CATCAGACTC	ACACCCATTC	TACACTGGAC	GTCAAAAGTT	1200
CACTCAAGCA	GATGGACGCG	TGGATCGTTT	CAACAAAAAA	TACGGTCTCA	AATAATGATA	1260
AGAGAACAGT	TTTGGCTGTT	CTTTTTTGTT	TCTTGAAATC	AACTGCTGTT	TTCATGTTCC	1320
AGACTCATCT	GTAGGTTCGA	TTTCCATGCT	ACTAGGCAGG	AAGGAAATAG	CTGTTTCAAC	1380
ACGTCCATAA	TGAGCTATAC	TATTGTCACG	AACCACACTT	TCATTGATGG	TCCAAGTGGA	1440
ATTCAATTTT	TTAAAAGCTT	CTCGGACTTT	TTCCAAATCT	TTGGAGGCAA	TGGCCTGCTC	1500
TAAGGTTTCA	AAACGAGGAC	TTATACTCAT	CTGCTTTCAA	AAAGCATTCT	AGTCCATCTC	1560
CGATTACCGA	TGGACTTTAT	CACCTCCTTC	TCCAGTCCTT	GTATGACATC	TTGAAGTTGA	1620
TTCATGACAT	CTTCCAAAGT	TCGAAAAGCT	TTATTCCTAA	ATCCACGTTT	ACGAATCTCT	1680
TTCCACACTT	GTTCAATGGG	TTCATCTCTG	GTGTGTATGG	AGGAATAAAG	GTAAAATCAA	1740
TATTAGTCGG	AATATTTAAG	GTACTTGATT	TATGCCATAT	AGCATTGTCC	ATAACGAGTA	1800
AAAGGATAAG	CTTGTGAAAG	CTCTTCTAAA	AAGGCGTTCA	TCCACACTCC	TTTTTATAAA	1860
CCTGAAATAA	GGCATCAATT	GTAACAAATT	CTCCTGCCTC	TGTAGCCTTC	AAATGACGGG	1920
CAAGAAAGGC	TTTCTCTTCC	TCAACTGTCA	TATATGCATG	GTTACGACCA	CCACGTGTTT	1980
CTTGAAGGAG	AGAGTCGAGT	CCGAACTCCT	CATATTTTTT	TACGTTTCGC	CAAATCGTTG	2040
TTTGATTACA	GTCTAAAAGC	TCTATAATCT	CTTTATAAGA	TTTGCCCATC	AGACGAAATA	2100
TAGTAGATTG	AAACTAGAAT	AGTACACCTC	TACTTCTAAA	ACATTGTTAG	AAATCGATTT	2160
GTCTGTCTCT	TGTTTCATTT	TACTATAGAA	CGATTTGAAG	GCGTTTATAA	TATTTAGCTG	2220
TACGAGAGTC	TTTTTAAAAGT	GTTTTGATGG	TTTGGATTTC	TTCTTTAGTT	GATTTTCATAT	2280
TACTATTATA	TAATGCTTTT	TGATTTTAGT	CTGGTATAAA	TATTGCTTTC	CTCCAAAATG	2340

1256

GTCATAGTTT TACTGGCAAA TCTAACATAT CACGGATAAA TTAACAAGTG ATTTCTGAAT	2400
TGCTAAACAT TTTCTTTTCT TATAGCATAC TTAAAGATTT TGTCTTTGAG AAAGATATTT	2460
CCAAGAAAAA CGTTCGTTTT TTGG	2484

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

CTAGATATAG CTATAATTTT ATTTATAACA AGAGGATAGA AATGACCGAA TTAGAAAGAA	60
AAAATCGAAA AATTAGCTAA GAAATATTCT GATAACTTAA ACATCAAAGT TCAAGAGAGA	120
GTTCGTGAAA TGGCAAATGA TAATAAGAGC CATTATTTGA TATACAGAGT TTTAGGTATT	180
TCATTTGAAG AAGGAGAAAA TATCGATTG TATCAAAATA AAGGTCGTTT TTTATACAAA	240
TATGCTGGTT CATTTTTAGA AGAAGCTGCA GTACTATGCT TTAACGAAAA ATTTGGTACA	300
GAAAATACTT AAAAAGTTAA CATTCCTAAT TCTGAAAGTA CAAAACCTAA GACTTTTGAA	360
ATTGATTGTT TAGTCGGAGA AAAACACGCA TACGAAATAA AATGGTGGGA TGCAACTACA	420
GATGGAGACC ATATAACTAA AGAACACACT AGAATAAAAG TTATTCATAA CAAAGGATAT	480
ATACCAATTC GGTTAATGTT CTACTATCCA AATAGAATC AAGCTATAAA AATTCAGCAA	540
ACTTTAGAAA CATTGTATAA CGGTATTGGA GGGAAATATT ATTATGGAGA TTCTGCCTGG	600
GAACATTTAA GAGCAGTGAC CGGTATTGAT TTACTIONAGTA TTCTAACAGA TATTGCAAAAT	660
AAAAAAACAG GGGTAAAATC AAAATGACAG TATTAAAAGG AGATAACTTA GAAATATTAA	720
AAACTATTGA ATCCTCAAGT ATTGATTTAA TCTATATGGA CCCTCCTTTC TTTACACAGA	780
AAACCCAAAA ATTATCTAAT AACAAAAATA TTATGTATTC ATTCGAAGAT ACGTGGACTT	840
CGATTGAGGA TTACAAAGAA TTTTGTCTG TAAGATTAGA AGAATGCAAA AGAGTGCTAA	900
AAAATAGTGG CAGTATTTTC GTTCATTGTG ATAAAATTGC AAATCATCAT ATTAGATTAA	960
TTTTAGATAA TATCTTTGGA GTAGATATGT TTCAAAGCGA AATTATATGG AACTATAAAC	1020
GGTGGTCTAA TTCAAAAAAG GGATTATTGA ACAATCATCA AAACATTTAC TTTTATTCAA	1080
AGTCAAAAGA TTTTAAATTT AATACAATTT TTACAGAGTA TTCTTCTACT ACAAATATCG	1140
ACCAAATACT AGTGAACGA AAACGAGATG GAAACTCTAA AACTATATAT AAGGTTGATA	1200
ATAATGGTAA CTATATTCTA GCAAAAGAGA AAAATGGAGT TCCCCTTTCA GATGTTTGGA	1260

1257

ATATACCATT TCTTAATCCA AAAGCTAAAG AAAGAGTAGG TTATCCTACA CAAAAACCTA	1320
TTCTGTTATT AGAACAAATT ATAAAGATTG CTAAGTATAA AAATGATATA GTTTTAGACC	1380
CGTTCTGTGG AAGTGGAAGT ACTTTAGTAG CCTCCAAGAT TTTGAATAGA AATTATATGG	1440
GGATTGATTT ATCTGAGGAA GCTATCAATA TAACTCAGCA ACGTCTGGAA AATGTTATAA	1500
AAACAAGTTC AAATTTATTG AATAAAGGAA TCGAAGCATA TAGAACCATA ACTGAGGAAG	1560
AGGAAAACAT TCTTAAATTA TTACAGGCAA AAATTGTTCA AAGAAATAAA GGAATTGATG	1620
GTTTTTTACC TAAACATTTT CAAAAAAAC CGATACCTAT AAAAATTCAA AAAAATAATG	1680
AATGTCTGAA TGAGAGTATC TCTTTATTAC AGAATGCTAT AACTCCAAA AAAGTTGATT	1740
TTGGAGTAGT TATAAAAGT CATTCG	1766

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 748 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

CCGAAAATCA AATTCAAACC ACGTCAACGT CGCCTTGCCG TACTCAAGTA CAGCCTGCGG	60
CTAGTTTCCT AGTTTGCTCT TTGATTTTCA TTGAGTATTA AACTAAATTA AATAATATTA	120
GCGCGGAGAA TTTCTAATTC TTCCTTGGTC AAGCGACGCC ATTCCCCTCG TTCTAGGTTC	180
TCATCTAATA CTAAAGTTC CATAGTCAAT CGTTGCAAGT CCACCACTTC CTTGCCACAG	240
TAGCCCCACCA TACGCTTGAT CTGATGAAAC TTCCCTTCTG CAATGGTCAC ACGGATTG	300
CTTTGATTCT TTTCTGTATC TATGGATACA AGCTCCAGTA TAGCGGGTTG ACAGGTAAAG	360
TCTTTGAGAG GAATACCCTC AGCAAATGTC TCCACATCTT CTGGGTCAT GATTCCCTTG	420
ACTTGTGCCA GATAAGTCTT GTCCACATGA CGCTTGGGCG AAAGAAGAAC ATGAGCCAGC	480
TGACCATCAT TGGTCAAGAG CAAAAGACCA TGCGTGTCAA TATCCAAGCG TCCTACTGGG	540
AAAAGTTCCCT TACTCCGCGC CAAGTCATCC AACAAGTCCA GAACGGTTCT GTGCTTGGGA	600
TCCTCAGTCG CTGAGATAAC TCCTTTGGGC TTGTTTCATCA TGTAGTAGAC AAAGTCTTCA	660
TACTCCAACA CTTGCCCATC AAAGCGAATC TCATCTATTT TTTCATCAAT CTGCAATTA	720
GCTGATTTTT CTTTTTGACC ATTTACAG	748

(2) INFORMATION FOR SEQ ID NO: 237:

1258

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

AAAAGATTAC ATTGCAACAA TTGAAAATTA TCCAAAGGAA GGCATTACCT TCCGTGATAT	60
TAGTCCTTTG ATGGCTGATG GAAATGCTTA TAGCTACGCT GTTCGTGAAA TCGTTCAGTA	120
TGCTACTGAC AAGAAAGTCG ACATGATCGT GGGACCTGAA GCTCGTGGAT TTATCGTGGG	180
TTGTCCAGTT GCCTTTGAGT TGGGAATTGG TTTTGC GCCT GTTCGTAAGC CAGGTAAATT	240
GCCACGCGAA GTTATTTCTG CTGACTATGA AAAAGAGTAC GGTGTCGATA CCTTGACTAT	300
GCACGCGGAT GCCATTAAGC CAGGTCAACG TGTCTTATT GTAGATGACC TTTTGGCGAC	360
AGGTGGAAC TTTAAGGCAA CTATCGAGAT GATTGAAAAA CTTGGTGGTG TTATGGCAGG	420
TTGTGCCTTC CTTGTTGAAT TGGATGAATT GAACGGCCGT GAAAAAATTG GTGACTACGA	480
CTACAAAGTT CTTATGCATT ATTAATGAAA ACAGTCCCTA GGGCTGTTTT CTCTACACTA	540
GGATATAAAA ATAGACTATA ACTAGTTAGA GAAAACTAT AATTGAAAAC TATATCTTCT	600
TGCAGTATAA TAAAAGGACT AAGTGTTTGA GATTTGTCTT CAAACATATG CAATTATTCC	660
TGAAAGAGTA CAGTTAGGAG AGGGTTATGC CGATTCGAAT TGATAAAAAA TTGCCAGCTG	720
TTGAGATTTT ACGGACAGAG AATATCTTTG TCATGGATGA TCAACGTGCT GCCCACCAG	780
ATATCCGTCC TTTGAAGATT TTAATTTTAA ATCTCATGCC ACAGAAAATG GTCACAGAGA	840
CCCAGTTGTT GCGCCACTTG GCTAATACAC CCCTACAAC TGGATATTGAT TTTCTCTATA	900
TGGAGAGCCA CCGTTCATAA ACAACTCGTT CAGAGCACAT GGAGACCTTC TATAAACTT	960
TTCTTGAAGT CAAGGATGAG TATTTTGATG GGATGATCAT CACGGGTGCT CCAGTTGAGC	1020
ATTTACCATT TGAGGAAGTG GACTATTGGG AGGAATTTAG ACAGATGCTT GAGTGGTCTA	1080
AGACTCATGT CTATTCGACC CTTCATATCT GTTGGGGGGC TCAGGCTGGG CTTTATCTGC	1140
GCTATGGTGT AGAAAAATAC CAGATGGACA GTAAGCTATC AGGTATTTAT CCTCAGGACA	1200
CCCTAAAAGA GGGTCACCTT CTATTTAGAG GCTTTGATGA TAGCTATGTA TCCCCTCATT	1260
CACGGCACAC GGAGATTCTT AAGGAAGAGG TCTTAAACAA GACCAATCTC GAGATTTTAT	1320
CAGAAGGACC TCAGGTTGGG GTTTCTATTw TGGCCAGTCG TGATTTACGA GAAATTTATA	1380
GTTTGGGTCA TTTGGAGTAT GACCGTGATA CTTTGGCAAA AGAGTATTTT CGAGATCGTG	1440
ATGCAGGTT	1449

1259

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 904 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

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TACCCGCTTC TTTCAAGAGT TGGAGCAGGG CTTGTTTGCG ATCTTTTGTC ATAGTTCTTC      60
CTTTTAACGG CGTTTTTCGAA GCACTTTTATA GACAGCTAGT GCTAATGTAT AGTCTACCAT      120
ACTATGGATA ATTGTACCAA ATCCAAC TAG TACAAATAGA ACATAAAACA TATTTTCTAC      180
ATTGGTACCA GAAGTTGCGT AAAAAACGAC ACAGGCCAAT ACTTCAGCAA GGGCATGAAC      240
AACAGCCAAA ACAAAGTTGA AAATCCAGGA AGATTTTGGT TTATCTAGGG TATCGGGGAA      300
TTTTTGTAGG TAAAGAGCTC CTAAAGCACC AAAAGATATA TGGGAAAAAG CCCGAAAAAC      360
GATAACCATG GGATAGCCAG CCATCAAAAA TCCAAAAC TA GAGGCTAGGA TGACAAAAAC      420
TGCCATCAAG GCGGACAAGA ACATGGCTAT AAAAATAGCG ATGTGGCTCC CCAAAGTATA      480
GGAAGCAGGT GGAATGACAA TCTTGAAAGG CATAACAATT GGAATCAAAA TCGCAATAGC      540
CGTTAAAAGG GCTGTCATTG TCATAAATTG TGTCTTTTTC CGTGATTCA CAAGAATCTC      600
CTTTTAACT GCATATACAC TAGTATGGTA CAATAAACCA GACAATAAAG CAAGAATTTA      660
CTTGGGTTTA TAGATCATTT TTTAGTTAAA AGTTATAGTA GATTGAACT AGAATAGTCC      720
ACCTCTACTT CTA AACATT GTTAGAAATC GATTGGCTG TCCTGATCGA TTTGTCCTGT      780
TCTTATTTTCG TTTTACTATA GTAAAGATTT CATTA AAAAG AACTGTATA GAGCAAAATC      840
TCCACCTTCA GGT TTGGAAA GCGGAGATTG TTTnTTATTT TTTCCAGGGT TTGTAGTCGT      900
GGGA                                                                                      904
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(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

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CACTCAAACA TGACTTATAT CAAGACGGAT GGACTTCAAG ACGATGCCAA TCGCTTGAAT      60
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1260

CGTAACATTC AGTTTGGTGT TCGTGAATTT GCAATGGGAA CAATCTTGAA CGGGATGGCC	120
CTTCATGGTG GACtTCGTGT ATACGGTGGA ACTTTCTTCG TCTTCTCTGA CTATGTGAAG	180
GCAGCTGTCC GCTTGTGAGC CTTACAAGGA CTTCTGTGTA CTTATGTCTT TACCCATGAT	240
TCAATCGCAG TTGGGGAAGA TGGTCCGACT CATGAACCAG TTGAGCATTT AGCAGGTCTT	300
CGTGCTATGC CAAATCTAAA TGTTTCCGT CCAGCAGATG CGCGTGAAAC GCAAGCAGCT	360
TGGTACCTTG CAGTGACAAG TGAGAAAACA CCAACTGCCC TTGTCTTGAC ACGTCAAAAT	420
TTGACTGTTG AAGATGGAAC AGACTTCGAC AAGGTGCTA AAGTGCTTA TGTTGTATAT	480
GAAAATGCAG CCGACTTTGA TACCATCTTG ATTGCGACAG GTTCAGAGGT TAATCTTGCT	540
GTCTCAGCTG CTAAAGAATT GGCTAGTCAA GCGGAAAAA TCCGCGTAGT CAGCATGCCA	600
TCTACAGATG TCTTTGATAA ACAAGATGCA GCTTACAAGG AAGAAATCTT TCCAAATGCA	660
GTCCGCCGTC GTGTTGCACT CGAAATGGGT GCAAGTCAAA ACTGGTACAA ATATGTTGGT	720
CTCGATGGTG CCGTTCTAGG TATTGATACT TCGGAGCCTC TGCCCCAGCA CCAAAAGTAT	780
TGGCAGAATA TGGCTTTACT GTAGAAAATC TTGTAAAAGT TGTTGAAAC TTGAAATAAT	840
CCTAAAAATC AGGGCGTAAG CTCTGGTTTT TCTTACCAGA AAAGTAAGGT ACAATCTTGT	900
AAAAGTAGCT GAAATTTGAT ATAGTAGTCC TATGTAAAAG ACAAAG	946

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2764 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

CGGGGCTCCc TAGTTCCTAG GGAGCTATTT TTGTTTTTTC AAGAAGTTAT CTTCTTGAT	60
TTTATACTCA ATGAAATCA AAGAGCAAGC TAGGAAACTA GCCGTAssTG CTCAAAACAC	120
TGTTTTGAGG TTGTAGATAA GACTGACAAA GTCAGGAACA CATATCTACG GCAAGGCGAC	180
GTTGACGCGG TTTGAAGAGA TTTTCGAAGA GTATTAGTTG TGAATCTGGT GCAGTCGTCC	240
CAGATTATTC TTATTAGTAG GGTCTTGTTT TCTATATCCC CTCGTAGTTA ACAAGACCTT	300
GAGCATTTTA GAAAGAGGAA TCTATGTCTA CGAAATATAT TTTTGTAAC TGGTGTGTGG	360
TATCGTCCAT TGGGAAAGGG ATTGTGGCAG CGAGTCTAGG CCGTCTCTTG AAAAATCGTG	420
GTCTCAAAGT AACCATTCAA AAGTTTGACC CTTATATCAA TATTGATCCG GGAACCATGA	480
GTCCTTACCA GCACGGGGAA GTTTTTGTGA CAGATGACGG AGCTGAGACA GATTTGGACT	540

1261

TGGGTCACTA TGAACGTTTC ATCGATATCA ATCTCAACAA ATATTCCAAC GTGACAACCTG	600
GGAAAAATTTA CAGTGAAGTT CTTCGTAAAG AACGCCGTGG AGAATACCTT GGGGCAACTG	660
TTCAAGTCAT TCCTCATATC ACAGATGCTT TGAAAGAAAA AATCAAGCGT GCCGCTCTAA	720
CGACCGACTC TGATGTCATT ATCACAGAGG TTGGTGGAAC AGTAGGAGAT ATCGAGTCCT	780
TGCCATTCCCT AGAGGCTCTT CGTCAGATGA AGGCAGATGT GGGTGCGGAT AATGTCATGT	840
ATATCCATAC AACCTTGCTT CCTTACCTCA AGGCTGCTGG TGAAATGAAA ACCAAACCAA	900
CCCAACACTC TGTCAAAGAA TTGCGTGGCT TGGGAATCCA ACCAAATATG TTGGTTATTC	960
GTACAGAAGA GCCAGCTGGT CAAGGAATTA AAAATAAACT GGCCAGTTC TGTGATGTGG	1020
CACCAGAAGC CGTTATCGAA TCGTTGGATG TTGAACACCT TTACCAAATT CCACTGAACT	1080
TGCAGGCACA AGGGATGGAC CAAATTGTTT GTGATCATTT GAAATTAGAC GCACCAGCAG	1140
CGGATATGAC AGAATGGTCA GCCATGGTGG ACAAGGTCAT GAACCTCAAG AAACAAGTTA	1200
AGATTTCCCT TGTGGTAAG TATGTGGAGT TGCAAGATGC CTATATCTCA GTGGTCGAAG	1260
CCTTGAAACA CTCTGGCTAT GTCAATGATG CAGAAGTTAA AATCAATTGG GTCAATGCCA	1320
ATGATGTGAC AGCAGAGAAT GTAGCAGAAC TCTTGCTCTGA TGCGGACGGG ATCATCGTAC	1380
CAGGTGGTTT TGGTCAACGT GGTACAGAAG GGAAAAATCCA AGCCATCCGC TATGCGCGTG	1440
AAAATGATGT TCCAATGTTG GGAGTCTGCT TGGGAATGCA GTTGACATGT ATCGAGTTTG	1500
CTCGTCACGT TTTAGGTCTT GAAGGTGCCA ATTCTGCAGA GCTTGACCA GAAACAAAAT	1560
ACCCTATCAT TGATATCATG CGTGATCAGA TTGATATTGA GGATATGGGT GGAACCCCTC	1620
GTTTGGGACT TTATCCGTCT AAGTTGAAAC GTGGCTCTAA GGCTGCTGCT GCTTATCACA	1680
ATCAAGAAGT GGTGCAACGC CGTCACCGTC ACCGTATGA GTTTAATAAT GCCTTCCGTG	1740
AGCAGTTTGA GGCAGCAGGT TTTGTCTTTT CAGGAGTTTC TCCAGACAAT CGTTTGGTAG	1800
AAATCGTGGA AATTCCTGAA AATAAATCTT TTGTAGCTTG TCAGTATCAC CCTGAACTGT	1860
CAAGCCGTCC AAACCGACCA GAAGAACTCT ACAC'GCCTT TGT'ACTGCA GCAGTTGAGA	1920
ACAGCAATTA GCAAAATCAG AACCTTTGAG AAAAATCTCA GAGGTTTTTT GCATACGATG	1980
ATATTGCAGT ATATCTGAGG TAGGGTCCCT CTGTATGTAC CTGCTACCGT TGAAATCAAT	2040
AGCGACTCCC TCTTGCCCTG TGCTAGTGAA TGGATTATC AGTATATTGA AATGAAATAA	2100
AATTTGAACA AATTAATTCG GAAAGCCAAA TCAATTTCTA GCAAAGTTTT AGGAACTGGA	2160
TTGTATAGTG AATTGAAATA AGATGTGAAC ATCTCTATCA GGAAAGTCAA ATTAATTTAT	2220
AGAAATATTT TAGCAGTCAA GATGTACTGT TATAGATTCA ATACATTATA CTTTTTAAAT	2280

1262

TTAATCCACT ATAGTAAAT GAAATAATAA CAGGACAAAT CGATCAGGAC AGTCAAATCG	2340
ATTTCTAACA ATGTTT TAGA AATAGAGGTG TACTATTCTA GTTTC AATAT ACTATCCCAA	2400
ATCATTCATA CCTCTCTCAA CTAGATGTAA CTTACAAAAC CCCTGACCTC ATGAGCCACT	2460
TTCTTCCTCC TCATGAGGTC AGTTT TACTT TCTGCTGTTC CAGTATCGTT TTCCTCGCT	2520
AGATTTCCCTC AAAAGGGCAG ACTCCTCCCT TGGTGCGTCA CACGATTTTT TCATCTCGAC	2580
TGTTCTTTAA TGCATCATTA ACGACGCTTT TCTTCTAGGT GGTCATAAG GAACAGGAAG	2640
ATTGAGGTTG ACTTTTCTAA TCCTAGAATA AAGTGCTGAA AACAATTCGG AATAGGCATA	2700
GAGACTAGAC AATTTGAGGA GCTGCTTGCG TCCTGTTCGA ACACATTTTC CCACCACGTG	2760
AAGA	2764

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

CCGTTTTTTT CATTGTT CAG TACTACAACT TACGTGTAG CGCCCTGCAC ATTGGTTCGT	60
CTGTTCAGT TTTCAAAGGT CTTGTCTACT TGCTTCTCTC AAGCGACAAC TATATTAGTA	120
TATCACAACT GCTTTCGCTT GTCAACACTT TTTTGAAGAT TTTTAAGTTT TTTTAACTT	180
TTTTTCATCA AGTGGTCCTG ACGCAACATA CCATAGTCCG TACGGGATTC GAACCCGTGT	240
TACCGCCGTG AAAAGGCGGT GTCTTAACCC CTTGACCAAC GGACCTGAGT TGTTATTTTC	300
AACTCTTACT ATTATACAGT CTTTTCAAAC TTTGTCAACT ACTTTTTTAA ACTTTTTTTA	360
TTAATTTTAC AACAGCTTCA GTTCGAGCTG TATGTGGGAA CATATCGACC GACTGGATAT	420
AATGAAGATC ATAGACTTCT ACTAAGCGTA CCAAATCACG AGCCAAGGTC GAAACATTAC	480
AAGAAATATA AACCATTTTT TCTGGTACAT AAGTAAGAAT AGTATCTAAT AACTTATCAT	540
CCAGACCTGT ACGTGGTGGG TCAACAATCA AAGCATCTGC TCGGTAGCCT TCCTTGTAAC	600
AACGAGGAAT AATCTCTTCT GCCGTTCAG CTTCATAATG AGTATTGTCA AATCCCATTC	660
TTTTAGCATT TCGCTTGGA TCTTCAATAG CTTCTGGAAT AATATCCATA CCTCTGAGTG	720
TTTTTACTTT CTTTGCAAAG GCAAATCCAA TCGTTCCAAC TCCACAATAA GCGTCAATCA	780
AATGGTCTTC TTTATCAACA TCCAGCGCTT TTAAGCTGCTC GCTATAGAGG ACTTCTGTTT	840
GCTCAGGATT TAGTTGATAA AAAGCTCGAG GGGATAGTGA AAATTCATAA TTGAGTACAC	900

1263

CTTCTTGAAT ACTCTCTTGC CCCCAGATAA TCTCTGTCTT TTCACCATAT ATCTCACTGG	960
TTTTAGCTGT ATTTGTATTA ACAGCTACTG TCACAACTTC TGGGAAATCT TTAACCAACT	1020
CTTTTACCAA TTGAGTTAAA TTAAGCTGGC GGTTTGTAAC AATAATAATC TGAACCTGTC	1080
CGGTCTTTCT CGCGCGTCGG ACCATAATAG TACGGACACC TAGAACTTTT CTCTCATCCG	1140
TGATTGGAAT CTGGTGATAA GTAAGTAATT CTGCTAAGCG ATTAGCAATC ACTTGGGTTT	1200
CCTTATCTTG TACCAGGCAG TCTTTCAACT CTACTAAATA GTGAGAGTTT TGTGCATATA	1260
AGCCCGCCTT GACCTGATTT TTAAATTTTC GAGTCTGAAA TTGTAACTTA GCTCTGTAAT	1320
ATTTTGGTTC CTGCATTCCA ATAGTTGGAC GAATTCATA ATTTTCATAT CCTGCAGGAG	1380
CAAATTTTTT CAGCGCTTGA TGAAGTAAGT CCGTCTGAA CTCCAGCTGC TTATCATAAT	1440
GCAGGTGCAT GATTTGGCAG CCTCCGCATT CATTATAAAT AGTACAAGAT GGCACAATTC	1500
GAAATTTAGA CTTCCTGTG ACCCTCAGTA ATTTTGCTTC AACAAAGTTG CGTCTAATAG	1560
AAGTAATCTG ACAATAGATA TCTTCGCCTT TGAGAGCTCC TGGTACAAAG ACTAATGTTT	1620
TTTGGTAAAA GCCGATTCCC TCACCGTTAA TTCCCATGCG CTTGATTTTT AATGGTATTT	1680
TT	1682

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TTAACTTTGG TCAATTCCTT AAAGTCATCC TCTGTAAGCA TGTCTAACCA TTGATGTTTC	60
CCTTTATTGC TAAATCACC AATCCGACT ACAGCTATAT CTAAATCTTT CCAACTATTT	120
TTCAAATTTT CAAAATATCT TGATTGCAAA ATACCATCTG CTAACAATTT ATTTTCTTGC	180
ACAATCGTTG CATTATAAA TGTACACTCT CCATGAAATT TTCTAGACAT TTCATAAATC	240
AGTGTATTCA CATGGTATTT AGCGTGTATG TGACTAGGAC CACCTGCTAG AGGATAGAAG	300
TGAACATTCG GGACACTTTT ACTGTGAATT AAATCTACTA AATTACTTAA ACTTTTCCCC	360
CAAGAAAAGC CAATTTTCAT ATTATCATCA ATTAGATTCC TAAGGACGCC TGCTGCAACT	420
TGAGAAATTC TTTCAGATAA AATTGTTGGA GTATCATCAA ATTCATTTGG AATAATTTCT	480
AAACTTTCCA AACTGTATTT TTCTTTTACA TAATTTTCCA ACTTAAACAT ATTGGTATCA	540

1264

AAATTCCTCTA TTTCAATTTT AACAAATTCCT ACATTCCTTG CTTCTGTAA CATTCTACTA	600
ATAGAGGTTC TATAAATTC TAATTTTGCT GCTATTTGTG ACTGATTTAA GTTTTCAATA	660
TAATACAGAT AAGCAATTTT AGAAAGCAGT TTATTCCTAT CTTGATTCAT AACTTAACC	720
TCTTACGAAA CTACCTTAAC CATTATCCCA GCATTTTCTA ATGTAGCTAT ATTTTGTTTA	780
GAAAGTTTTT CGTCTGTTAT TACTTCATAG ACTTGACTTA AAGCAAATCT TCTTACTGTA	840
CCTCTTTTAT CAAATTTACT TGAGTCAGTT AGGACAATGA CTTTATCCGA CACTGCTGAA	900
ATATATTGAA CTACCTCACT GCGCATTAAG TCTTTTCCGG TAAAGCCCAT CTCTTTATCG	960
TAACCATCTG TCCCAACAAA AGCTTGACAC ACATGAAAAG TCTGTATCAT TTCTTTTAAT	1020
AAAGGTCCTA CAGTCACCTG TGAATCTTTC TGAAACTCAC CACCAAGAAC AATAACACGA	1080
CATGAATCAT AAGCTCTCAC AAAATTTGCT ATAAAAACG AATTGTGTAC AATCGTAACA	1140
TTTCTTTTTT GCTTGCAAAT TTCCTCAGCA AGTAAAGCAC AGGTCGATCC AGATTCTATC	1200
ATTATTGTTT CATATCTGA CACCAATTTT ACTGCTTCCT GAACAATTTT TCTCTTAGTT	1260
TCATAATTAA TTGACAAACG TACATTTAAG TCATCTCCAC TATTTAATAC AGCATATCCA	1320
TGCTCTCTGT GTAATAAACC TTTTGACTCT AATTTATCTA AATCTTTTCT AATCGTTACT	1380
TTTGATACAT TTAATTTTTC CGATAATGTA TTAACGTCGA TCTTTTCATA TTCTGATACT	1440
AATTTAATAA TTTGTTCCAA TCTTTTCATT TTACACCTCC GTTTTATTCT ACCAAAATAA	1500
AAAGCAAAA ACAACAAATT AACCTTTCGT TCGTAATTGT TTTTCTTTCTG TTTTGTGTAT	1560
AGGATAGACT TATGAAGAGG AGGAACTCTT ATGGAATAT CTAAAGGAAT TATTTTAAAT	1620
ATTCAACACT TTTCAATTCA TGACGGTCCG GGTATTGCTA CAACTGTTTT TTTAAAGGA	1680
TGTCCTCTGC GCTGTCCATG GTGTTCTAAT CCTGAATCTC AAAGAATGAA ACCTGAAAAA	1740
ATGAAAGATG CTCAACGAGA GAAATTCACC TTAGTCGGTG AAGAAAAGAC TGTAAGAGAA	1800
ATTATTACAG AGGTATTAAA AGACAAAGAA TTTTACGAAG AATCCGGTGG AGGTTTAACT	1860
TTATCAGGAG GTGAAATATT TGCTCAGTTT GAATTTGCTA AAGCCATCTT AAAATCAGCT	1920
AAAGAACATC ACATACACAC TGCCATTGAA ACTACTGCCT TTGTTGATCA TGAAAAATTT	1980
ATTGATTTAA TTCAATATGT GGATTTTATC TACACAGACC TAAAACATTA TAATTCTATA	2040
AAACATAAAA AAGTGACTGG GGTTTTTAAT CAAATGATTA TTAAAAACAT TCATTATGCT	2100
TTTTCACAAA ATAAAACTAT CGTTTTAAGA ATCCCAGTTA TTCCTAATTT TAACAATAGT	2160
TTAGAGGATG CAGAAAAATT CGTACTCTA TTTAACTCAT TAAATATCGA CCAAGTTCAA	2220
CTACTCCCTT TTCATCAATT TGGTGAAAAC AAATATCGTT TATTAAATCG GAAATATGAA	2280
ATGGATGGAA TCAACGCACT TCATCCwGAA GATCTTATTG ATTATCAAAA GGTATTTCTG	2340

1265

AACCACCATA TTAATGTGTA TTTCTAGTTT ATTTCCCTGA AATGCTCTAG CTATTTGCAG	2400
ATAACAAGCA TCTATAATAC ATACTTAACT TTTCAAAAGG TTTAGCTAAA AAATTTTAGC	2460
CAAACCTTTT CTATTTTACC TTGCTCTAGA ATTTTAAAC TGCTATACTT ATCACAAAAA	2520
AACG	2524

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

CGTGCTTGGG GGCTTGTGGT CAAAAGGAAA GTCAGACAGG AAAGGGGATG AAAATTGTGA	60
CCAGTTTTTA TCCTATCTAC GCTATGGTTA AGGAAGTATC TGGTGACTTG AATGATGTTT	120
GGATGATTCA GTCAAGTAGT GGTATTCACT CCTTTGAACC TTCGGCAAAT GATATCGCAG	180
CCATCTATGA TGCAGATGTC TTTGTTTACC ATTCTCATAC ACTCGAATCT TGGGCAGGAA	240
GTCTGGATCC AAATCTAAAA AAATCCAAAG TGAAGGTCTT AGAGGCTTCT GAGGGAATGA	300
CCTTGGAACG TGTCCCTGGA CTAGAGGATG TGGAAGCAGG GGATGGAGTT GATGAAAAAA	360
CGCTCTATGA CCCTCACACA TGGCTAGATC CTGAAAAAGC TGGAGAAGAA GCCCAAATTA	420
TCGCTGATAA ACTTTCAGAG GTGGATAGTG AGCATAAAGA GACTTATCAA AAAAATGCGC	480
AAGCCTTTAT CAAAAAAGCT CAGGAATTGA CTAAGAAATT CCAACCAAAA TTTGAAAAAG	540
CGACTCAGAA AACATTTGTA ACACAACATA CAGCCTTTTC TTATCTAGCG AAGAGATTTG	600
GGCTTAATCA ACTTGGTATT GCAGGTATCT CTCCTGAACA AGAACCAAGT CCACGACAAC	660
TAACAGAAAT TCAGGAATTT GTTAAGACCT ATAAGGTAA AACGATTTT ACAGAAAGTA	720
ACGCTTCTTC AAAAGTAGCT GAAACTCTTG TCAATCAAC AGGTGTGGGT CTTAAAACTC	780
TGAATCCTTT AGAGTCAGAC CCACAAAATG ACAAGACCTA TTTAGAAAAT CTTGAAGAAA	840
ATATGAGTAT TCTAGCAGAA GAATTAAAGT GAGGAAAGAA TGAAAATTAA TAAAAAATAT	900
CTAGCAGGTT CAGTGGCAGT CCTTGCCCTA AGTGTGTGTT CCTATGAGCT TGGACGTTAC	960
CAAGCTGGTC AGGATAAGAA AGAGTCTAAT CGAGTTGCTT ATATAGATGG TGATCAGGCT	1020
GGTCAAAAG CAGAAAACCT GACACCAGAT GAAGTCAGTA AGAGGGAGGG GATCAACGCC	1080
GAACAAATTG TTATCAAGAT TACGGATCAA GGTTATGTGA CCTCTCATGG AGACCATTAT	1140

1266

CATTACTATA ATGGCAAGGT TCCTTATGAT GCCATCATCA GTGAAGAGCT CCTCATGAAA	1200
GATCCGAATT ATCAGTTGAA GGATTCAGAC ATTGTCAATG AAATCAAGGG TGGTTATGTC	1260
ATTAAGGTAA ACGGTAAATA CTATGTTTAC CTTAAGGATG CAGCTCATGC GGATAATATT	1320
CGGACAAAAG AAGAGATTAA ACGTCAGAAG CAGGAACGCA GTCATAATCA TAACTCAAGA	1380
GCAGATAATG CTGTTGCTGC AGCCAGAGCC CAAGGACGTT ATACAACGGA TGATGGGTAT	1440
ATCTTCAATG CATCTGATAT CATTGAGGAC ACGGGTGATG CTTATATCGT TCCTCACGGC	1500
GACCATTACC ATTACATTCC TAAGAATGAG TTATCAGCTA GCGAGTTAGC TGCTGCAGAA	1560
GCCTATTGGA ATGGGAAGCA GGGATCTCGT CCTTCTTCAA GTTCTAGTTA TAATGCAAAT	1620
CCAGCTCAAC CAAGATTGTC AGAGAACCAC AATCTGACTG TCACTCCAAC TTATCATCAA	1680
AATCAAGGGG AAAACATTTC AAGCCTTTTA CGTGAATTGT ATGCTAAACC CTTATCAGAA	1740
CGCCATGTGG AATCTGATGG CCTTATTTTC GACCCAGCGC AAATCACAAG TCGAACC GCC	1800
AGAGGTGTAG CTGTCCCTCA TGGTAACCAT TACCACTTTA TCCCTTATGA ACAAATGTCT	1860
GAATTGGAAA AACGAATTGC TCGTATTATT CCCCTTCGTT ATCGTTCAAA CCATTGGGTA	1920
CCAGATTCAA GACCAGAAGA ACCAAGTCCA CAACCGACTC CAGAACCTAG TCCAAGTCCG	1980
CAACCAGCTC CAAGCAATCC AATTGATGAG AAATTGGTCA AAGAAGCTGT TCGAAAAGTA	2040
GGCGATGGTT ATGTCTTTGA GGAGAATGGA GTTCTCGTT ATATCCCAGC CAAGGATCTT	2100
TCAGCAGAAA CAGCAGCAGG CATTGATAGC AAATGGCCA AGCAGGAAAG TTTATCTCAT	2160
AAGCTAGGAA CTAAGAAAAC TGACCTCCA TCTAGTGATC GAGAATTTTA CAATAAGGCT	2220
TATGACTTAC TAGCAAGAAT TCACCAAGAT TTAATTGATA ATAAAGGTCG ACAAGTTGAT	2280
TTTGAGGCTT TGGATAACCT GTTGGAACGA CTCAAGGATG TCTCAAGTGA TAAAGTCAAG	2340
TTAGTGGAAG ATATTCTTG	2359

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

TTCTTTCTGC TATAATCGTA TAAAATACTT ACTTTAGGAG TTCTTATGAA AGTTGTTAAA	60
TTTGAGGTA GTTCTCTTGC CTCTGCTAGT CAATTAGAAA AAGTTTAAA CATCGTCAAA	120
AGCGATTGAG AGCGTCGTTT TGTAAGTCGTT TCTGCGCTG GTAAACGCAA TGCTGAAGAT	180

1267

ACTAAGGTTA CGGATGCCCT GATTAAATAC TACCGCGACT ATGTTGCGGG TAACGATATT	240
AGCAAGAACC AAAGCTGGAT TATCGACCGC TATGCTGCTA TGGTTAGTGA ATTGGGACTA	300
AAACCAGCTG TGCTAGAAAA AATTTCTAAA AGCATTACAG CCTTGGCCAC TCTTCCTATT	360
GAAGAAAATG AATTTCTCTA CGATACTTTC CTAGCAGCCG GTGAAAATAA CAATGCCAAA	420
TTGATTGCTG CCTACTTTAA CCAAATGGT ATCGATGCAC GCTATATGCA CCCTAGAGAA	480
GCTGGGATTG TGGTCACAAG TGAACCTGGT CACGCTCGCA TCATTCCATC AAGTTATGAC	540
AAGATTGAAG AATTGACAAA CACCAATGAA GTCCTTGTC TCCCTGGTTT CTTTGGTGTC	600
ACTAAGGAAA ATCAAATCTG TACTTTCTCA CGTGGAGGTT CTGATATTAC AGGTTCTATC	660
ATTGCTGCTG GTGTCAAAGC TGACCTCTAT GAAAACTTA CGGACGTTGA TGGTATCTTT	720
GCAGCCCACC CTGGTATTAT CCACCAACCA CACTCGATTC CTGAGTTGAC CTACCGTGAA	780
ATGCGCGAGT TGGCCTATGC AGGCTTCTCA GTCCTTCATG ACGAGGCTCT TCTTCCTGCC	840
TACCGTGGA AAATTCCTCT GGTATCAAG AATACCAACA ACCCTGACCA TCCAGGTACT	900
CGTATCGTTC TAAACACAG TAATGATGAA TTTCCAGTTG TGGGAATTGC TGGTGACTCA	960
GGCTTTGTCA GCATTAACAT GTCGAAATAC CTCATGAACC GTGAGGTTGG ATTTGGCCGC	1020
AAGGTTCTGC AAATCCTGGA AGAACTTAAC AT	1052

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

CCCTCGAAAA CTAAGCCGAT GAAGTCAGAA CACTTCAATC CTGTTCTGTA CTGGTGGGAA	60
AATCGTGAAG AGATTCTGGA AGGTAAGTTC TACAAATCTA AATCATTTAC ACCTAGTGAA	120
TTGGCTGAGT TGAATTATAA TTTAGACCAG TGTGACTTTC CAAAAGAGGA AGAGGAAATC	180
TTAAATCCCT TTGAGTTGAT TCAGAATTAT CAAGCGGAAA GAGCAACTTT AAATCATAAG	240
ATTGATAATG TATTAGCTGA TATTTTGCAG TTGTTGGAGG ACAAATAATG ACACCAGAAC	300
AACTTAAAGC AAGTATTCTC CAAAGAGCGA TGGAAGGGAA ATTAGTGCCG CAAAATCCCA	360
ATGACGAACC TGCAAGTGAA TTATTAAAGA GAATTAAAGC TGAAAAAGAA AAACCTATCA	420
GTGAAGGAAA AATCAAACGA GATAAAAAGG AAACCTGAGAT ATTTCTGTGGT GATGATGGGA	480

1268

AACATTATGG GAAGTTTGCT GATGGAAGCA CTCAAGAAAT TGATGTTCCCT TATGATATTC	540
CTGATACTTG GGAGTGGGTG AGGATAAAAT CAATTTATTG GAATTTTGGG CAAAATAAGC	600
CAGAGAAATC CTTTAGGTAT ATAGATACGT CTAGTATTGA TAGAAAAAAG AACATAATCA	660
ACTACAAAAA TCTACAATAT CTTTCACCTG AACAAGCGCC TTCCCGTGCT AGAAAATTAG	720
TTTCGCAGAA TAGTGCTTA TTTTCAACAG TTAGACCATA TCTAAAAAAT ATTGCTGTAG	780
TTAGAGAACT TAAAGAGTAT TTGATAGCTA GTACAGCATT TAATGTTTTG GGATACTTTA	840
CTTAACGAAA CATAT	855

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

TTTAGGAAGG CTATCCGTAA TTTTACAAAG GATTTAGATA TTACAGAGGA ACATTTAGAT	60
ATTATCAAAA GAGAGATGTT TGGCGAATTT TTCAGTAGCA TGAAGTCTCT TGAATTTATT	120
GCAACGCAAT ATGATGCTTT TGAAATGGT GAGATAATTT TTGATTTGCC GAAAATTTTA	180
CAGGAAATTA CTTTAGAGGA TGTCCTTGAT GCTGGACATC ATTTAATAGA TGATGGTGAC	240
ATAGTTGATT TTACAATATT CCCATCGTAG TAACCTATTA TAATAGACAC TAGAAAGAAG	300
GGATGACAAG TATGAGAAAA AAAACAATTG GAGAGGTTTT ACGATTAGCT AGAATCAATC	360
AGGGATTGAG TTTAGATGAA TTGCAGAAAA AGACAGAAAT CCAGTTAGAT ATGTTGGAAG	420
CAATGGAAGC AGACGATTTT GATCAACTTC CAAGTCCTTT TTACACGCGT TCTTTCTTGA	480
AAAAATATGC ATGGGCTGTT GAGTTAGATG ACCAAATTGT TTTGGATGCT TATGATTCTG	540
GGAGTATGAT TACTTATGAG GAAGTAGATG TTGATGAAGA TGAGTTGACA GGTCTGAGAC	600
GTTCAGTAA GAAAAAGAAG AAAAAACAT CATTTTTACC TTTATTTTAT TTTATCCTGG	660

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1805 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

1269

CCGGTTGCAC AGGATCGTGC ATAGTCAACT CTCAAGTAT AGCATATCTC CTATTTTCTT	60
ACAAGTAATA ACACCTAAAA TGAAGCTTTT TCTTTTACTT TTTTCTGCCA AGAGGCAAAA	120
AGCATGCTGA GGTAAAAAAC GTCATCATA ATAGGAACAC CAAGAATGGT CTTTTCATGA	180
TAGAAAATCG TCAAAATAGGC TGAAAAGACA ACGCCAAGGA CAAAAC TACT AAGCAGGCTA	240
ACAAATATGA ATCCTTCACG CAAAAAAGGA GTGTGCTTGG TTCGGAAATA ATCTCCAAAA	300
GCCAGCATGG TCCGTTTGAT ATTCCTGTC ATAAAAGCGT TATTATAGGC AATACCCGAC	360
ACTTCTCCAA AAGCAGTTGT CACCAGTCCC ATACAGAAGG CCAAGGGCGG CACTAGATAG	420
ATATTATCCA CAGTTTGCGG CACAAAAGCA ATAATGATTG ATAAGATTGC CAAGGGAATC	480
AAGGACAGAA TAGGTTTTTT CACAATTCTC AATTTTTCCT TATAAATCGT TAATAAAAAG	540
ACTCCCATCA TAAACGCTAG CAAGGTGAGA ACCTTGTCCT TAACATCCGA AACATTATTT	600
TTAATTAATT C TACTGAAAG AAAGACAACA TTTCCAGTTT GTCCAGCTAC AAGGGTATTC	660
CCGCGAACAA TAAAAGTGTA AGCATCCACA TATCCAGCAC AAAACGTCAA AAAAAGTGCT	720
AACCTTTTAG ACTGACGTA TATTTTCTT ATAGGTAATA ACCTCATTTT ACCTCCCATT	780
GTATTTTCTC TTAGAAATAT TGTACCATTT TCTTCTAAA AAATCGTAGG CTACCATTTA	840
GATTTTACTA TTAGCATAAA AATAATAATA GACAAC TATT TATCCAAAA TAGATAGATG	900
TAACATGTTT GCAAACAAAG CATACGAACC TTTAGTAAAA TCATTTCCAT GAAACTAGAA	960
TAGAGCCCTC TTAGCAAAAA TCATTATTTT AATTTATTTT TAATCACTCC TTGACATAAA	1020
TAACTCTCAC CAATAAAAGA CTATGTCTTA AAAAAATGGT ATAATAAAAT CAATACTTGG	1080
GCTTGATGGC TATGCTACTA ATAACAATTA GGAGAGAAAA TCAGGCACTT GTTAACAACA	1140
AGGATTATCC CCTTGAGATG AAAGGAACTT TAGAAATCTT ATGATGAACA TGCAAAACAT	1200
GATGCGTCAA GCACAAAAAC TTCAAAAACA AATGGAACAA AGCCAAGCTG AACTTGCTGC	1260
TATGCAATTT GTTGGCAAAT CTGCTCAAGA TCTTGTCCTA GCGACCTTAA CTGGCGATAA	1320
GAAAGTTGTC AGCATTGATT TCAATCCAGC TGTCGTTGAC CCAGAGGACC TTGAGACTCT	1380
TTCTGATATG ACCGTTCAAG CCATCAACTC TGCTCTTGAA CAAATCGATG AACTACCAA	1440
GAAAAAACTG GGTGCTTTCG CTGGGAAATT ACCTTTCTAA AAACAAGGAG CTAGAACAAT	1500
GCTTGTCGAT AACAAAGGCT AAGAAAGGTG CAAAAATGAC TCTATAATAT TTGTAGTGGG	1560
TAAATCCCCT ATGGATATTA TGGAGCCTAT TTTTGTGTAG AAAAAAGTCC CATATGACCT	1620
ATAATGAAA GCGACAAAAC AACTCATTAG AAAGAATCAT ATGGAACAAT TACATTTTAT	1680
CACAAAATTA CTAGACATTA AAGACCCTAA TATCCAGATT TTAGACATCG TCAATAAGGA	1740

1270

TACACACAAG GwAATCATCG CCAAAC TGGr CTATGAAGCT CCATCTTGTC CTGAGTGCGG 1800
AAGTC 1805

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2516 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

CTGCATCTAG TTTGTTTCTC CCTACAGTTT TAGCTAGACA GATTGGAGAT TATGATTTAA 60
 CGTCGCCGCG TTGGGGTTCG GATACAACTA GTGAGCTTGA GAAAGAAAAC TCCTCTGCTG 120
 GAATTAATAA TAATGACAGC ACTGGTGGCG GTAAAAGGTT AAATACCTCT ATTCGTAGCG 180
 CCTATAGTGG GTCAGATATT ACCCCGGTAT ATTCATTGGG GTCTGGCTCT AGGATTGTCA 240
 TGTACTATAA TGGAGGTGGT GACAATTATA TTGGTTCTGG TACTAGATTA GCTATGGCGC 300
 CACAATTGGG AAATCATGTA AGAATTCATA CTTCAGGTTC TTGGAATCCA GATTCTTATT 360
 AACTTACTTG TCAGAGTAAG CCTTAAAGAT GGTGATTGT GGGTGTAGCA TGAAAAAAGA 420
 ATGCTACACC CTATTTTAT TATAAGGAGG AGTAAGGATG GAATTTTCA TTTGTAATCT 480
 TGTACGAGTC GTTCAATCAC CTCGATTTTA TATGTCTTTA TTTTGGACCC TTCTTTGCAT 540
 GAGTTTAGGA AATTCCTTG CTTTCAATGG TATTTATAAA ATTGAAGGT TATCGATTTT 600
 TTTTGCCGCT TCTTCTATTC GAGGATTTTC ACCGATTAGC CTAGTAGCTG CACTTATCTG 660
 TACACTGCCC TATTCTAGTC AGATAATAGA GGATGCTGAG AGTCATTTTC TAACAGCACA 720
 ATTGTGTCGA ATTTCTAAAA AGAAGTATCT GGCTATTGTG GGTAGTACTG TAATTATTTT 780
 TTCTTTTCTA GTCTTTTTC TCCCCTATTT ATTATTATTA GGAATTAATC TTTTAGTGAC 840
 TCCTTATCAG GAAATTATA TTGGAGATTA TAGTGGTGCC TTAAGAAGAT TATTTGATTC 900
 CAATCAGTTT CTCTATAGTC TTGTAACGAC TCTCTGGTAT GGAGTTTGGG GCGCTGTGTT 960
 CTCTATTTTT GGACTAGCTA GTGCTTTGCT AGTGAAGAAA AAAATAGGAG CTATTTTCAT 1020
 CCCAGTTGCC TATATGATGG TTGGTGGTAT TTTTGGGCT ATTTTAGGGC TATCTTACTT 1080
 AGAACCTGTG ACAACGCTAG CTTTGGGATA TCAGAAAGAT ATCAGTCTTT CCTTAGTTAG 1140
 TGCTCATCTT GCTTTTATTT TATTTGTTAG TTGTTTGGTT GTTTATGGTA CATTTTCTT 1200
 ACATTCAGAG GACTATGTAT AATGAAACAA TTTGTTCAAT TTTATAAAAA AGATTTCTTA 1260
 GCAGTATTGG TTTATTTTAT ATTACTGCTA TCCTGTGTTT TATCTAGTAC AGTATATTTA 1320

1271

TTGCGCtGTC	GCCAATATTC	AATCCATCCA	AATGTATTAG	AATGGATCTT	AGTTTTACTT	1380
CAAGATATGA	CGACTGGAGT	ATATTGCTTT	CCG TTCACAT	ATATATTGTT	CTTTTTTTAT	1440
TTGATGAATA	ACTATTTTAA	TAGGTTGGAG	TGTCGCATTC	GTCTGAAATC	AATTAAGCAC	1500
TTTACCAGTT	TTAGTTTCAA	ATTAGCAGCT	CTTAGTACGG	GGATTTGGAC	GGCGACTTTA	1560
TTTTTATTGA	TTTTTCTAAT	TGCATTTAGT	AATGGTTTTA	GCTTCTCTTT	GGAGATAAAG	1620
GAGGTTGATT	TTTAAAGAGA	ATTTTATGGT	ATAAGTATTG	CAAACAATGC	TAGTTTCTTT	1680
ATAGGATTTT	TTTTCTCTTA	TATAGCATAC	TATTTCTTTT	TATCCTTACT	TACTATTAGC	1740
AGTTTTTCTT	GGTTTAAAAA	ATCAAACATG	AGCTTAGTAT	TTCTGTTTAC	TTTTTTATTT	1800
GTAGAATCCT	TATTCCTGGAT	TTATCAGTTG	GACAATGGGA	TAATTGGATT	ATTGCCAATT	1860
TTTCAGTATA	TGGTAAATTC	CAATCCGTAT	GCATTGATTT	ATTGGCTTAC	ATTACTATCT	1920
ATCATAATTC	CATTGACTGT	ATTTTCTGTT	CATAGAAACT	GGAGGAGAGT	GTAAAAGTTG	1980
GAAATGGGAA	AGTTAAGTAG	TCACATGTGG	AGGTTGAATC	AGATAATCTA	TACCAAGTAC	2040
TTTTGGGGTT	ATGTTCTTTT	TTGGATATTG	ATTTGTTTAG	GATTATGGTA	TTGGTTAGAA	2100
GGAAATGATA	GACTTGTTAT	AGAAATTTTA	AAAGGGCCTA	ATCTGAGTCA	AAACTCTTTT	2160
TTAGTCTTAT	CTATATGGTT	GCTTCATTGG	TTTATTATTC	ATACATTTT	TCTAGCAGTT	2220
GTATATCGTA	GAAGAGCATC	CGATTTCTTT	ATGGAAGTGA	TTCGATTTTC	TTCTATTAAAG	2280
CTCTGGATTA	GGTATCAGAT	TTGGACCTGT	TTCTTTTATG	GACTCATTTT	AATCATGGTA	2340
AAAGTCTTAG	TGATTCAATT	TATGTTACAG	TTACCAAAC	GGGATATAGG	AGTTTTGTTT	2400
ATAGTTGATT	CTTTGAATGC	TTGTGTGTTA	GTCTTGTTTT	GCTTTATGTT	ATACGCACTA	2460
GGAGCGAATG	TACAAATGAA	CTTGCTTGC	GTTAGTTTCT	TTTTACTCAT	GATTGG	2516

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1364 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

CGGTGTTTTT	TTGTAAATTT	TCTAGCACTT	GTATGGTAAA	ATAGATACAG	GTGTTCATTA	60
AAC TAGACTA	AAAACCTATT	TAAGCAGGCA	AAATGAAGAA	ATACCAACAA	TTATTTAAGC	120
AAATCCAAGA	AACCATTCAA	AACGAGACTT	ACGCTGTCGG	AGATTCCTT	CCTAGCGAGC	180

1272

ACGACCTTAT GGAGCAATAT CAAGTGAGTC GTGATACCGT CCGAAAGcCC TGTCTCTCCT	240
CCAAGAGGAA GGATTGATCA AAAAGATAAG AGGGCAAGCT TCTCAAGTCG TCAAAGAAGA	300
AACCGTCAAT TTCCCTGTAT CCAACCTAAC CAGCTACCAA GAACTAGTTA AAGAACTTGG	360
ACTGCGCTCT AAAACCAACG TGGTCAGTCT GGACAAGATT ATTATTGATA AAAAATCCTC	420
ACTGATAACC GGTTCCTCCAG AGTTTCGGAT GGTTCGGAAG GTGGTCCGCC AGCGTGTGGT	480
GGATGATCTG GTATCCGTTC TGGATACGGA CTATCTGGAT ATGGAACCTCA TCCCAAATCT	540
CACTCGCCAA ATTGCTGAGC AGTCTATCTA TTCTTATATA GAAAATGGCC TCAAACCTCT	600
TATTGATTAT GCTCAGAAGG AAATCACCAT TGACCACTCA AGCGACCGAG ACAAGATTCT	660
CATGGACATT GGCAAAGACC CTATGTTCGT TTCGATTAAA TCAAAGTCT ATCTCCAAGA	720
CGGACGCCAA TTTCAGTTTA CCGAAAGTCG CCATAAGTTA GAGAAATTTA GATTTGTAGA	780
TTTTGCAAAA CGCAAGAAAT AAAAGACTGA GACACCAGAT CTCAGCCTTT TTCGGCTCTA	840
TAATATTTGT AGTGGGTAAC CCCCTATGG ATATTATGGA GCCTATTTTG TGTAGAAAAA	900
AAGTCCCAT A TGACCTATAA TGAAAAGCGA CAAAACAACT CATTAGAAAG ATTCATATGG	960
AACAATTACA TTTTATCACA AAATGCTCG ATATTAAAGA CCCAAACATC AAGATTCTAG	1020
ACATCATCAA TATGGATACC CACAAAGAAA TTATCGCTAA GCTGGATTAT GAGGCTCCAT	1080
CTTGCCCTGA TTGTGGAAGT CTAATGAAGA AATATGACTT TCAAAAACCG TCTAAGATCC	1140
CTTACCTCGA AACAACTGGT ATGCCTACTA GAATTCCTCT TAGAAAGCGT CGTTTCAAGT	1200
GCTATCATTG TTCTAAAATG ATGGTCGCTG AAACCTCTAT CGTCAAGAAG AATCATCAA	1260
TTCCCTCGTAT TATCAACCAA AAAATTGCGC AAAAGTTGAT TGAGAAGATT TCTATGACCG	1320
ATATTGCTCA TCAGCTGGCC ATTTCAACTT CAACTGTCAT TCGG	1364

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CCATGAAGAC CGCTTGGAAT TGGAATGGCA CAAGTCTTTG TTGAATGGTC TATTTCCATT	60
GACAATCGGT GGAGGAATTG GACAATCTCG TATGGCCATG TTCCTACTTC GCAAGAGACA	120
CATCGGAGAA GTGCAACAA GTGTTTGGCC TCAAGAAGTC CGCGATACTT ACGAAAATAT	180
TTTGTAGAGA ATCGAACC GC AAGGTTCGGT TTTCTTTCTC TTTTGTCTA TAATTTGGTA	240

1273

TAATAAACAG TATGAAAATC GTATCAGGAA TCTATGGGGG ACGTCCCCCTC AAGACACTAG 300
 AAGGCAAGAC GACAAGACCT ACTTCGGATA AGGTTAGGGG AGCCATTTTT AACATGATTG 360
 GTCCCTACTT TGAAGTGGGA CGAGTCTTGG ACCTTTATGC AGGTAGTGGT GGTTTATCTA 420
 TCGAAGCAGT ATCGCGTGGC ATGTCCAGTG CTGTTTTGGT GGAGCGAGAC CGTAAGcTCA 480
 GACCATCGTG GCTGAAAATA TCCAGATGAC CAAGGAAGTT GGAAAATTTC AACTCCTCAA 540
 GATGGATGCA GAAAGGGCAT TGGAACAGGT ATCTGGGGAA TTTGACCTCG TTTTCTTAGA 600
 CCCTCCCTAT GCCAAGGAAC AAATCGTAGC AGATATTGAA AAAATGGCTG AGAGAGAGCT 660
 TTTTCTGAA GATGTTATGG TTGTGTGCGA GACGGATAAA GCCGTTGAAC TTCCAGAAGA 720
 AATTGCCTGT CTGGGTATCT GGAAGGAAAA GATTTATGGA ATTAGTAAGG TGACAGTCTA 780
 TGTCAGATAA GATTGGCTTA TTCACAGGCT CATTTGATCC GATGACAAAT GGGCATCTGG 840
 ATATCATTTGA ACGGGCGAGC AGACTTTTTG ATAAGCTTTA TGTGGGTATT TTTTPTAATC 900
 CCCACAAACA AGGATTTCTC CCTCTTGAAG ATCGTAAACG GGGGTTAGAA AAGGCTGTGA 960
 AACATTTGGG AAATGTTAAA GTCGTGTCTT CTCATGATAA ATTGGTGGTC GATGTCGCAA 1020
 AAAGACTGGG GGCTACTTGC CTAGTGCAGG GTTTGAGAAA TCGGTCGGAT TTGCAATATG 1080
 AAGCCAGTTT TGATTACTAC AATCATCAGC TGTCTTCTGA TATAGAGACT ATTTATTTAC 1140
 ATAGTCGACC TGAACATCTC TATATCAGTT CATCAGGCGT TAGAGAGCTT TTGAAGTTTG 1200
 GTCAGGATAT TGCCTGCTAT GTTCCCG 1227

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

CCGGTCAAGT TAAAAACGCT ATTTCTTCCC ATTTTATTTA TTTTITAGGA GTGGTAACGT 60
 ATCAAAATAG CCCAAGCGTT CTCACCCGTG TGAGTTTGAA TAATGGAACC CGTTTCCAAA 120
 ACAGAAATG GCTTTTCAAC ATAAGCTTGT AAGCTTTCCT TCATCTCTTT TGCCCAATCA 180
 TCACTACCAG AATATGAAAT TCCAATCTCT GCTACAGCAC GTTCAGAAAAG CGATGTTATC 240
 AACTCATCTA ACCATTTTTT AAATGTTTTA GTTCCACGAC CTTTAACCAT TGGCTGCAAT 300
 TCATGGTCTT TCATTGTCAT GACAGCACGG ATATTGAGAA GAGAGCTCAA CAAGCCAGTT 360

1274

ACACGGCTAA	TTCGTCCACC	TTTGACAAGA	TTTTCCAAAG	TTGAAACACC	AATATAAAGC	420
TCGTGTATGGT	TTTTAACCTC	TTCTACATGA	GATAAAATTG	CCTCCATATC	TTTACCTTCT	480
TGAGCTAACT	TCGCAGCCTC	AACAACTTGG	AATTTCAGGG	CTTGGTCAGT	GAAGGAACTA	540
TCAACAACAG	TCACATCTGC	AGTAGATAGG	CTAGCACCTT	GGCGTGCTGC	TTCTACCGTA	600
CCCGAAAGAG	CATGGGACAT	ATGAATAGCA	AGAATCTGGC	CACCATCTTT	GCATAGGTCT	660
TCAAAAATCT	CAGCAAAGAC	ACCTACAGGT	GGCTGACTTG	TTTTCGGAAG	ATTCTTACTT	720
TCTTGCATCA	ACTGAAGAAA	TTTACCTTCT	TCTTTCAAAT	CCGCATCAGA	ATAAACAACA	780
TTATCAATCA	TTACAGATAA	TGGAACAATT	GTAATATCTA	ATTGCTTTAC	TAGTTCAGGT	840
TCAATAGTAA	CAGATGAATC	GGTTACAATC	TTAATTTTGG	TCATAGTATC	AATCTTTCTA	900
TTTTAGGATT	CAGATTGGTT	TCCTTACTTC	TAATTATATC	AAAAAAAAGA	TTAAAAATCC	960
TAATGGAGTC	AATCAAATTT	TCCGTAAAAT	TTGATATAAT	CAACTTATAA	GAAAAGAGGT	1020
GTCTTATGAT	TAAAAAAATT	TACCCCATTT	TTACCATTTT	ACTAGGTGCT	GCTATTTATG	1080
CTTTTGGACT	GACTTATTTT	GTAGTTCCCC	ATCATCTCTT	TGAAGGAGGG	GCGACAGGCA	1140
TTACCCTCAT	CACCTTTTAT	CTTTTAAAA	TCCCTGT'TTC	CCTCATGAAC	CTGCTGATTA	1200
ATATTCCCCT	TTTCATCCTA	GCTTGGAAGA	TTTTTGGAGC	CAAATCCCTC	TATTCTAGTT	1260
TACTAGGAAC	CTTAGCTTTG	TCCGGCTGGT	TAGCTTTTTT	TGAGCATATT	CCCCTTCATA	1320
TTGATCTTCA	AGGTGATTTA	CTAATCACAG	CCCTTATAGC	GGGAATCCTA	TTGGGAATTG	1380
GCCTTGGAAT	TATTTTAAAT	GCTGGAGGTA	CAACTGGCGG	AACTGATATT	CTAGCTCGTA	1440
TTCTCAACAA	ATACACTCAT	ATATCCATAG	GAAAACCTGCT	CTTTATCTTA	GATTTTTGTA	1500
TTCTCATGTT	GATTCTCCTA	ATCTTCAAGG	ATTTGAGATT	GGTTTCCTAC	ACGCTTTTGT	1560
TTGATTTTAT	TGTTTCTCGT	GTTATTGATT	TGATTGGTGA	AGGAGGATAT	GCCGGCAAAG	1620
GCTTTATGAT	TATCACAAAA	CGTCCTGACC	AACTTGCTAA	GGCGATTAAT	GATGACCTCG	1680
GAAGAGGTGT	TACTTTTATT	TCTGGTCAAG	GCTACTATAG	TAAAGAAAAT	TTGAAAATCA	1740
TCTACTGTAT	TGTCGGAAGA	AATGAAATTG	TGAAAACGAA	GGAAATGATT	CATCGAATCG	1800
ATCCTCAAGC	CTTTATAACT	ATTACAGAAG	CCCATGAAAT	CCTAGGAGAA	GGCTTCACCT	1860
TTGAAAAAGA	ATAAAAAGAG	GTAATGTCGT	GACCTCAAAA	GTTAGACTAA	ATCATCTATC	1920
TTTTGGGTTA	CAGACAACCT	CTTTTTTATT	TTATTTACTC	AAGCTCTTAA	GACCAATTCC	1980
GAGTTACTTC	TTCATCAGCC	TTTAACTGAT	CCACTAATTG	GTCAACTGAG	TCAAATTTGG	2040
TCATATCTCG	AATGCGATCA	AGCCAATAAA	CCATGACGGT	TTCCCCATAA	ATATCTTGAT	2100
TAAAATCAAA	AATATTGACT	TCAAAACGTG	CTTCTTCTCC	ATCAAAGGTC	ACATTTTTC	2160

1275

CGACACTAGC CATAGCACGA TACTTCTGTC TTTGAATCTC AACATCAACA ACATAAACGC	2220
CATCTGCTGG CATATAAGTA CGGTCTAAAA GCACTAAATT CGCTGTCGGA TAACCAATTG	2280
TACGACCACG AGCATTACCA TGAACCACCA TACCTCTTGA TGGAAAGCGGT GCCCCCCAAAA	2340
GTTTTCTGTC TTCTTTCACA TTTCCATCTA AAATAGCTTG ACGGATACGA GTTGAACATA	2400
TCTTTCCTTT CTCATCTTCT ACAGGTGGAA CAATGATAAC TTCTCCATCA AAGTAATTCT	2460
TTAAATCTTC TGCTGTTTTT TTGTCAGAAC CAAATGTATA ATCAAAACCT GCAACAATAA	2520
TTTTGGCATT CATAGCCTTG ATATAAGTTG CAAAGAATTC TTGTGCAGTG AGACTAGCGA	2580
ATTGACTACT AAAATCAAGG AGATATAATT CTCTACACC TTCGCGCTTT AATTTTCTTT	2640
CACGTTCAAG AGGGTTCAAA ATATGCAAAA ACAAATCTGG ATGATAAGGC TCTAAAGCGA	2700
TCTTTGGAGA TTCATTAAAG GTCATAACGA CGATAGGCAA CAAATCCTTT CTCGCAGCCT	2760
TGTTGGCAAC ACGAAATAAT TCTTGATGCC CCTTATGTAT GCCATCAAAA TAGCCGAGAA	2820
CAACGACTGA ATCAGATGGT GTGCCAATAT CTTTTTGGTT TTTTATAGGA ATAGTAATAA	2880
TCATAAAATA ATTATATCAT AGCGATAGCT ATTTCTGGAA CAGAAAATCT GAAATGTTGT	2940
TTTTTTCACA TGAAGGTAC CTGTTTTCAA AAAGCACTTT ATTCTATCGT TGCTTAACTA	3000
TGAACCTTGC AATATTCTTC TCAAAAACCT GTAGGACATC TTCAAAATTT TGCAAGGAGT	3060
GATTAGACTT GTTCGGTAAC CATAAAGTGT CATACTATGC TTATGTATGA AAAAGCAATG	3120
CAACTAACTC CTGAGAACTT TAAATTACTA ATTGGTGCCG AAAAGGTAGA ATTTAGAATC	3180
GAGGTACACC TATGGCTGTA AAATTTACAA AATGAGACAA CTGGGCAAG ATGTTTGAAG	3240
AATTTCTTAA ACTCCCTGAT TTGAAGCAAG TCACTTTCCC TAATGACAAA GAAAAAGCC	3300
AAAACAGCAA AGAAAACTA GATGACTGCT TTCCAACAAC TCCCATCTAG TGTGCTTCAG	3360
ACTGGGCTAT TTTTCTCTCC ATCTGTTAGC TTGGATTCTC AGACCGTTTC AGCTAAAGAA	3420
TATCTTTTCC CTTATCAGAA GGAACGGCTC AAGCCATTCA GACAAGTGAA GGGACGACAA	3480
GCCAATATTT GAAACCAGAT AGCAGTTCTT ATAGTCAATT GAAATAAAAT CTGAAGAAAT	3540
CGAGTAGGAA ACTCATATCA ATGTTTAACA GTGTTCTATT CCAGATTCAT ACTCAATGaw	3600
AATTAAAGTG CAAACTAGGA AGTTAGCCGC AGGTGATACT TTGGGTACGG CA	3652

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 743 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GTACCGTGGT GCCAAAGTAC AGCAAGGTTG GCTTTTGTGAC AAACAATACC AATCTTGGTT	60
TTACATCAAA GAAATGGAA ACTATGCTGA TAAAGAATGG ATTTTCGAGA ATGGTCACTA	120
TTATTATCTA AAATCCGGTG GCTACATGGC AGCCAATGAA TGGATTGGG ATAAGGAATC	180
TTGGTTTAT CTCAAATTG ATGGGAAAAT GGCTGAAAAA GAATGGGTCT ACGATTCTCA	240
TAGTCAAGCT TGGTACTACT TCAAATCCGG TGGTTACATG ACAGCCAATG AATGGATTG	300
GGATAAGGAA TCTTGGTTT ATCTCAAATC TGATGGGAAA ATAGCTGAAA AAGAATGGGT	360
CTACGATTCT CATAGTCAAG CTTGGTACTA CTTCAAATCC GGTGGTTACA TGACAGCCAA	420
TGAATGGATT TGGGATAAGG AATCTTGGTT TTACCTCAAA TCTGATGGGA AAATAGCTGA	480
AAAAGAATGG GTCTACGATT CTCATAGTCA AGCTTGGTAC TACTTCAAAT CTGGTGGCTA	540
CATGGCGAAA AATGAGACAG TAGATGGTTA TCAGCTTGA AGCGATGGTA AATGGCTTGG	600
AGGAAAACT ACAAATGAAA ATGCTGCTTA CTATCAAGTA GTGCCTGTTA CAGCCAATGT	660
TTATGATTCA GATGGTGAAA AGCTTTCCTA TATATCGCAA AGTAGTGTG TATGGCTAGA	720
TAAGGATAGA AAAAGTGATG ACA	743

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4010 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

TTTTGGTTGA TGATACGAGG GATTTGGTGA TTCTTCTTGA CGATAGAAGT TTCAGCGACC	60
ATCATTTTTG AACAGTGATA GCACTTGAAT CGACGCTTTC TAAGGAGAAT TCTAGTAGGC	120
ATACCAGTCG TTTCAAGATA AGGAATTTTA GAAGGTTTTT GAAAGTCATA TTTCTTCAAT	180
TGGTTTCCGC ACTCAGGGCA AGATGGGGCG TCGTAGTCCA GTTTGGCGAT GATTTCCTTG	240
TGTGTATCCT TATTGATGAT GTCTAAAATC TGGATATTAG GGTCTTTAAT GTCTAGTAAT	300
TTTGTGATAA AATGTAATTG TTCCATATGA TTCTTTCTAA TGAGTTGTTT TGTCGCTTTT	360
CATTATAGGT CATATGGGAC TTTTTTCTA CAATAAAATA GGCTCCATAA TATCTATAGT	420
GGATTTACCC ACTACAAATA TTATAGAACC GAATTAATTT AATTAGAGAG CCAACTTTCT	480
AATATAGTAA TCGCGTCATA ACAAGGTATC TATCATTCAT GGAGTTCCTC CTGTATACTA	540

1277

TTAGTAAAGT AAAACTATTG GAGGATATTT TAATGCCACA ACCTATTGTT CCTGTAGAGA	600
TTCCACAATC TCGTCGTTTT GATTCTAAAA AGAGAAATGA TATTCTGCTT AAAATTCGTA	660
TTGGCAAGCT TGAAGTAAGT TTTTTCAT CTCTCAATCT CGAAATGGTA GAACAGCTTT	720
TGGATAAAGT GTTGCTCTAT GACAATTCAT CTATCTAGCC TAGGGCAGGT CTATCTCGTA	780
TGTGGGAAAA CGGATATGAG GCAAGGCATT GATTCAATTGG CTTATCTGGT TAAAACCCAC	840
TTTGAATTAG ATCCTTTCTC CGGTCAAGTT TTTCTCTTTT GTGGTGGACG TAAAGACCGC	900
TTTAAAGCCC TTTACTGGGA TGGTCAAGGA TTTTGGCTAC TATATAAACG CTTTGAGAAC	960
GGAAACTGA CTTGGCCCAG TACAGAAAAG GATGTCAAAG CTCTCACACC TGAACAAGTA	1020
GATTGGCTTA TGAAGGGCTT TTCTATCACT CCAAAAATAA ATTTATCAGA AAGTCGTGAT	1080
TTCTATTGAA ATGAGGACTT TCTTTTtagT TATAATAAAG TTAGGAAATA AGGAGAGGAA	1140
GCCCATGGAA GAAGATTGAA AATCATTCAA CAACAGAGTG CTACAATTGA TAGTCTCACC	1200
AATGAACTTG CCCTTCTTCG TGAACAAGTG GCTTATCTAA CGCAAAAGCT CTATGGAAAA	1260
TCCTCTGAGA AAAGTGTTCG CCCATCTGGA CCACTCAGTC TTTTGAAGA GGAACAAAAT	1320
ATGGAAGAAG ACTCTGACTT ACCCAGTTGA AAGAGAAGAA ATCACCTATA AACGTAAGAA	1380
AGCTAAAGGG AAACGTCAAG CTCTTCTTGC CCAATTTGAT TCAGAAGAAG TTCATCATCA	1440
AGTAGAAGAG AGCATTTGCC CTGATTGTCA GGGAGATCTA AAAGAGATTG GAGCAACCCT	1500
TCAACGACAA GAATTAGTCT TTATTCCTGC GCAATTAAAA CGAATAGATC ATATCCAACA	1560
CGCTTATAAG TGCCAAGCAT GCAGTGATAA AAATCCGAGT GATAAAATCG TGAAAGCTCC	1620
TATTCCTAAA GCCCCTTTGG CGCATAGCCT TGGCTCAGCT TCTATTATCG CTCACACCAT	1680
CCATCAGAAG TTTAATCTGA AGGTACCCAA TTATCGCCAA GAAGAAGATT GGGCTAAGAT	1740
GGGTTTACCA ATCACACGTA AGGAAATTGC TAATGGCAT ATCAAGGCGA GTCAATACTA	1800
TTTGGAGCCC CTTTATAATC TTTTACGAGA AAAGTTGTTA GAACAAGCTC TTCTTCATGC	1860
GGATGAAACC TCTTATCGGG TTCTAGAGAG TGATAGTCAG TTGCCTTACT ATTGGACTTT	1920
TTTGTCTGGG AAAGCTGAGA ATCAAGCAAT CACGCTGTAC CACCATGATC AGCGTCGGAG	1980
TGTTTTAGTA GTACAAGAAT TCCTAGGAGA TTATTCTGGC TATGTTCAAT GTGACATGTT	2040
GCGGCAGTAA CTTAGGACTT TAGTCCTCTA GTTCTGCCTA TGCGATAGCA GTCCAAGGTT	2100
TAGGAGTAAG GCGACGCTAA GCTTGGTAAA CTGCGAACAG CTAGAAGCTT ATCGTCAACT	2160
GGAAGAAGCT GCACTTGTG GATGTTGGGC GCATGTGAGA AGGAAGTTTT TTGAAGTGCC	2220
CCCCAAGCAA GCAGATAAAT CATCCTTAGG AGCTAAAGGT TTAGCTTATT GTGATCAGTT	2280

1278

ATTTTCCTTG	GAAAGAGACT	GGGAGGCTTT	GCCAGCTGAT	GAACGACTAC	AGAAACGTCA	2340
AGAACATCTC	CAGCCCCTAA	TGGAAGACTT	CTTTGCTTGG	TGCCGCCGTC	AGTCAGTTTT	2400
AGCAGGTTCA	AAACTAGGAA	GGGCAATTGA	ATACAGCCTC	AAGTATGAAG	AAACCTTTTAA	2460
GACTATTTTG	AAAGACGGAC	ATCTGGTCCT	TTCCAATAAT	CTAGCTGAAC	GCGCCATTAA	2520
ATCATTGGTT	ATGGGACGGA	GTAAAAGAGT	CCAGTGGACT	CTTTTAGCCT	GAGCTCAGTT	2580
TAAAAAAGCG	AGGGTGGTTA	TTTTCTCAAA	GTTTTGAAGG	AGCTAAAGCA	AGAGCTATTG	2640
TTATGAGCTT	GTTGGAAACA	GCTAAACGTC	ATCAATTATA	GTGCGTTGAA	TCTATAACAG	2700
TACGCATCGA	CTGCTAAAAC	ATTTCTATAA	ATCAATTTTC	CTTTCCTAAT	CGATTGTGTC	2760
ATATCTTATT	TCAATCCATT	ATAAATAGCG	AGAAATATCT	ATCCTATCTT	CTAGAATGTC	2820
TTCCAAACGA	GGAAACTCTC	GTAAACAAAG	AGGTTTTAGA	GGCCTATTTA	CCGTGGACTA	2880
AAGTTGTACA	AGAAAAGTGC	AAATAAGAAA	TCTCCAGATT	AGGAACATATC	CGTGAGTTCT	2940
CTAGTCTGGA	GATTTTTCAA	TAGACTTCGT	TATTGGACGG	TTACAATTTA	TTATATGAAA	3000
ATCCCATATT	ATTCTCCAAT	TCTATATTTT	ACCTTTCTAA	ATGTATAGAT	TAACTACCTA	3060
ATTATAGCAT	ATAACGCAGA	TCCTTTTCAA	TCGTATGATT	TACTGCATTA	AATTAAGTAA	3120
AAAAATAAAG	GCAGTCCGAA	GACTGCCGAT	ATTTATCTCT	CATCTCTTTA	ATTATGGTAA	3180
GTAAATAAAT	AATTTCCCTA	AAGATATGGA	AATTATTAAT	ACTATAAATA	CATATTATAA	3240
AGTTTATAAA	TACTGTAAAA	ATCCTGAAGT	TAATTTTCTA	ATAAATATCA	ATATGTGTTA	3300
GTATCTTTTA	AATTTTLAGA	CAATTTACTA	GTTCTATAGA	CATGTTTAAC	AGACTCTATT	3360
TTACAATTCA	AAAATTTTCAT	CTGCCACTTC	ATTTAAAAAT	TCTATATCAT	GGGAAACAAT	3420
AAAAATTATT	TTATCCATGG	TTTTTACTTT	ATTAATCAGT	TCAGATATTT	TTATCATATT	3480
GGAATAATCC	ATACCACTTG	AAGGTCGTC	AAAAAAGACA	AATGGAGAAT	TCTTGACAT	3540
AACAGATGCT	ATTGCAAGCC	TTTGCTTTTG	CCCTCCTGAT	AAACTCATCG	GATGCCCTTC	3600
AATAAATTCG	TCCAGGCATA	AATCTTTTAA	CCCAAATCAT	TCATACCTCT	CTCAACTAGA	3660
TGTAACCTAC	AAAACCCCTG	ACCTCATGAG	CCACTTTCTT	CCTCCTCATG	AGGTCAGTTT	3720
TACTTTCTGC	TGTTCCAGTA	TCGTTTTTCC	TCGCTAGATT	TCCTCAAAAG	GGCAGACTCC	3780
TCCCTTGGTT	CGTCACACGA	TTTTTTCATC	TCGACTGTTC	TTTAATGCAT	CATTAACGAC	3840
GCTTTTCTTC	TAGGTGGTTC	ATAAGGAACA	GGAAGATTCA	GGTTGACTTT	TCTAATCCTA	3900
GAATAAAGTG	CTGAAAACAA	TTCGGAATAG	GCATAGAGAC	TAGACAATTT	GAGGAGCTGC	3960
TTGCGTCCTG	TTCGAACACA	TTTTCCCACC	ACGTGAAGAA	AAAGATGGCG		4010

(2) INFORMATION FOR SEQ ID NO: 254:

1279

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

ATGCATCCGT TTGTCAAGCC TAAATTGTAA TTTTTTTC	60
GAAAAATGACA TAAAAATATC ATTCCTAGGC CTATTTATGC	120
GAGTATTCAG TCGGTCAAAT GAAGCTGAAC GAACTCATTT	180
TTCGATGACA TTGTTGGGCT ACATAAGCAT CGTGGGTCAC	240
CTCGATTTCAT CTCTAAGAGA AACTTCAAGA CCAAACTCTCT	300
CTGTCGGTTC ATCGGCTAAA ATCAGCTGGC TGGGTTTAA	360
TTCGTTGTTG TTCGCCCCCA GACAACTCGG AGACCCTTTG	420
CTACTCTCTC TAAATCTCT TCCACCTTTT TGAGCTTGTC	480
ATTTTCAGCGC CACATGAGAT TGTACTCGAC CGTTTCATCA	540
AAACAGATAA GAGATATGTT CACGGATTAT TGTTTGCGAC	600
ATTTGTCTGA CCAAAAATCT CATACCGTCC GCTATAATCA	660
ATTTAACAAG GTCGACTTCC CACTACCACT CTTACCAACA	720
ATCAATCCTG AGAGATAAGT TATCCAAAAT CACTTTTCCC	780
TTTCAACTCA ATCATAAGAT GCCCCCTTTC AATAACTCTA	840
CTAGAAGCTA AGCCTAGCAC AAATAGTATA TCCAGACATG	900
AGTGGTAAGA ACGCATGGGC AAAGAAAATC AAGACTAGAA	960
AAGAGCAGAA CGAGGAGAGG ACGGTAGCGA TCGACCAGTT	1020
GTAATGATAT CCCTGCGCTT CAATAAGAAA GTTGTACTA	1080
ATGCTAAGGA GACCAAACAA AGCAAAGAGT AGGTAAAAAT	1140
GAATCCACTT TCTCTTGTG AATGGCTTGA ATAGATGAAA	1200
GACAATTTCT CAACTAACTC TGTAATCTCT TTTTGATGTT	1260
ATCGGATTAT TTAAGCCAGT TGTTGACAGG GAGGCTTCT	1320
TCATTGACCA AGCTAATAAT TGGATTGGAG AGATTTTCCT	1380
AAAAATGACC AATCTCCTTC ATAATAGGCA ATCTCGACAT	1440

1280

TTTTGCTGCT CTTCATACTT CATCGAATGA AAGGCAATTA ACTTCCCCAA GAGCTGATTT	1500
TTATCTTCTT CACCTTTCGT ACTTGCTGGC ATCAAAATAA CTTTTTTAAT ACCGGTATTT	1560
GGTAGCTTGA ATCCCTTGCT CTTTAGAAAA TTGCGATTGG CATAGTAAAC ATCCACCGTA	1620
TCTGTAACT GATATTGCTG AATCTGTTCT GATTGGACAA AATTTTTTAC AGGAAGACTG	1680
CTACTCTGCA CATAGCCCGC CTGCGTTTTT TCTACCAAAT CCTGATAAAA TCGATAGAAA	1740
TAATCTGTAG ATTTCCCTGA CCCTGCTAGC TCTTCTTGCC ACAGATTATC ATTGAGTTTG	1800
AAGGTTTCTA AGGTCAGGTA ATTACCTTGA CTTACCCACT GTTGCTGATA AGCAAGTTCT	1860
TTGTTTTCTT GTTCTAACT TCTGCCCACC CCAATCAGTA AGGCCGTCAG TAAAATAGTT	1920
GTCCCTATTT TCATCACATA ATTGAAGATA AGACCAAATT TGAAAGATGA AAAACCTTTC	1980
AGCAGAGAGC TGATTGTCAT TTTTGGATT AAGAGGTAAG TCAACCAACT GATAAAGAGA	2040
TAAAGCTGCA ACAGCAAAAA ATGAGACAAC CACAGCATAG GAAACAAATC TTTTGGCTTA	2100
TAATCAAGCA AGAAAAACAC GCCTAGATTG ATCACAAGAG CCCCACCTAG GAGGAGGTAA	2160
AGGTTGCCTT TTACAACATC AGCTAAAACA GCCCTATCTT GAAAACCAAG TAATTTTGT	2220
ACCCCAACTC TTTTCATCTC CATCATCGGT TGATACACTG TCACTAACAC AAGAAGCAAA	2280
ATAGCCAAGA CAAAAACAAT GGCAGATAAA AGCAAATCTC GATTTATGAC TTCCACTGCA	2340
CTTTTGTAGG TCGGCTCTAG CAAGGTAGCC TGGTCTATCT TGAAAAAATC GCTCCATTTT	2400
TGTACAATCC TATCCTTGTC CATCTCTGTG GTAGAAGTTA TCGTATAGCG ACCATTTAAA	2460
CTACGAGATG TATCCTTGAT ATAGGTTTGA AAAGTCATAA GCTGAATAGG TTTGGCTTTT	2520
AGAAAGGTCG GAATCGTACC AAGTTTATTG GAAATTTCTT TATTACTATA GACTCCTTCA	2580
CCATCTGTGG TAAATCAAG AGAAGAAATC CCAAATCTT GGTAGGGGAA GGTATCTTTA	2640
TCAAAAACAC CAGACTTGAC CACCTCATCA CCACTGTCTG TTTTGATGAT GGAGACTTTA	2700
TACTCCTTTG ATACATCCTC AAAAAATCGA AGAACAGACG CTGCAGGTTC GTTAATATCT	2760
TTCAAATACA AATCCAAAGA ATCTACAGG	2789

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

CTGCGAATTT TATTAAAGAT AATGTGTAA TTACAGCGGC TCACAACTAC TACAGACATG	60
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1281

ACTATGGGAA AGAAGCGGAT GATATTTATG TTCTTCCGGC TGTTAGTCCA AGTCAAGAAC	120
CATTTGGAAA GATCAAAGTA AAGGAAGTTC GTTATTTGAA GGAATTTAGA AATTTAAATT	180
CTAAGGATGC AAGGGAATAT GACTTGGCTT TATTAATTCT AGAAGAGCCC ATTGGTGCAA	240
AATTAGGGAC TTTGGGTCTT CCTACTAGTC AAAAAAATTT GACAGGAATA ACTGTGACTA	300
TCACAGGCTA TCCATCATAT AATTTTAAAA TTCATCAAAT GTATACAGAT AAGAAACAAG	360
TTTTAAGTGA TGATGGCATG TTCTTGGATT ACCAAGTTGA TACTTTAGAG GGGTCTAGTG	420
GATCTACAGT TTATGATGCT AGTCACCGTG TAGTAGGAGT GCATACTTTA GGAGATGGAG	480
CTAATCAAAT TAACAGTGCA GTTAAATTAA ATGAACGAAA TTTGCCATTT ATTTAWTCGG	540
TTCTTAAAGG TTACTCTCTT GAAGGATGGA AGAAAATAAA TGGTAGTTGG TACCATTATA	600
GACAACATGA TAAACAAACG GGTGGCAGG AGATAAATGA TACCTGGTAT TATTTAGACA	660
GTTCGGTAA GATGCTTACA GATTTGGCAA AAGTCCATGG AAAATGGTAT TATCTCAATT	720
CAAAATGGAGC AATGGTTACA GGTAGCCAAA CTATCGATGG TAAAGTTTAT AACTTCGCTT	780
CATCTGGTGA GTGGATTAA TGTTGGAGGA TATATAAAAT GAAGCTTTTG AAAAAATGA	840
TGCAAATCGC ACTAGCCACA TTTTCTTCG GTTTGTTAGC GACAAATACA GTATTTGCAG	900
ATGATTCTGA AGGATGGCAG TTTGTCCAAG AAAATGGTAG AACCTACTAC AAAAAGGGGG	960
ATCTAAAAGA AACCTACTGG AGAGTGATAG ATGGGAAGTA CTATTATTTT GATCCTTTAT	1020
CCGGAGAGAT GGTGTTCGGC TGGCAATATA TACCTGCTCC ACACAAGGGG GTTACGATTG	1080
GTCCTTCTCC AAGAATAGAG ATTGCTCTTA GACCAGATTG GTTTTATTTT GGTCAAGATG	1140
GTGTATTACA AGAATTTGTT GGCAAGCAAG TTTTAGAAGC AAAAAGCTGCT ACGAATACCA	1200
ACAAACATCA TGGGGAAGAA TATGATAGCC AAGCAGAGAA ACGAGTCTAT TATTTTGAAG	1260
ATCAGCGTAG TTATCATACT TTAAAACTG GTTGGATTTA TGAAGAGGGT CATTTGGTATT	1320
ATTTACAGAA GGATGGTGCC TTTGATTCGC GCATCAACAG ATTGACGGTT GGAGAGCTAG	1380
CACGTGGTTG GGTTAAGGAT TACCCTCTTA CGTATGATGA AGAGAAGCTA AAAGCAGCTC	1440
CATGGTACTA TCTAAATCCA GCAACTGGCA TTATGCAAAC AGGTTGGCAA TATCTAGGTA	1500
ATAGATGGTA CTACCTCCAT TCGTCAGGAG CTATGGCAAC TGGCTGGTAT AAGGAAGGCT	1560
CAACTTGGTA CTATCTAGAT GCTGAAAATG GTGATATGAG AACTGGCTGG CAAAACCTTG	1620
GGAACAAATG GTACTATCTC CGTTCATCAG GAGCTATGGC AACTGGTTGG TATCAGGAAA	1680
GTTGCACTTG GTACTATCTA AATGCAAGTA ATGGAGATAT GAAAACAGGC TGGTTCCAAG	1740
TCAATGGTAA CTGGTACTAT GCCTATGATT CAGGTGCTTT AGCTGTTAAT ACCACAGTAG	1800

1282

GTGGTTACTA CTTAACTAT AATGGTGAAT GGGTTAAGTA ATGAAGGCTA ATTGTAAACT	1860
GTGATGGATA CTTAACTTTG TATAATAGGT GGATAAAAGT CTTCAACAATC AAAAAACGCA	1920
TAGTATCAAG GTTTTCTGT ACTGCCCTCA AACAGTTAGA CAATTAATTT ATCCGAAGgA	1980
TTTAGTTCTG TATTGCACAG GGCTAAGTCC TTTTAGTTTT ACCTTAATTC GTTTATTGTT	2040
GTAGTAATCA ATATAGTCTA TAATGGCTTG TTCCAATTGC TTAAGCGACT GAAACGACTT	2100
CTCATAACCG TAAAACATTT CCGATTTCAG AATCCCAAAG AAGGACTCCA TCATACTATT	2160
GTCTGGGCTG TTTCCCTTAC GTGACATGGA TGCTTGAATT CCCTTACTCT CTAGGAACCG	2220
ATGATAAGAA TCGTGTGGT ATTGCCAGCC TTGGTCACTA TGGAGAATCG TATTCTCGTA	2280
GTGCTTCTCT GTGAATGCCT GTTCCAACAT TGTTTGTACT TGTTCTAAGT TGGGTGAAGT	2340
TGAAAGATTA TAGGCGATAA TTTGCTATT AAAGCCATCT AAAACTGGTG ATAAGTAAAG	2400
CTTTTGAGTA CTTGCTGGAA TGGCAAATTC TGTCACATCT GTGTAGCACT TTTCCATTGT	2460
TTTAGAGCCT TCAAATTGGC CTTGAATGAG ATTCG	2495

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 870 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TACCACCGTA TTCATCCAGC AAGATTGCCA TTTGTCTTTG GGTATTTCGC AGTTCTTTTA	60
GCAAGTCATC CACAAAAATA GTTTCAGGTA CAAAAAGTGG ATCTTGTAAG ATTCTCTTCC	120
AAACAATATT GTCAAAACCG TCCACAAAGC CTGCCTTAAG GAGACTCTTG GTGTGAATGA	180
TTCCAATTAC ATTGTCTTA TCCCCATCAT AAACCGGAT ACGAGAATAA TTTTGTTTTA	240
AAATACTTTG GATAATGGCT TGACTATCAT CCTGAATATC CACCATAAAG GCATCCGTTT	300
GAGGAACCAT AACCTCTCGT GCCATCAGTT CATCGAGCGA AAAGACACCT TGTCATCATCT	360
CAATCTCATC AGCATCCAAT GTTCTTTCAC TATTTGTCAG CATATAGGCA ATTTTCATCAC	420
GGGTCATCTT TTCATCCGCA TCATCGAATG ACATAGGAGT CAAATGGCTC AAGAAATTGG	480
TCGAAGCAGC TAAAAGCCAA ACAAAGGAC TGACTAGTTT TCCGATCCCA ATGATAATCG	540
GCGCTGTACG AATTGCCAAG GCATCCTTTA GATTAAAGAGC GATTCTCTTA GGATATAATT	600
CCCCAAAAAC GATGGAAATA TAGGTCAAAA ATGCCAAGGA TAGAAAAGTT GCCACGGCTT	660
GTGCTGTTTC GCCATTCCCA AGCCAAGAGG CAATCACACG TCCTAGAGTA TCAGTTAAAC	720

1283

TCGCCCCCTGA TAAGATTGTA ATCAGGGTGA TTCCTACCTG GATGGTTGAT AAAAAGTGGT	780
TAGGATTTTC TAGTACCTTC AGCAGGCGGA TGTCGCTCT GTCTCCTTCT TCCGCCTTTT	840
GTTCAACTCG GGCACGATTA AGAGAAACGG	870

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

CGTTCACAGA AGCCCGCATT CTCATCGCCA ATGTCGTGAT TGATTTGGCC CTTTCTCCAA	60
AATCCAATC AGCCTATGTA GCTATGGATA AGGCACTTGC TGACCTCAA ACATCAGGGC	120
ACTTGCCTAT TCCGCGACAC CTGCGTGATG GGCCTACAG TGGAAGCAAG GAACTGGGGA	180
ATGCCCAAGA CTATCTCTAT CCACACAAT ATCCTGGAAT TTGGGTCAAG CAAGACTATC	240
TGCCAGAAAA AATTCGTAAT CATCACTATT TCCAAGCAGA AGATACTGGT AAATATGAAC	300
GGGCTTTGGC TCAAAGAAAG GAAGCTATCG ACCGTTTGC AAAAACTGA AATCCTTTTC	360
AAAAAATTGC ACTTCTCTCT TGATTTTTTT TGAAGAAAGT GTATCATATA AATATAGAAA	420
CGCTGTGGTG TACGACTTCA CACTTAAGTG TTGACCGACT ATTTTGTGTA TTATTAGGGA	480
AACAAAAGTC TTCTAACAGC ATGTAGGCCG TCTCACACGG AACAGCTTC AGTTAGAGCG	540
AGTTGCCAC CTGCTTAATT GCGCGGGTTC AATACAAACC GTGAAGTTTC GGCACCAATA	600
CAGCTTTTTT CTTTGCCTCC TTAGCTCAGC TGGCAGAGCA GCGGACTCTT AATCCGTGGG	660
TCACAGGTTG GATCCCTGTA GGGGCGATAT AAATACAACA GGAAAGCCT TATAATATAG	720
GGCTTTTTTT GCTTCTCTTT TAAAAATTGT CGTGCAATTG GCCGTGTTT TACAACAAAC	780
TTTTCACAGC CATAACTCC TACTAATTT TTTCTCCAA GGTATGCCCA TAAACGTCAA	840
TCAACATGGA GATATCTTTA TGTCTAAAA TTTGGCTCTT TGTCAACTGT AGTGGGTGGA	900
AGTCAGCTAA GCTCGAGAAA GGACAAATTT TGTCTTTCT TTTTGTATAT TCAGAGCGAT	960
AAAAATCCGT TTTTGAAGT TTCAAAGTT CCGAAAACCA AAGGCATTGC GCTTGATAAG	1020
TTTGATGAGA TTATTGGTCG CTTCCAATTT GCGGTAGAA TAGTGTAGTT GAAGGGCGTT	1080
GACGATTTTC TCTTGTCTCT TTAGAAAGGT TTAAAGACA GTCTGAAAA GAGGAGGAAC	1140
CTGCTTTAGA TTGTCTCTCA TGAGTCCGAA AAATTTCTCC GGTGCCTTAT TCTGAAAGTG	1200

1284

AAACAGCAAG AGTTGATAGA GCTGATAGTG ATGTTTCAAG TCTTG

1245

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1684 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

ATGCCTATGT AACTCCACAT ATGACCCATA GCCACTGGAT TAAAAAGAT AGTTTGTCTG	60
AAGCTGAGAG AGCGGCACCC AGGCTTATGC TAAAGAGAAA GGTTCGACCC CTCCTTCGAC	120
AGACCATCAG GATTCAGGAA ATACTGAGGC AAAAGGAGCA GAAGCTATCT ACAACCGCGT	180
GAAAGCAGCT AAGAAGGTGC CACTTGATCG TATGCCTTAC AATCTTCAAT ATACTGTAGA	240
AGTCAAAAAC GGTAGTTTAA TCATACCTCA TTATGACCAT TACCATAACA TCAAATTTGA	300
GTGGTTTGAC GAAGGCCTTT ATGAGGCACC TAAGGGGTAT ACTCTTGAGG ATCTTTTGGC	360
GACTGTCAAG TACTATGTCG AACATCCAAA CGAACGTCCTG CATTCAGATA ATGGTTTTGG	420
TAACGCTAGC GACCATGTTC AAAGAAACAA AAATGGTCAA GCTGATACCA ATCAAACGGA	480
AAAACCAAGC GAGGAGAAAC CTCAGACAGA AAAACCTGAG GAAGAAACCC CTCGAGAAGA	540
GAAACCGCAA AGCGAGAAAC CAGAGTCTCC AAAACCAACA GAGGAACCAG AAGAATCACC	600
AGAGGAATCA GAAGAACCTC AGGTCGAGAC TGAAAAGGTT GAAGAAAAAC TGAGAGAGGC	660
TGAAGATTTA CTTGGAAAAA TCCAGGATCC AATTATCAAG TCCAATGCCA AAGAGACTCT	720
CACAGGATTA AAAAATAATT TACTATTTGG CACCCAGGAC AACAATACTA TTATGGCAGA	780
AGCTGAAAAA CTATTGGCTT TATTAAAGGA GAGTAAGTAA AGGTAGCAGC ATTTTCTAAC	840
TCCTAAAAAC AGGATAGGAG AACGGGAAAA CGAAAAATGA GAGCAGAATG TGAGTTCTAG	900
TTCTCATTTT TTTCATGAAA ATGTGCAAAA TATAGTAGAT TGAAACTAGA ATAGTATACC	960
TCTACTTCTA AAACATTGTT AGAAATCGAT TTGACTGTCC TGTTCCTTATT TCATTTTACT	1020
ATATCTTAAC AGATAGTGTA AATAAGATA AACTATTTAC TGGCTAATTA ATCAGTTAAA	1080
CACTAGTTAA GGAGTAATGA TGAAAAAAG AACAATACTA TTATTGATGG CCAGTCTGTT	1140
AGCTCTTGTC TTAGGAGCAT GTGGTTTCTT GGACATATTG ATCCTGGATC ATTCTCATCA	1200
GGATTACTCT TTAGTGCTAT TTTAGAACT GGGGTGGTTT GATGGAAAGT ATTGGTCTTG	1260
TTATCGTTTC ACATTCCAAA CACATTGCAG AAGGTGTTGT TGAACGATT AGTAAAGTAG	1320
CTAAAGATGT TCCGATTACT TATGTAAGAG GAACCGAGGG CGGAGGAATT GGAACGAGTT	1380

1285

TTGAACAAGT AGATAGGGTT GTTCCGAAA ATCCAGCAGA TACTTTACTT GCCTTTTTTG	1440
ACCTAGGTTC TGCTAAAATG AACTTAAAAA TGGTGAAGTGA TTTCAGTGAT AAAAGTATCA	1500
TCATCAACAG GGTTCCAATT GTAGAAGGTG CCTATAATGC AGCTGCTCTT CTCAGGCTG	1560
GTGCAGAACT GTCAGTTATT CAAACACAGT TaGCGGAgCt TGAAATCAAT AAATAAGGAA	1620
TTTTACTATA ACTCTTTTTA TAGATAAGCT ATTGaTTATC TCAACTATAA TAATGTTAAG	1680
TnAA	1684

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 970 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGGAGTGGAG AnATATGAAG ACACAAATTT TCACATTATT GAAAATCGTT GCTGAGATTA	60
TTATTATTTT GCCATTCTA ACTAATCTAT AAGTCTTTA TATTGCTGAA AACGCAATTC	120
AAAAAGGGCT ATTAATTGTG GATTTTCTAA TACCTGCAGA GATTGGATAA AGCGTTCAAT	180
CTCTTTTGA TTGCTTCCCT TTGTTTGAAG AAAGACACTC ATCTTCTTTA AAAATTGCCA	240
CGATACTTTT TCAAAAACAT CACACGGTCG TAACATCCTC TCCAACCTCGG CTCGAAGAT	300
TGGGATGTAG GAGAAAAGTT TTCGCTCCAT GAGTCTGAT AAGATATTTA AGAGTCCTTG	360
CTTCATATAC AATCGATTGT GTACTAACTC TTAAATTTCT TTGGATTTTT CGAGTAAGGA	420
GGTTGATAAA AAAATCAGAT CTGATTGCT CAAGAAGGGC ATGGTATTGC AAAAGAGATA	480
GAGTTCAAAC CAGGTCCAAG ACTCGATAGC ATAGAGATAG GTGGTCAAAA ACTCGCTATC	540
CTCCTCTGCT AGTGGGTAGC TTTTATTTAG TGAATGGATG GCATCTTTAA TCACGATGGC	600
ATTCAAACGA CGATAGGTCT GCGCCATCTG TTCTTGATCG ACTTCTTCCA ATAGCTGCTC	660
TAAAGCAGCT ATATCCTGAT GGGCAAAGCG ATTCACAACC TTTCGACCGA TTCGCATATG	720
TGGAGATTCT TGATAGTTGT TGAGCTTGTG CCCAACTCA TCAAAGGTCA CATTTATACC	780
TTGGATAGCT AGAATCAACT TATCCGCAGA CAGCATAGAC TGCCCTAGTT CAAACTTGGA	840
CAACTGAGAA GCTGTTAGAC CCTCACAAGC CACATCTGAC TGCTTGAGCT TTCTCGCCAA	900
ACGTAATTCC TTGTAAAATT CCCCAGTTC CATCTCTCA ATCATCTGAC CACCTCCTAG	960
CTTTTGCAGG	970

1286

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2996 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

GTGACCACG GGTAAACTA CCCTAACTGC AGCTATCACA ACTGTTTTGG CACGTCGCTT	60
GCCTTCATCA GTTAACCAAC CTAAAGACTA TGCCTCTATC GATGCTGCTC CAGAAGAACG	120
CGAACGCGGT ATCACTATCA AACTGCGCA CGTTGAGTAC GAAACTGAAA AACGTCACCTA	180
CGCTCACATC GACGCTCCAG GACACGCGGA CTACGTTAAA AACATGATCA CTGGTGCTGC	240
TCAAATGGAC GGAGCTATCC TTGTAGTAGC TTCAACTGAC GGACCAATGC CACAAACTCG	300
TGAGCACATC CTTCTTTTAC GTCAGGTTGG TGTAAACAC CTTATCGTCT TCATGAACAA	360
AGTTGACTTG GTTGACGACG AAGAATTGCT TGAATTGGTT GAAATGGAAA TCCGTGACCT	420
ATTGTCAGAA TACGACTTCC CAGGTGACGA TCTTCCAGTT ATCCAAGGTT CAGCACTTAA	480
AGCTCTTGAA GGTGACTCTA AATACGAAGA CATCGTTATG GAATTGATGA ACACAGTTGA	540
TGAGTATATC CCAGAACCAG AACGTGACAC TGACAAACCA TTGCTTCTTC CAGTCGAGGA	600
CGTATTCTCA ATCACTGGAC GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTATCGT	660
TAAAGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTCAA AAGCAGTTGT	720
TACTGGTGTT GAAATGTTCC GTAAACAACCT TGACGAAGGT CTTGCTGGAG ATAACGTAGG	780
TGTCCTTCTT CGTGGTGTTT AACGTGATGA AATCGAACGT GGACAAGTTA TCGCTAAACC	840
AGGTTCAATC AACCACACA CTAAATTCAA AGGTGAAGTC TACATCCTTA CTAAAGAAGA	900
AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACTAC	960
TGACGTTACA GGTTCATCG AACTTCCAGC AGGTACTGAA ATGGTAATGC CTGGTGATAA	1020
CGTGACAATC GACGTTGAGT TGATTCAACC AATCGCCGTA GAACAAGGTA CTACATTCTC	1080
TATCCGTGAG GGTGGACGTA CTGTTGGTTC AGGTATGGTT ACAGAAATCG AAGCTTAATT	1140
CGATTTAGTT CCCAGAAGAA CAATTATTTA AGTTAGACAC TAAAAGAATC TTGCTTGCA	1200
AGGTTCTTTT TTTAGATATT GAACTAATAC TCAATGAAAA TCAAAGAGCA AACTATAATA	1260
TATTGAAACT AGAATAGTAC ACATCTACTT CTAAAACATT GTTAGAAATC GATTTGACTG	1320
TCCTGATCGA TTTGTCTTGT TCTTATTTCA TTTTACTATA GAAAGTTAGC TACAGACTGC	1380
TCAAACATT GTTTTtaggt TGTAGATAGA ACTGACGAAG TCAGtAACAT CTATACGACA	1440

1287

AGGCGAAGCT GACGCGGTTT GAAGAGATTT TCGAAGAGTA TAATACTAGA CTAAAATCAA	1500
AAAGCATTAT ACAATAGTAA TATGAAATCA ATTAAAGAAG AAATCCAAAC CATCAAAACA	1560
CTTTTAAAAG ACTCTCGTAC AGCTAAATAT CATAAACGCC TTCAAATCGT TCTATTTTCGT	1620
CTGATGGGCA AATCTTATAA AGAGATTATA GAACTTTTAT AGTGGTTTGA AATAAGATGT	1680
GAACAACTCT ATCAGGAAAG TCAAATAAT TTATAGAAAT ATTTTAGCAG CCAAGGTGTA	1740
CTGTTATAGA TTCAATACAC TTTAGACTGT AATCAAACAA CGATTTGGCG AAATGTAAAA	1800
AATATGAGGA GTTCGGACTC GACTCTCTCC TTCAAGAAAC ACGTGGTGGT CGTAACCATG	1860
CTTATATGAC GGTGAGCAA GAGAAAGTCT TTCTTGCCCG CCATTTGAAG GCTACAGAGG	1920
CAGGAGAATT TGTTACAATT GATGCCTTAT TTCAGGCTTA TAAAAAGGAG TTAGGTCGTT	1980
CCTACACACG TGATGCCTTC TATCAACTGT TGAAGCGCCA TGGTTGGCGA AATATTACGC	2040
CACGTCCAGA ACATCCTAAG AAAGCAGATG CTCAAACCAT TGTCGCGTCT AAAAAATAAG	2100
TCTCAATTCA AGAAGACAAG TGAAGTGCAC CCCAAAAGTT AGACAGAAAA AATCTAAGTT	2160
TTGGGGTGTT TTTATTATGA AATTAAGTTA TGATGATAAA GTTCAGATCT ATGAAGTTAG	2220
AAAACAAGGA TATAGCTTAG AGAAGCTTTC AAATAAATTT GGGATAAACA ATTCTAATCT	2280
TAGGTACATG ATTAAATTGA TTGATCGTTA CGGAATAGAG TTCGTCAAAA AAGGAAAAAA	2340
TCGTACTAT TCTCCTGATT TAAAACAAGA AATGATTCAT AAAGTCTGAC ATGAAGGCTG	2400
GACTAAAGAT AGAGTTTCTC TTGAATACTG TCTCCCAAGT CGTACGATAC TTCTTAAGTG	2460
GCTAGCACAA TACAGGAAAA ACGGGTATAC TATTGTTGAG AAAACAAGAG GGAGAGTACC	2520
TGAGAGCGGA GAATGCCATC CTAAAAAGT TAAGAGAACT CCGATTGAAG GAGGAAAAAG	2580
AGAAAGAAGA AAGACAGAAA TTATTCAAGA ATTAATGACT GAGTTTTTCGT TAGATATTCT	2640
TCTAAAAGCC ATTAAACTAG CTCGTTTGAC CTACTACTAT CACTTGAAAC AGCTAGATAA	2700
ACCAGATAAG GACCAAGAGC TTAAAGCTGA AATTCAATCC ATTTTATATCG AACACAAGGG	2760
AAATTATGCT TATCGTCGGA TTTATTTAGA ACTAAGAAAT CGTGGTTATC TGGTAAATCA	2820
TAAAAGAGTT CAAGGCTTGA TAAAAGTACT CAATTTACAA GCTAAAATGC GACAGAAACG	2880
AAAATATTCT TCTCATAAAG GAGACGTTGG CAAGAAGGCA GAGAATCTCA TTCAAGGACA	2940
ATTTGAAGGC TCTAAAACAA TGGAAAAGTG CTACACAGAT GTGACAGAAT TTGCCG	2996

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 837 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTTATCAACT CCCGACATGG CTCTCAGACC AATCCAAATC CCTAAAAAAA TCAGAACAAG	60
GATGGTGGTC AAGATCAAAC TCTCGAAATA TAAAGAAAAT AGTTGCAGTA GCATGATTTC	120
TCTCATTTCT ATCTTTTTTA AAGAGTAAAC TCAGCTAGTC CAACTAACTG AGTTTTCTCT	180
TATCTATTAT ATCAAATATA AGTCCGTTTG TAACTAGCGA AGAATTCTTT TGTCCGCTCT	240
TCTTTAGGGG TGTGGATAAT CTCATCCGGA GTTCCAGACT CGATGATTTT CCCCTTATCT	300
AAGAAGAGAA TTTTATCCGC AACTTGGGCT ACAAAGGACA TGTCATGACT GACCAAAATC	360
ATGGTCTGAC CTGACTTAGC AGCATCTGCA ATAGACTTTT CTACTTCACC GACCAATTCT	420
GGGTCAAGGG CTGAAGTTGG TTCGTCTAAG AGCAAAACAT CTGGTTTCAT AGCAAGCGCA	480
CGCGCTAGGG CAACCCGTTG CTTCTGTCCA CCTGATAAAT GGCGAGGATA ATGGTTTTC	540
CGGTCCGAAA GCCCAACCTT AGCCAACTCT TCCTTGCGAA TCTTAGTCGC TTCTTGGTCA	600
GATAATTTCT TGACAACAAC CAAGCCTTCT TTCACATTAT CAAGTGCTGT TCGGCGTTCA	660
AACAAATTAA ACTGTTGGAA AACCATAGAC AACTTACGAC GTAGGGCAAG GATTTCTTCT	720
TGAGTGATTT TAGAAAAATC AACTGAAAAA CCATCAATCT GAATAGAGCC ACTGTCAGGT	780
GTTTCTAGAT AATTGAGACT GCGAGAAAGG TTGATTTTCA GCTCTGAAGA CCAATCA	837

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 868 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CCGAACAAAA TGGGCTAATT AGATTATAGT AAGAAAGGTA AGTTAAAAAT GAGAATTGCA	60
ATTGGATGTG ACCACATCGT AACTGATGAA AAAATGGCGG TTTCAGAATT TTTGAAATCA	120
AAAGGATATG AAGTCATTGA CTTTGGTACC TATGACCATA CACGGACTCA CTACCCAATC	180
TTTGGTAAAA AAGTAGGGGA AGCTGTAAC TACGGTCAAG CTGATCTTGG AGTATGTATC	240
TGTGGTACTG GTGTTGGTAT CAACAACGCT GTAAATAAAG TTCCAGGTGT TCGTTCTGCC	300
TTGGTTCGTG ATATGACAAC AGCCCTTTAT GCTAAAGAAC AATTGAACGC TAACGTTATT	360
GGTTTGGTG GTAAAATTAC TGGTGAATTG CTTATGTGTG ATATCATCGA AGCTTTCATC	420

1289

CATGCTGAAT ACAAACCAAC TGAAGAAAAC AAAAAATTGA TTGCGAAAAT TGAACATGTT	480
GAAAGTCACA ATGCTCAACA AACAGACGCA AACTTCTTTA CAGAATTCCT TGAGAAATGG	540
GATCGTGGAG AATACCACGA CTAAGAGGTG ACCTATGATT TTAACAGTCA CAATGAACCC	600
ATCCATCGAT ATTTCTATC CCTTGGATGA GTTGAAGATT GATACTGTCA ATCGTGTGGT	660
GGATGTAACC AAAACGGCTG GTGGTAAGGG ACTCAATGTT ACCCGAGTAC TTTCAGAATT	720
TGGCGATTCT GTTCTTGCTA CTGGTTTAGT GGGTGGCAA CTGGTGAGT TTTTGGTTGA	780
ACATATCGAT AATCAAGTAA AGAAAGATTT CTTCTCAATT AAGGGAGAAA CTCGTAAC TG	840
TATCGCTATT CTCCACGGAG ACAACCAA	868

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CCGTTCAAAG TCTTCATAAG ACTCGAAAGT CACAGTTCTT TCGTTCTTGC TGGCATCTAT	60
ATAGGTAATT TCAATCATGT TTAAACTCC TTTGTTAAT GCTAACTTA TTTTACTCCT	120
TATAAAGAG AATGTCAAGA AAAATGATTG CGCACGCAAC TTTTTTTAAA ATCATCTTAA	180
ATCAAGAAAT CCAAACCTGC TTCCAAGCTT TCTTCGACAG TCTTTTGTAG CGAGGCCAGT	240
GTCTTTTGCC CATCATTTGT CAGGCAGATA AACTAGAGC GTCTATCTTG ATGGCAACAC	300
ATGCGACTGA GTAGACCGCA ATTTT TAGCT TCCAAGCGAG CCACCATCCT AGAAACTGCG	360
CTCGGGCTCA GATGAAGCTT ATCTGGCAGG TCAATCTGGC GTAGAGATTT TTCTTCAGCC	420
AAGTCCAGAT AGTAGAGCAG GTAGAACTCT TTCAAGGTCA GACTTTGCTC GCTCTGTTGG	480
GCAATGGTCT CTTCCAAGAG ACTTTCAATT TCTTTCTGAC GCCGATTGAA GTCAAACCAT	540
TTTTCCAAAT AGGTCAAGT GTCTCCTTTC TTTT TAGAGT CATAAATAGA AGAAAGTCCA	600
TTAACGGGCA GTCTCTGCGT CACAAGATGA TTGCGCATGC AATAATTATA CTACTTTTCA	660
AGAATGCTGG CAAGCTCTGT TTTT TAGTGG TTTTATTTT GTGTGAATAA TGGGGGAATC	720
CTATTGTTTC AATTTCTAAC TCCTTATCAC ATTCGAATTC AGATTTTATT TCATTTCTCT	780
ATCTATAGTT GCTTAGTTTA AAATAAGCAT GGTCTAATAA AGCTATGCAT ATAGTACTGA	840
TTTTAAACAA GGAGCATTAG ATTCCATTAA AGGAGGGCAC AGACATGTCG AGGCGGCCAA	900

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AGTTTTTGAT	GTGCGCGTCA	GAAGTCTCTT	CACGTGGGAA	AAGAAAGACG	TAAACAAGGG	960
AACTTAGAGC	GGAAAAAGCG	AGTCGTCAAA	AAGCGTAAGA	TCCCTTTAGA	AGAATTGAAA	1020
GCCTTTGTAG	AGGCTCATCC	AGACGCTTTT	TTACGGGAAA	TTGCGGCCCG	TTTTGATTGT	1080
GCTTTGCCCT	CCGTATGGGC	AGTTTTAAAG	CAGATTAAGG	TCATTTTAAA	AAAGACGACC	1140
AGTTTTAGGG	AACAAAAGCC	TGAGAAAGTT	TCTGAGTTTC	TTGATATTTT	GGATAACCTA	1200
AAAGATTTAC	CAGTCCTATA	TATTGACGAA	ACGGGAATCG	ACCGCTACCT	CTATCGTCCT	1260
TATGCAGGGG	CTCCTAGAGG	GGAGAAAGTC	TATGGCAAGA	TTAGCGGACG	GCGTTTTGAG	1320
CGGACTAATG	AGGTGGAGCA	AAACTCAAT	GGTAGTTTTC	TAATCAGATA	TATTGATTCA	1380
CAAAATTAGAG	AATGAAAGAA	TAATTATGCA	TAAAAATAGG	AATATAAACC	AAAAATTAGC	1440
TGATTTATAC	TCATTTGCGT	GTCTTTATAA	AAAACCTTATC	TTATAATATA	TATATATATA	1500
TATACAAAAT	AGTAAAATGC	TTTTTTTTTT	TAGCAAAAAT	ACCTCAAGTT	TCTTGCTATT	1560
TTGGGTTCCT	TATTCTATAA	TTATAGTATG	GTAATTTTAT	TATATCCATA	CATGAAAATA	1620
ATACTCGAAA	GGAAATTTC	AAATATTTTT	TAGACGTCAG	AAGGGTGAAT	ATAGAGAAAC	1680
AGACCGAGTA	ACTCGGTTC	AATTAATCAA	ATCAGGGAAG	CATTGGCTAC	GGGCCTCGAC	1740
TTCTCTTTTT	GGCTTGTTTA	AGGTCTTGCG	AGGTGGTGTT	GATACTACTC	AGGTCATGAC	1800
CGAAACGGTA	GAAGATAAAG	TAAGTCATTC	AATTACTGGG	CTTGATATCC	TCAAGGGGAT	1860
AGTTGCTGCG	GGAGCTGTCA	TAAGTGGAAC	CGTTGCAACT	CAAACGAAGG	TATTTACAAA	1920
TGAGTCAGCA	GTAATTGAAA	AACTGTAGA	GAAAACGGAT	GCTTTGGCAA	CAAATGATAC	1980
AGTAGTTCTA	GGTACGATAT	CTACAAGTAA	TTCAAGCGAGT	TCAACTAGTT	TGTCAGCTTC	2040
AGAGTCGGCA	AGTACATCTG	CATCTGAGTC	AGCCTCAACC	AGCGCTTCGA	CCTCAGCAAG	2100
TACAAGTGCA	TCAGAATCAG	CAAGTACATC	GGCTTCGACA	AGTATTTCTG	CATCATCTAC	2160
TGTGGTAGGT	TCACAAACAG	CTGCCGCTAC	AGAAGCAACT	GCTAAGAAGG	TCGAAGAAGA	2220
TCGTAAGAAA	CCAGCTAGTG	ATTATGTAGC	ATCAGTTACA	AATGTCAATC	TCCAATCTTA	2280
TGCTAAGCGA	CGCAAGCGTT	CAGTGGATTC	CATCGAGCAA	TTGCTGGCTT	CTATAAAAAA	2340
TGCTGCTGTT	TTTTCTGGCA	ATACGATTGT	AAATGGCGCC	CCTGCAATTA	ATGCAAGTCT	2400
AAACATTGCT	AAAAGTGAGA	CAAAAGTTTA	TACAGGTGAA	GGTGTAGATT	CGGTATATCG	2460
TGTTCCAATT	TACTATAAAT	TGAAAGTGAC	AAATGATGGT	TCAAAATGA	CCTTTACCTA	2520
TACGGTTACG	TATGTGAATC	CTAAAACAAA	TGATCTTGGT	AATATATCAA	GTATGCGTCC	2580
TGGATATTCT	ATCTATAATT	CAGGTACTTC	AACACAAACA	ATGTTAACCC	TTGGCAGTGA	2640
TCTTGGTAAA	CCTTCAGGTG	TAAAGAATA	CATTACTGAC	AAAAATGGTA	GACAGGTCTT	2700

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ATCCTATAAT ACATCTACAA TGACGACGCA GGCTAGTGGG TATACTTGGG GAAATGGTGC	2760
CCAAATGAAT GGTTCCTTTG CTAAGAAAGG ATATGGATTA ACATCATCTT GGACTGTACC	2820
AATTACTGGA ACGGATACAT CCTTTACATT TACCCCTTAC GCTGCTAGAA CAGATAGAAT	2880
TGGAATTAAC TACTTCAATG GTGGAGGAAA GGCTAGTTGAA TCTAGCACGA CCAGTCAGTC	2940
ACTTTCACAG TCTAAGTCAC TCTCAGTAAG TGCTAGTCAA AGCGCCTCAG CTTCAGCATC	3000
AACAAGTGCG TCGGCTTCAG CATCAACCAG TGCCTCGGCT TCAGCGTCAA CCAGTGCGTC	3060
AGCTTCAGCA AGTACCAGTG CTTCAGTCTC AGCATCAACA AGTGCTTCAG CCTCAGCATC	3120
GACAAGTGCC TCGGCTTCAG CAAGCACATC AGCATCTGAA TCAGCGTCAA CCAGTGCTTC	3180
GGCTTCAGCA AGTACCAGTG CTTCAGCTTC AGCATCAACC AGCGCCTCGG CCTCAGCAAG	3240
CACCTCAGCT TCTGAATCGG CCTCAACCAG CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC	3300
TGAATCGGCC TCAACCAGCG CCTCAGCCTC AGCATCAACG AGTGCTTCGG CTTCAGCAAG	3360
CACAAGCGCC TCGGGTTCAG CATCAACGAG TACGTCAGCT TCAGCGTCAA CCAGTGCTTC	3420
AGCCTCAGCA TCAACAAGTG CGTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA	3480
ACGAGTGCGT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT CAGCAAGCAC CTCAGCTTCT	3540
GAATCGGCCT CAACCAGTGC GTCACCTCAG CATCGACAAG CGCCTCAGCT TCAGCAAGTA	3600
CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG	3660
CATCAACCAG TGCGTCAGCC TCAGCAAGTA CTAGTGCATC GGCTTCAGCA TCAACCAGTG	3720
CCTCGGCTTC AGCGTCAAAC AGTG	3744

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

CGATAAAGAG GCCTTGAGTA ATCTCAATTT GCAGATTGAA AATGGAGAGA TTATGGGCTT	60
GATTGGTCAT AATGGGCTG GAAAATCGAC CACTATAAAA TCCCTAGTCA GTATCATTTT	120
ACCCAGCAGT GGTCGTATTT TGGTAGACGG TCAGGAGTTA TCGGAAAATC GCTTGGCTAT	180
TAAACGAAAG ATTGGCTACG TAGCAGACTC GCCTGACTTA TTTTACGCT TAACGGCCAA	240
TGAATTTTGG GAATTGATCG CCTCATCCTA TGATCTGAGT AGATCTGACT TGGAGGCTAG	300

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TCTAGCTAGG CTATTGAACG TTTTGTGATTT TGCTGAAAAT CGCTATCAGG TTATTGAAAC	360
TCTTTCTCAC GGAATGCGTC AGAAAGTCTT TGTCATCGGA GCACTCTTGT CTGATCCCGA	420
TATTTGGGTC TTGGATGAAC CCTTGACTGG TTTGGATCCC CAGGCTGCCT TTGATTGAA	480
ACAGATGATG AAGGAACATG CACAAAAAGG GAAGACAGTC TTGTTTTCAA CTCATGTCTT	540
AGAGGTGGCA GAGCAAGTCT GTGATCGGAT TGCCATTTTG AAAAAGGGGC ATTTGATTTA	600
TTGTGGTAGT GTAGAGGACT TGAGAAAAGA TTACCCAGAC CAGTCTTTGG AAAGTATCTA	660
CCTTAGTCTT GCTGGTAGAA AAGAGGAGGT TGCGGATGCG TCTCAAGGTC ATTAATAAAT	720
TAGTTGATAT CAATATCCTT TATTCATCTC AAGAAGCTAA TCTGGCTAAT CTACGAAAGA	780
AGCAGGCTAA GAATC	795

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TGGTAATGTG CTTGGCAGCw TCCTTGACAC TGCTACTACC ATTTCCCATATA GCGACCGACA	60
TACCAACGCC AGCCAGCATT TCAAGATCAT TATCTGAGTC ACCAAAAGCC ATGACTTGGT	120
TGAGGTCAAA GCCATATTCT TTCCCAACTC GCGGAATGCC TTCTAATTTA GAATTTCCCT	180
GATTGATGAC ATCCGATGCA AAAGGATTGC TACGTGTCAA TTTCAAGTCT TCAAAATCAG	240
CTGCCGCCTT CTCAGATTCT TCTGGTGTCA TCAGCATCAA AACTTGGTAG ATAGGCTGAT	300
TCATCAGGTG AAGCAGGTCC TCTTCCTTTT GGGGAACAAC CTTGCTGACC ATGCGATTAA	360
AAGACTGACT CACCGTCCGA GTTAAAACAG AGGGAACGAA GCGACTAATT CGTTGGGAAA	420
AAGAACCCAG ACCAAAGGAC ATGATTTTAG AACCCAACAT GGCATCCTTG GTCCCTAGAG	480
CAATCTCCGT GCCCTCTTTT TTAGCATAGC TAATTAGATG GCGCAAATGT AACTTGGA	540
TAGGGCTCGT GAACAAGACT CTGTCTTTAC TAAAGATATA CTGGCCATTA TAGGTTACCG	600
CAAAATCCAG ATCCAAATCG TCCATCAATT CCTTAACAAA AAAAGGTCCCT CGCCCTGTCTG	660
CTACGCCAAC TAGTACCCCT TGTTCTTTGA CAATCTTAAT CGCATCCTTA GTGGATTTC	720
AAACTCTTT GCGATTGTTG ACCAAGGTTT CATCGATATC AAAAAAACA GCTTTGACTT	780
CCATCCTATC CCAATCTCCC CTTTTGTGAT ACAATGATTA TACCACATTT CAGAAAGAGT	840
GAGTAAATCA TGCCTAAGAA AATCCTTGTT TTACATACGG GTGGAACATAT TTCCATGCAG	900

1293

GCCGATGCTT CTGGCGCTGT TGTGACGAGT TCAGATAATC CCATGAACCA TGTGTCCAAC	960
CCACTTGAAG GAATCCAAGT CCACGCCTTG GACTTTTTTA ACCTTCCAAG TCCCCATATC	1020
AAACCCAAAC ATATGCTGGT CCTCTACCAG AAAATTAAAG AGGAAGCAGA TAACTACGAT	1080
GGAGTGGTGA TCACACACGG AACCGATACT TTAGAGGAAA CAGCCTATTT CCTTGATACC	1140
ATGGAAGTTC CCCATATGCC TATCGTTCTA ACAGGAGCCA TGCGTACTCC AATGAGCTCG	1200
GTAGTGATGG TGTTTATAAT TACCTAAGTG CTTTACGAGT GGCCAGCGAT GACAGGGCTG	1260
CTGACAAAGG AGTTTTGGTC GTTATGAACG ATGAAATCCA CGCTGCCAAG TATGTCACCA	1320
AAACACATAC GACTAATGTC AGCACCTTCC AGACTCCAAC ACATGGCCCC CTGGTCTCA	1380
TCATGAAACA GGAAATCCTC TACTTCAAAA CAGCTGAACC TCGTGTTCCG TTTGACCTTG	1440
ATCACATACA AGGTTTAGTC CCTATCATCT CGGCTTATGC TGGTATGACA GATGAGCTGA	1500
TTGATATGCT GGATTTAGAA CACTTGACG GTTTGATTAT CCAAGCCTTC GGAGCTGGTA	1560
ATATTCCCAA AGAAACGGCT CAAAAATTAG AAAGCCTTCT GCAAAAAGGA ATTCCAGTCG	1620
CTCTGGTATC ACGATGCTTT AACGGTATTG CCGAGCCTGT TTATGCATAC CAGGGTGGGG	1680
GCGTACAGTT GCAAAAAGCA GGCGTTTCT TGTAAAGA ACTCAACGCC CAAAAAGCTC	1740
GCTTGAAACT CCTCATCGCC CTCAATGCCG GACTAACAGG ACAGGCTTTG AAAGACTATA	1800
TGGAAGGCTA ATACTCTTCG AAAATCTCTG CAAACCACGT CACGTCGCCT TACCGTATGT	1860
ATGGtACTGA CTTCGTCAGT TTCATCTACA ACCTCAAAAA CATGTTTGA GCTGACTTCG	1920
TCAGTTCTAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTCGTCAGT TCTATCTACA	1980
ACCTCAAAAA CATGTTTGA GCTGACTTCG TCAGTTCTAT CTACAACCTC AAAAACATGT	2040
TTTGAGCTGA CTTCGTCAGT TCTATCTACA ACCTCAAAAA CATGTTTGA GCTGACTTCG	2100
TCAGTTCTAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTCGTCAGk TCTATCTACA	2160
ACCTCAAAAA CATGTTTGA GCTGACTTCG TTAGTTTCAT CTACAACCTC AAAAACATGT	2220
TTTGAGCTGA C	2231

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

1294

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GAGTCAAAGG CTCCGAGGTT GACTTTTTTAC AAGGGGACAG GTGAATATTA TCTAGACCTG      60
TCAGAAATTC TCTTCTTTGA AACAGAAGGG AGCAAGATCT ACGCTCATAA CCAGAAGGAA      120
GCTTATGAGG TTCGCCTCAA GCTCTATGAG TTGGAGTCTA TCTTGCCTCG CTATTTTAAT      180
CGAGTTTCCA AGTCAACGAT CGCAAACATC CGTCAGATTT ACTCAGTGGA CAAGTCCTTT      240
TCAGGAACGG GCACCATTTC CTTTATCAG ACGCACAAGG AGGTTCATGT CTCACGGCAT      300
TACCAATCCC TCCTAAAAGA AAATCTAAGA AACATGAGGT AAAAAACATG AAAAAGAAAG      360
CATTTGGTAT TGTTTTATTG GTTTTAGCAG CTTGGATCTT GCTGCAAGGG AATTTTGGAA      420
TTCCTTCTTT GGATGGTAAA ATATGGCCTT TACTAGGTAT TGTTTTTTTT GCTTATAAGT      480
CCATTGAGTC CATCCTTAGA CGTCATCTCA CTTCGGCAGT TTTTACAGGT TTACTGGCGC      540
TCATCATTCG AAATTACGCT TATGACTTGT TACCAGTTAC CAATCATTCT CTTATTTGGG      600
CTAGCATCTT GGTGGTACTT GGTGTTGGTT ATCTGACGCA TTCAAGTAAG TTCTGGAATG      660
AAAAAAATG GTGGTACAAT GGGAAAAAAA CAGTCGTCAC GGATAAGGAA GTCGCTTTTG      720
GTAGCGGGAC CTTCTATAAG CAAGATCAAG ATCTCGTAGA TGACCAAGTG GAAGTCGCTT      780
TTGGGGATGC TAAATCTAC TATGATAATG CAGAGATGCT AGGTGATTTT GCAACTTTAA      840
ATATTGAAGT GGCCTTCGGG AATGCAACCG TCTATGTTCC ACAACACTGG CGTGTAGATT      900
TGAAAGTAGA AACCTCCTTT GGTGCAGCTA AGGCTGACGC TCCTGTAGCC CCAACCAGCA      960
AAACCTTGAT TATCCGTGGA GATGTGGCTT TTGGGAAGTT GGAAATTGTC TACGTTAAAT      1020
AAAAAATCT TCACCTCAAC CATCAAAATA GACGTACTAA GAGTAGGAAA TTGATGCCTT      1080
GCTCTGATTT CAGTTCATAG GTTGTTAGAC TTTAAAAAAT GAAATGCTGC CTTTAAAAGT      1140
TGTATATTTT TCGATATTTT GGCTTTTACG TTTGATGTAT CTATGTACTA CAGCGTAGAT      1200
GATGTAGTGT CAAATGCTTT TAAAAAACGG ATGATATTGG ACAGTTTTTT TGCCTTTAAT      1260
TGCTCAGGAA CCATGAAAGT CAGTACCTGG GTTTATGACA AGGAGAATG      1310

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(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5922 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

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ACTCTGATTT GATTGGAACG ACAGTCGGTG CCATTGCAGT TACTTCAAAC GTAACGACTT      60
ATGTTGAGTC TGCTGCTGGT ATCGGTGCAG GTGGACGTAC TGTTTGACA GCCTTGTTG      120

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1295

TAGCTATCTG	TTTTGCGATT	TCAAGCTTCT	TTAGCCCACT	TCTAGCGATC	GTACCAACAG	180
CGGCTACAGC	TCCAATCTTG	ATTATCGTTG	GGATTATGAT	GCTTGGTAGC	TTGAAAAATA	240
TCCATTGGGA	TGATATGTCT	GAAGCAGTTC	CTGCCCTTCT	CACATCTATC	TTTATGGGAT	300
TCAGCTACTC	TATCACTCAA	GGGATTGCAG	TTGGTTTCTT	GACTTACACT	TTGACTAAGC	360
TTGTTAAAGG	TCAAGTTAAA	GATGTTTCATG	TCATGATTTG	GATTTTGGAT	GCCTTGTTTA	420
TCCTTAACTA	CATCAGCATG	GCCTTATAAT	AGAATGACCC	AGGGGGATTT	CCCCCCTTTT	480
TTAATACAaG	GAGATAGGTG	ATGAAAGAGA	AAAATATGTG	GAAAGAATTG	TTGAATCGTG	540
CAGGCTGGAT	TTTGGTCTTT	TTACTTGCCG	TCCTTTTATA	TCAGGTTCCC	CTAGTGGTTA	600
CCTCTATTTT	GACTTTAAAA	GAAGTAGCCC	TGCTACAGTC	AGGGCTGATA	GTGCTGGCC	660
TTTCAATTGT	GGTCTGGCT	CTATTTATTA	TGGGAGCTCG	TAAAACCAAG	TTAGCTAGTT	720
TTAATTTTTC	TTTTTTTAGA	GCTAAAGATT	TGGCACGTTT	GGGCTTGAGT	TATCTAGTTA	780
TTGTGGGGTC	AAATATACTT	GGTTCCATTT	TATTGCAACT	GTCAAATGAG	ACGACAACAG	840
CTAACCAGTC	TCAGATTAAT	GATATGGTTC	AAAATAGTTC	GTTGATTTCC	AGTTTCTTCT	900
TGCTAGCCTT	GCTTGCTCCG	ATTTGTGAGG	AAATCTTGTC	TCGTGGGATT	GTTCCCTAAAA	960
AGATTTTCCG	AGGCAAGGAG	AACCTGGGAT	TTGTAGTCGG	TACGATTGTG	TTTGCTTTAT	1020
TGCATCAACC	AAGTAATTTA	CCTTCTTTAT	TGATTTATGG	AGGTATGTCG	ACAGTTCTAT	1080
CTTGACAGC	CTACAAGACC	CAACGTTTGG	AAATGTCGAT	CTTGCTTCAC	ATGATTGTTA	1140
ATGGGATTGC	TTTCTGTTTG	TTGGCTCTTG	TGGTGATTAT	GAGTCGGACA	TTAGGAATTT	1200
CTGTTTAAAA	GTTTTTATGT	AGGAACCGAC	CTCTTCTTAC	CAGGGAAAGA	TGAATGCAAT	1260
CGTGTCATC	TTTTTCTTTT	TATGGTAAAA	TAGAAAAATA	ATATGATGAA	AATCCTTGAG	1320
GGAGTGACCG	ATATGTCAAG	TAAAGCCAAT	CATGCAAAGA	CAGTTATTTG	CGGAATTATC	1380
AATGTAACCC	CAGACTCCTT	TTCGGACGGT	GGTCAATTTT	TTGCTCTTGA	GCAGGCGCTC	1440
CAGCAGGCTC	GTAAATTGAT	AGCAGAAGGA	GCCAGTATGC	TAGATATCGG	CGGAGAATCG	1500
ACTCGCCCGG	GAAGTAGCTA	TGTTGAGATA	GAAGAGGAAA	TCCAGCGTGT	TGTTCCAGTG	1560
ATCAAAGCGA	TTGCAAGGA	AAGTGATGTC	CTCATCTCTA	TTGATACTTG	GAAGAGTCAA	1620
GTAGCAGAGG	CTGCTTTGGC	TGCTGGTGCC	GATCTAGTCA	ATGATATCAC	TGGTCTTATG	1680
GGTGATGAGA	AAATGGCTTA	TGTGGTAGCT	GAAGCGAGAg	CGAAAGTGGT	CATCATGTTT	1740
AACCCAGTTA	TGGCTCGACC	TCAGCATCCT	AGTTCGCTTA	TCTTCCCTCA	TTTTGGTTTT	1800
GGTCAAACCT	TTACAGAAAA	AGAGTTAGCT	GACTTTGAAA	CATTGCCAAT	CGAAGACTTG	1860

1296

ATGGTGGCTT	TCTTTGAACG	AGCACTAGCG	AGAGCGGCAG	AAGCTGGTAT	TGCACCAGAA	1920
AATATCCTGT	TGGATCCAGG	AATTGGCTTT	GGTCTGACCA	AGAAAGAAAA	TCTGCTTCTT	1980
TTACGGGACC	TGGATAAACT	ACATCAGAAG	GGCTATCCAA	TCTTTCCTCGG	AGTGTGCGCGC	2040
AAGCgATTTG	TCATCAATAT	CCTAGAGGAG	AATGGTTTTG	AAGTCAATCC	TGAGACAGAG	2100
CTTGGTTTCC	GAAATCGGGA	CACGGCTTCG	GCTCATGTAA	CTAGTATCGC	TGCGAGACAG	2160
GGTGTAGAAG	TGGTGCGCGT	GCATGACGTA	GCTAGTCACA	GGATGGCAGT	TGAAATTGCC	2220
TCTGCCATTC	GTCTGGCTGA	TGAAGCGGAA	AATTTAGATT	TAAAAACAATA	TAAATAAGAT	2280
GAAAGAAATT	GAAAACAATC	AGTGGATTGC	TAAC TACCGG	ACGGATCAAC	CGCATTTTGG	2340
CTTGGAACGA	ATGGTGGAAC	TGTTAGCTTT	CGGTGGCAAT	CCCCATCTCA	AACTCAAGGT	2400
CCTCCATATC	GGAGGGACTA	ACGGCAAGGG	CTCGACTATT	GCTTTTTTGA	AAAAGATGCT	2460
AGAAAAGCTA	GGGTTGAGAG	TTGGCGTGTT	TAGCTCGCCC	TATCTCATTC	ATTACACAGA	2520
CCAGATTAGC	ATCAATGGGG	AATCGATCTC	AGAAGCGAGG	CTAGAAGCTC	TCATGGCAGA	2580
CTATCAGTCT	TTGCTGGAGG	GAGAAGCGGT	CGCCAATTTA	CAGGGCACAA	CCGAGTTTGA	2640
GATTATCACA	GCCCTGGCCT	ATGACTACTT	TGCCTCAGAG	CAAGTAGATG	TGGCCATCAT	2700
GGAAGTTGGC	ATGGGTGGAC	TTTTGGATAG	TACCAATGTC	TGTCAGCCCA	TTTTGACAGG	2760
AATTACAAC T	ATTGGCTTGG	ATCATGTGGC	TCTACTTGGT	GACACCTTGG	AGGTCATAGC	2820
AGAGCAGAAG	GCAGGTATTA	TCAAACAAGG	GATGCCCTTG	GTAACAGGGC	GTATTGCTCC	2880
AGAAGCCTTG	GCTGTGATTG	ACCGCATTGC	GGAAGGGAAA	GATGCGCCGA	GACTTGCCCTA	2940
CGGGACAGAT	TATCAGGTTC	GTCATCAAGA	AAGTGTGGTG	ACAGGGGAAG	TCTTTGACTA	3000
TACAAGTGCT	GTCAGACAAG	GTCGCTTCCA	GACTAGCCTG	CTTGGTTTGT	ACCAAATAGA	3060
GAATGCTGGG	ATGGCCATAG	CTTTACTTGA	TACTTTTGT	CAAGAAGATG	GTCGAGAGCT	3120
AGCAAGCAAT	GATTTTCTTG	GTCAAGCCTT	GGAAGAAACA	AGTTGGCCAG	GGCGTTTGGA	3180
AATCGTGTC A	AGAGATCCCT	TGATGATTTT	GGATGGAGCC	CACAATCCCC	ATGCTATCAA	3240
GGCCTTGTTG	GTAACCTTGC	AAGAACGTTT	TGCGGATTAT	CATAAGGAAA	TCCTCTTCAC	3300
TTGTATCAAA	ACCAAGGCCT	TGGAGGATAT	GTTGGACTTG	CTGGGAGCCA	TGCCAGTTAC	3360
CGAGCTTACT	CTAACACATT	TTGCGGATAG	TCGGGCGACG	GATGAAAACG	TGCTGAAAGA	3420
GGCAGCTAAG	TCTAGAAATC	TCAGCTACCA	AGATTGGCAT	GATTTTCTAG	AGCAGAATTT	3480
GACAGATAAA	AAAGAAGAGA	AACAAACAGT	TAGGATTGTC	ACAGGTTCCCT	TGTATTTCTT	3540
GAGCCAAGTG	AGGGCCTATC	TGATGGAGAG	GAAGAACGAG	AATGGATACA	CAAAAGATTG	3600
AAGCGGCTGT	AAAAATGATT	ATCGAGGCTG	TAGGAGAGGA	CGCTAATCGC	GAGGGCTTGC	3660

1297

AGGAAACACC	TGCTCGTGTA	GCCCGTATGT	ATCAAGAGAT	TTTTTCAGGT	CTTGGTCAAA	3720
CAGCAGAGGA	ACATTTGTCA	AAATCCTTTG	AAATTATTGA	CGATAATATG	GTGGTAGAAA	3780
AGGATATCTT	TTTCCATACC	ATGTGTGAAC	ACCACTTCTT	GCCATTTTAT	GGTAGAGCGC	3840
ACATTGCCTA	CATTCCAGAT	GGTCGTGTGG	CAGGCTTGTC	TAAGCTAGCC	CGTACGGTTG	3900
AAGTTTATTC	GAAAAAACCA	CAAATTCAAG	AACGTTTGAA	TATCGAAGTG	GCCGATGCCT	3960
TGATGGACTA	TCTAGGTGCT	AAAGGAGCCT	TTGTTGTCAT	TGAGGCGGAA	CATATGTGTA	4020
TGAGTATGCG	TGGTGTTAGA	AAACCAGGCA	CTGCAACCTT	GACGACAGTA	GCTCGTGGTC	4080
TATTTGAAAC	AGATAAGGAT	CTCCGTGACC	AAGCTTATCG	TTTAATGGGG	CTATAAAAAAG	4140
AATCCGCTTC	AAGCGGATTT	TTCTAGAAAG	GAATCATTAT	GGATCAACTG	CAGATTAAGG	4200
ATTTGGAAT	GTTTGCCTAT	CATGGTCTTT	TTCTTAGTGA	GAAAGAATTG	GGGCAGAAAT	4260
TTGTCGTTTC	AGCCATCCTA	TCCTATGATA	TGACCAAGGC	AGCTACAGAC	TTGGATTTTAA	4320
CAGCCTCTGT	CCATTACGGA	GAATTGTGTC	AGCAGTGGAC	GACTTGGTTT	CAGGAAACGA	4380
GTGAAGATTT	GATTGAAACG	GTAGCCTATA	AACTGGTGGA	ACGTACCTTT	GAGTTTTATC	4440
CTCTTGTCCTA	AGAAATGAAG	TTGGAACCTGA	AAAAACCTTG	GGCACCGGTG	CATTTGTCAC	4500
TAGATACTTG	CTCGGTAACC	ATTCATCGCC	GCAAGCAACG	AGCCTTTATC	GCCCTAGGAA	4560
GCAATATGGG	AGATAAACAA	GCAAACCTGA	AGCAAGCCAT	TGACAAACTG	CGAGCTCGTG	4620
GCATCCATAT	TCTCAAAGAG	TCCAGTGTCT	TAGCGACGGA	GCCTTGGGGT	GGAGTGGAGC	4680
AGGATAGCTT	TGCCAATCAA	GTGGTTGAGG	TGGAACCTG	GCTACCAGCA	CAAGACTTGT	4740
TAGAAACCTT	GTTAGCCATT	GAGTCAGAGC	TGGGACGGGT	GAGAGAAGTG	CATTGGGGAC	4800
CTCGTTTGAT	TGATTTGGAC	TTGCTCTTTG	TGGAGGACCA	GATCCTTTAT	ACAGACGACC	4860
TCATATTGCC	TCATCCTTAC	ATAGCGGAAC	GCCTTTTGTG	CCTTGAGTCT	TACAGGAAAT	4920
TGCGCCTCAT	TTTATCCATC	CGATATTAAA	ACAACCGATC	CGCAACTTGT	ATGATGCTTT	4980
GAAAAAATAG	AAAAACTCTA	GTTTTTCAGTT	ACTTGCAACT	GAAGGCTAGA	GTTTTTATAC	5040
TCTTCGAAAA	TCTCTTCAAA	CCACGTCAGC	GTCGCCTTAC	CGTACTCAAG	TACAGCTTGC	5100
GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	TAAAATAGGT	CATTTTCTTC	5160
TGGGAGGAGG	ATAGTTTCTC	TACCGTCCAT	GTCTAAAACC	AGTACTCTTG	GGGGATAACG	5220
AGGGTCGAAA	GGATGGTTAA	AGTCAAAATC	AATGGCTGTA	GGGAGGTGTT	GACTTGAAAA	5280
GTGGAAGGTA	ATCTTTCCTT	GGTTATTAAG	CAATTGAAAC	TCGAGTTCCT	CTTCCAATTC	5340
AAAGACATTT	TTTAAGAAAT	GGTCGATGAT	ATACCAAAAA	GAGTCAATGA	TGTCATCAGG	5400

1298

CAAGCTGGTA ACAATACCAA AACTAGCAGA TCGCATGTGG GTATTGGTAA AAGCCATATC	5460
TCTGTCCCCC TTCTTTTCCC TTATCATACA GCAAATAGGA TTAAAAATCA AGAAAAGGTG	5520
ATTTTGTGAA AAGGATTTTA GTTACAGGGA GAAATAGGGA AAAAATTCCT AAAAATCTAC	5580
CGAAGTTAAT AGGTAAATTC CCAAATTAAC TTGATTATAT AACTTTCAGT TACTTTGAGA	5640
AGTTACCGAA AAATATTTTT CATATCTATT GACTTTTAGG GGTAATAATT GGTATGATAG	5700
TAGGCGGTAT TGTTTACCCC ATTTGAAAGG CCCCAGGAACC TTCCAAATAC TTTTCGATGG	5760
GAAGGAACAC CCATCACCGT AAACAAAAAT CGAACTATAT ATAGGAGAAA TCATGAACAA	5820
AACAACATTT ATGGCTAAAC CAGGCCAAGT TGAACGTAAA TGGTACGTAG TTGACGCAAC	5880
TGATGTACCA CTTGGACGTC TTTCTGCAGT AGTTGCTAGC GT	5922

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1988 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TAACATCTA CGATGAGCTG TTGTGATTCT CATTAGTTCC CCTTTCCCAA GAGGCATAGG	60
GGTGCGCATA ATAGATGTGC TCCTCAGAAA ATATATCAAA CAAGCGATTG AATTCCGTTT	120
CATTATCTGC CGTGATGGAA AGAATCTTGT GTTGTTTTAA GATGAGTTT AGAGCCTGAT	180
TGACCACCTC AGCACTTTTA TTTGGAATCA ATCGGATGAT CTGATGTCTA CTCTTTCGAT	240
CCGTCAAGAC AATCAAGCAG TAGTTTTTCG ATCTCGTAAG TAGAACCGTA TCAATCTCAT	300
AATGCCCATT CTCCAAGCGA AGATTGATAG CTTCAGGCCG CTGTTTCGATG GATTGACCAG	360
CAGGTTTAAA GTTGGTGCTA GCCTGTTTCT TAAGCGCTTT TCCTTTTCTA GGGTAAAGCA	420
AATCCTGCTT GCTTAACCCC AATTTTCCAT GATGAATCCA ATAGTAAATG GTTGAAATTC	480
CCACGTTAAC CCCTTTAGCC ATAACCATCA TTTCAGGCGA AAATTTTGG TTATGATAGT	540
GGAGAATCTT TTCCTTTAGT TCCTTGGTCA AGCTTGATTT CTTGACCGAG CGCTTGCGAT	600
TGTTTTCATA AGACTGTTGA GCGTAGTCGG CAGAATAAAC CTCTTTGAAG CGCCCTTTTC	660
CAAGACATTG TCGGACTGTC CCACGCTTGA TTTCAAGTGT ATAGTTTGAG GAGCTTTTCC	720
AAGTAGAGAG GCAATTCTC TATTTGATTT TCCTTCTTTT TTCCATCTTT CGATTAAGCG	780
ACGGCTATCG ATTGTCAAAT GTTTGGCTTT TGTAAGTATAA TTGTCTTGCA TCTCTGTGCC	840
TTTCTTGTGT TTGTGGTTGA ACAACAAGTA TAACACAGAG GTGCTTCTTT ATGCCTACAA	900

1299

GAGCTTTCAT TATTTCCATT TTCTTTTGGA TTCTACTCTA TTCTGAAAAA CTTGTGTATA	960
TTTACTGAAG CTAGCAAGTC TTACCTGTAA ATTTAATGAA AGCAACACAA AATCCGAGAG	1020
GGGAATCTCG GATTAATAGA TAGAGAGTTT TAGTTTAAA TAAATTGTTT AAAATATCAA	1080
CAACATCACT TCTTTTCTTA ACCTGATAAG TCTTGATTCC TAATTTTGGG GCTACGATTA	1140
TATTGTCCTC AATATCGTCT AGAAAGACAC AATTTCTAGG TTATAACTGG TATTTATCGA	1200
TAGTTACTCA TATACATCAG TCCACCTCCA TACTTATGTG CGAGCCTCTC TTTGTATTAT	1260
ACCTCCATAC TCACCTTACA GATTCTTTTG GTAATAATAT CTTTGCCTAA TGTAAGAGACA	1320
GTCTTGCAAA GAAAAAATT CCTTGTAGCC ATGTTTCTGA TAAAAGTCCG GTGCCTGGAA	1380
CTGGTAAGTA TTGACAAAGG CAAAACAACA ATTCGATTC TTAGCTTCAC TTTCTGCCTG	1440
TTGCAATAGT TTTGAACCGA TTCCTTGCCC TCGCAGTTCC TCTTTTACAA ACAAATACTC	1500
GATTTCTAGC CAATTTCCAA AAGTCTCTGC TATCAAACCT GCCAGGAGAT TGCCCTTTTC	1560
ATCTTCGACA TAAAGATTAA GTGGCTCACT TTCAGCCTCT TCTCTTTTTC AACGGTTATA	1620
AACACGAATC AGATTCCCTA TTTCTTGCGA TTTATGTGAT TCCTTATTTT CCAATCTAAA	1680
GTATAGTGAA ATGAAATAAA ACATGCGCAA ATCGATTAAAG GAATTTAATC TAATTTCTAA	1740
CAATGTCTTA GAAATCAAAG TGTACTATTT TAACCTCAAT GCACTATACA TCTAATACTC	1800
AATAAAAATC AAAGAGCAAA CTAGGAAACT AGCCGCAGGT TGCTCAAAAC ACTGTTTGA	1860
GGTTGTAGAT AGAACTGACG AAGTCAGCTC AAAACATAGT TTTGAGGTTG TAGATGAAAC	1920
TGACGAAGTC GGCTCAAAAC ATGGTTTGA GGTGTAGAT GAAACTGACG AAGTCAGCTC	1980
AAAACAGG	1988

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

CCGGATATTT GTTTTATGTA ATTTTCTTGC AAGTTTCTTC TTAGTAGCTT GTCAGTCAGG	60
TTCTAATGGT TCTCAGTCTG CTGTGGATGC TATCAAACAA AAAGGGAAAT TAGTTGTGGC	120
AACCAGTCCT GACTATGCAC CCTTTGAATT TCAATCATTG GTTGATGGAA AGAACCAGGT	180
AGTCGGTGCA GACATCGACA TGGCTCAGGC TATCGCTGAT GAACTTGGGG TTAAGTTGGA	240

1300

AATCTCAAGC ATGAGTTTTG ACAATGTTTT GACCAGTCTT CAAACTGGTA AGGCTGACCT	300
AGCAGTTGCA GGAATTAGTG CTAAGTACGA GAGAAAAGAA GTCTTTGATT TTTCAATCCC	360
ATACTATGAA AACAAAGATTA GTTCTTGGT TCGTAAGGCT GATGTGGAAA AATACAAGGA	420
TTTAAGTAGC CTAGAAAGTG CTAATATTGC AGCCCCAAAA GGGACTGTTC CAGAATCAAT	480
GGTCAAGGAA CAATTGCCAA AAGTTCAATT AACTTCCCTA ACTAATATGG GTGAAGCAGT	540
CAATGAATTG CAGGCTGGAA AAATAGATGC TGTTCATATG GATGAGCCTG TTGCACTTAG	600
TTATGCTGCT AAAAACGCTG GCTTAGCTGT CGCAACTGTC AGCTTGAAGA TGAAGACGG	660
CGACGCCAAT GCCGyTGCTC TTAGAAaATA GTGATGATTT GAAAGAAGT	709

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

TATAAAATGT TAAGTTAAAT GATTTCAAAA TTCAGAAAGG GATTGCTTTA TGCAGTTCCT	60
TTTTATTTTA ACAGGAGTGA AACTATAGTG TTTCTAAATT GTGAATCAAT CAAACTGAT	120
TGTGATGGGG CTATTCTAGC TTTAGAAACC TTCAAAAATT AAAATTTAAG GCAATCAATT	180
ACTTGGAAGA GTATGAAAGC ATTTAGTTTA TAGGAATTCT AGGTCTAGAA TTACATATAT	240
ATATTTATGA AGACGGGGTG TTCGATAGTT AGTATTGTTC TATTCTGAAA GATTGAGCT	300
GTCAGTTGTA TAGAAAGTGT TCGAATTTTT TTAAGTGATT AAATTAGTTA ATTGTATGAG	360
GTGCTTTATG ATATAATGTT CTTAATGAAT TTTCAGAAAG GAAAACCTCA AATTGTTCTA	420
CAAATTTCTA CTCTTCGACC TCGACCACAC TCTTCTTGAT TTTGATGCTG CTGAGGATGT	480
GGCTTTGACC CAACTTCTAA AAGAAGAAGG AGTTGCGGAT ATTCAGGCTT ATAAAGATTA	540
TTACGTTTCT ATGAACAAGG CTCTCTGGAA AGACTTGAG CTGAAGAAAA TCAGTAAACA	600
AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT TTTGGACAGG AAAAAGACGG	660
TAGTTTCTTT GCCCAGCGTT ACCAATTTTA CCTCGCCCAG CAGGGACAAA CACTATCGGG	720
CGCTCATGAT CTCTTGGA CA CCTCATTGA GCGTGATTAT AACTTGTATG CTGCGACAAA	780
TGGCATTACT GCCATTCAGA CAGGACGTTT GGCTCAATCT GGTCTAGCAC CTTATTTCAA	840
TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAGCCG GATGCTCTTT TTTATGAAAA	900
GATTGGCCAG CAAATTGCTG GATTTAGTAA AGAAAAGACG CTGATGATTG GAGATTCTCT	960

1301

AACCGCCGAC ATTCAAGGTG GCAATAATGC GGGGATTGAC ACTATCTGGT ATAATCCTCA	1020
TCACCTCGAA AATCACACAC AAGCCCAGCC GACTTACGAA GTCTATTCTT ACCAAGACTT	1080
GCTGGATTGT TTAGATAAAA ATATCTTGA AAAGATCACA TTTTAAAGGA GACGAGCTAA	1140
TGACTACAAA AAAGCTAATA TTAGTATTGA AGAGTACATT GAAATGTCTG AAGTTGATTT	1200
TAATGAAGCT GTTAATTATG AATTACATC TGACACTTGT CAATTAGCAA ATAGTATTTA	1260
TCAATCTCTT TTTAAGTTTT TTGATAAGAA AAATTCTCTT GCGGATTTAA TTTTACTTG	1320
GAAATCTCCA TCATTAGTCA AAGAAGGGGA TTATATTGGG AGAAGGGATT CACAAGTAGA	1380
TAATCTTAGA GTAATAGGAA ATATATTTCC GAATTATCTT ACTAATCGAA AATATAGCCT	1440
CAATATGAAT CGTAATGGCT GTATGGGAGA TTTTCCTCAT GACTTTTTTG ATATATACCT	1500
AGATCATGTA GCAAAATATG CCTACGAACA AAAAGTTAAT AATATTAAAG AGTATTATCC	1560
TTTAAAAAGA GCGATTTTAC ACCAAGAGAA TGCATTGTAT TTTGATTTT TTTCTAATTT	1620
TGACGACTTT TTAGAAAAAA ATTATTTAAA GACTATATGG CAAGTTTCTA AAGAACTCC	1680

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 598 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

AGCTCGGTAC GTAGTATnTG TGGTGCATAA ATGAGTGAAA AGAGGATAGA GAGGATGAGG	60
CCGATAAGAA CACCGGTAGC TGCATCGTGA AATACTTGTT TTTTCATAGT TCTAATTTCT	120
CCTTGATGGT TTTTAGATAA CGGCGTGAAG AGTAGGTGAA GCTTTCGTTT TTCAAGAAAA	180
TTTCTACCAG ACCGTTTGGC GTGagCTTGA GGTGAGAGAT GGAATCGATA TTGATGATTT	240
CTGATTGGGA AATTTGGATA AAATGGTTG GCAAGAGTTT AAGAACCTGA TAGAGTCGCA	300
AATCAATGCT GTAGGTCTGA CTCGCGGTTT CTGCTAGAAC CTTCCGATTC TCGATATAGA	360
AGCGCTGAAT CTTGCCAATC TCAACTAGAT AGACCTGATC ATCGATTTTT CTTTGATTT	420
TTTCTCTTTG GTCCAGATTT TCTGCGAACT CGATGACTTT CTGGACTTTT TCGGTTTCTT	480
GAGGTGCTTG GACAATCAGC TTTTCCTCCT CGTAAGTCTC ACTAATCTGT AGTTCTACTT	540
TCATAGTTTT CTCTCCTTTT CAGTTATACA AGGTTGTGAT CACTTCCTGT ATATCCGG	598

(2) INFORMATION FOR SEQ ID NO: 272:

1302

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1099 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CCAGCAAATC AATAACTGCA ATTGCTATAA AATGGATTCT ATAGAGTTTT TTCATGACAA	60
GACCTCCCTC TTTTATCTAA CTTCATTCTA CTCCAAAAGA ATGGGAGTTA CAACTAAAAT	120
GATAAAAATA GCAGAAGGGA GATTCTCTTA AGTTGGCTAG TATTCTTTAT TTGAGTTTCC	180
TTCTATTATC TAACTTCTTC ATCATTCAG ACAAATAAAG CTCCGATTGC ATTGAGGATA	240
TAAAAGATGT ATTTACCGAT ATTGGCGAAG TTTCCTTGAA TACCAGCTTT TGTCAGCTGA	300
ACGAAATTGT AAATCAACCA AAAGCCCCAC TGAGTTGTGA GTTTTAATGC ATTCAAAGCA	360
TTGGCAATGA GGGACAGTGC AAAGGCAATA GTTGTTACGT AGGCAAGGAG ATTCATCTTG	420
CCCCCATATC CGATATAGTT GGTCACAAAG GCAAAGAGGA AGGCGATGAT GGAAATGATG	480
ATGGCCGCCA ATTTTACCTG TTTTGGGCTC ATTTGGTTGG GTCTGCCTTC TTGCGAAGCT	540
TCCCACCTCT TTATAGCAAA GGTATAAATG AGGAAGGTGA CGGGATAGGT AATGATGGCC	600
GCCTTATTTT CAAGGATATA ATCAATAGCA CCGGACAAAA TGGTATTAAC AATACCAAAG	660
TAATTTCCCC ATTTGCTTAA TTTCCCCGTG AAACGAGTGG ACAACATGGA AATCCCAACG	720
TTGGTTACGG AAATCAATCC AAAGGTACA AGAGCTGTCC ATGATCCCCA GTCTACAAAT	780
TTATCGAGGT GTGAGTTGAG GTAACCAGAT GCAATCGCAA TCCCAACGAC CAAAGCAACC	840
CCGAAGAGGT CAAACTATTT AGATGTAGCA AAAATTTTGA GTGATTTTTT CATAGGTAA	900
ACTACCTTTC TTTTTTCAA ATATTCTCCC ACCAAATGAA AGTAAATAA AATGATAGAA	960
ATAAAACCCCT GAAAATAAAG GTTCTATAAT ATTTGTAGTG GGTAAATCCA CTATAGATAT	1020
TATGGAGCCT ATTTTATGT AGAAAAAAG TCCCATATGA CCTATAATGA AAAGCGACAA	1080
AACAACTCAT TAGAAAGAT	1099

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

1303

CTGGGATTCA	CGTGAAAAGG	AAGCCCAGAG	AGTAGCCAGG	TGTACTGCTA	GAACAGTGAG	60
TGAAATTGAA	TATTACCATA	GAGAGTCAAC	CCAGATAGCT	CAGGCTTTAG	TTGAAAATCA	120
AGCTCGTATC	GAGGGAATCT	ATAAATACTT	TAGCCTTAGC	ATGCCAGACT	ATTTTACTG	180
GCAATTAGAG	CGGAAAGCTT	CGCCTTATAT	ATCAGTCTCT	CTGTATGAAA	ATGTTGATGA	240
CCTCTATGTT	CGAAATGATT	TTGTAACTGG	GGTGGCCATT	GCTTTTCAAG	ATTACAAGGA	300
AGTCTATGTT	TCTACTAAAG	ACAAACGTAG	GkKAGAAAAA	ATCAGGGCTG	AGGATTTCOA	360
ACCAGCAGGA	AATAGTTTGG	CCATTCCAGT	GTCAGATCCA	GTGTCAGATC	AAGACTTAGG	420
AGTGATTAC	ATCTCCTTGG	ATCCTGCTGT	TTTATACCAT	GCCATTGATA	ATACTAGAGG	480
TCATACTCCG	ATGGCAGTAA	CAGTGACCTC	ACCTTTTGAT	ACGGAGATTT	TTCATATGGG	540
TGAGACAGTT	GATAAGGAGA	GTGAAAATTG	GCTAGTTGGC	TTAACTTCTC	ATGGATATCA	600
GGTTCAGGTG	GCAGTTCCTA	AAAAC'TTGT	TTTACAAGGA	ACAGTGACTA	GCTCTGCTTT	660
GATTGTGGGT	TFGAGCCTTC	TCTTTATGT	CATTCTTTAT	CTGACTTTGA	GGCAGACTTT	720
TGCTAATTAC	CAAAAGCAGG	TAGTGGATTT	AGTAGAATCC	ATTCAAGTCA	TTGCTCAAGG	780
CGAAGAGGGG	CGTCGGATTG	ACATTTCCGA	GAAAGATCAG	GAATTACTCC	TAATCGCGGA	840
GACGACCAAT	GATATGTTGG	ATCGATTGGA	AAAGAATATC	CATGATATTT	ACCAGTTAGA	900
GCTTAGTCAA	AAAGATGCCA	ATATGCGAGC	CTTGCAGGCG	CAAATCAATC	CTCATTTTAT	960
GTATAATACG	CTGGAGTTCT	TGCGCATGTA	TGCAGTTATG	CAGAGTCAAG	ATGAGTTGGC	1020
AGATATCATT	TATGAATTCA	GTAGTCTCTT	GCGTAACAAT	ATTTCCGACG	AAAGAGAGAC	1080
CCTCCTCAAA	CAGGAATTAG	AATTTTGCCG	TAAATACAGC	TATCTCTGCA	TGGTTCGCTA	1140
TCCCAAGTCC	ATTGCCTATG	GTTTCAAGAT	AGATCCAGAG	TTAGAGAATA	TGAAGATTCC	1200
CAAGTTTACC	TTGCAACCGC	TGGTAGAAAA	CTATTTGCGG	CATGGTGTTG	ACCACAGGCG	1260
GACAGATAAT	GTGATTAGCA	TCAAGGCTCT	TAAACAGGAT	GGTTTTGTGG	AAATTTTGGT	1320
GGTCGATAAT	GGTAGAGGAA	TGTCGGCTGA	AAAGTTGGCA	AATATCCGAG	AAAAATTAAG	1380
TCAGAGATAT	TTTGAACACC	AAGCCAGCTA	CAGTGATCAA	AGGCAGTCTA	TCGGGATTGT	1440
CAATGTACAC	GAGCGTTTTG	TGCTCTATTT	TGGAGACCGC	TATGCCATTA	CTATAGAGTC	1500
TGCAGAGCAA	GCCGGTGTTT	AGTATCGTAT	TACAAATCAA	GATGAGTAGA	AAGGGAGAAA	1560
ATGTATAAAG	TATTATTAGT	AGATGATGAG	TACATGGTGA	CAGAAGGTCT	GAAGCGTTTG	1620
ATTCCCTTTG	ATAAGTGGA	TATGGAGGTC	GTCGCAACAG	CCAGTCATGC	CGATGAAGCT	1680
CTAGAATATG	TTCAGGAAAA	TCCTGTCGAT	GTCATCATTT	CCGATGTCAA	TATGCCAGAC	1740

1304

AAAACAGGGC TTGATATGAT TCGGGAGATG AAAGAGATCT TACCAGATGC TGCCTATATC	1800
CTGCTCTCAG GTTATCAGGA GTTTGATTAT GTAAAAAGAG CAATGAACCT TACTGTGGTG	1860
GACTATTGTTG TCAAGCCTGT TGATAAGGTA GAGCTGGGAA ATCTGCTGGA GAAGATTGCA	1920
GGTCAGCTCG GCGAGAGAGG GAAGAAAAGT CAGACTCTTA GTCAAGAATT AGACGAGGCT	1980
GGATTTGTTA GTTATTTAGG GGATAAGGAG AATTGGTGGA TAGGTCTATC CAAGGAAAAA	2040
CAAGGTTCCCT TCACCATTCCT CTACTATGTC TTGGGTCAAG ACTGGCAGAT TTTCATTTCT	2100
GGCCACCCCC TAGATGGTTT AGTCGTTACA CCTTTTGAAG CTCCTTATCA AGAACACTTT	2160
GAACGCTGGA AGCTGAATGC TGAGAAAACC CTCTTTTACG GTTCTGTAAA TCTGCAGCAG	2220
TCTGAGAGTC TCTTTGCCTA TTACGAACCG ATTTATAGGG TTATCATTC A GGGAAATCTC	2280
AATCAAATCG TAGAAGAGTT AAATCTCTTG GAGAAGGTAG TTCTTGAAAA TACACCTCGT	2340
GTTTCGATTA CTAAACAGCT TTTTATCCAG TTTGTCATGG ATGTTTTCCA TTTATTTGAA	2400
CATCTCAAAG CTGATGATAT GACGGACATT GTCAAAACCA TTCATGCTAT TCAATCCTTC	2460
GATGAATTGG TTTCTTATAT CAAGGAACT CTGATCAGCT TTTTCGGTCA ATACCGTATG	2520
AATGAAAATG TGGTCAGTGT GCTGGAAGTC ATTGGTCGTG ATTACCAAAA AGAGCTTTCC	2580
CTCAAGGATA TCAGTAAGGC CCTCTTTATC AATCCTGTCT ATCTAGGGCA GTTGATTAAG	2640
CGTGAAACCG ATTCGACCTT TGCAGAGTTA CTAAACAAAC AACGTATTAA GGCTGCCCCAG	2700
CAGCTCTTGC TTTCAACTAG TGA	2723

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 836 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CCGCAGTTTT TTAAACCGT ATATAAGTAT AGCATAGTCA AAAAAAGAAT GCAAGATTTT	60
TGCAAACTTT TTAAATTT TTCGTAATTT TTCTTTTAAA GTTCTACTGT CAGGACTTGA	120
CCTTGCTTAA CAACCTGTTT TCCGGCGATA TAAACATCAT CTACATCACT AGATTTAACT	180
GCATAAACCA GGTGAGACAG CATATTTTCC TGAGGTTGGA GATGAATTTT CCCTTGTTGGT	240
TGAATGACCA GAAATCTGC TTGCTTGCCG ACTTCCAGAC TTCCTATCTG ATTTTCCATT	300
CCAAGGACCT TAGCCCCTTC GATTGTCAGT ACCTTGAGAG CTGTTTCGAT TGGAAACTGG	360
CTGGCATCCC CACTTTTCAT CTTCTGAAGA AGAGCTGCAG TCCTTCCTTC CTCAAACATA	420

1305

TCTAGATTGT TATTGGAAGC AACCGAGTCA GTCGCAATTC CGACTGCTAC TCCCGCTTTT	480
TGGAGCTGGA TAATTGGAGC AATTCCTGAT GCCAGTTTGA GGTTACTGAT AGGATTGTGG	540
GCGATAGCnA CTTGAGAAGA TGCCAAGCGT TCAATTTCTC TCTCGTTTAA TTCGACCCCG	600
TGAGCAAATA CGGACGGATG ATCTAAATAA CCCAGTTCTT CAAGAAAAGC AAGGGGGCGT	660
TTGCCGTATC GTTTGAGGAT AATTCCTGAC TCCTCCTTGG TCTCCGCCAC ATGGACATGG	720
AGCGGAATAT TTAGCTCTTT TGCCATTTC AACTCGCTT CCAGCAAGTC TCTACTGCAG	780
CTATACGGAG AATGAGGTGC TACCATAACC TTGAAATTG GATTTTTATA TTTTAA	836

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ATTTTATTTT ACTTTT TAGG TGGTCTGGGG CTATTCTTAT ATAGCnTCAA GACCATGGGA	60
GACGGTTTAC AACAAGCTGC TGGAGATCGC CTGGGTTTTT ACATTGACAA ATATACTAGT	120
AATCCTTTGT TTGGAGTTCT GGTTGGTATT GGGATGACTG CTCTAATTCA GTCTAGTTCT	180
GGTGTAACAG TTATCACAGT CGGCCTGGTC AGTGCCGGTC TCTTAACCTT ACGTCAGGCT	240
ATCGGGATTG TCATGGGTGC TAATATTGGG ACAACTGTCA CATCCTTTCT CATCGGTTTT	300
AAATTAGGTA ACTATGCCCT ACCTATGCTC TTTATCGGTG CCGTCTGTCT TTTTTTTACG	360
AAAAATCGGA CAGTCAATAA TATCGGACGC ATCCTCTTTG GTGTCGGTGG TATCTTTTTT	420
GCCCTCAATC TCATGAGCGG CGCAATGGCT CCACTCAAGG ATTTACAGGT CTTTAAGGAC	480
TATATGATTG AGCTAAGTAA GAATCCTGTT TTGGGTGTCT TTGTCGGTAC TGGCTTGACC	540
TTGCTAATTC AAGCTTCTTC GGCTACCATT GGGATTTTAC AAAACCTCTA CGCCGGCAAT	600
CTAATTGATC TACAGGGAGC TTTGCCAGTT CTATTTGGTG ACAATATCGG GACAACCATT	660
ACAGCCATCA TTGCCTCTTT AGGGGCTAAT ATTGCAGCTA AACGGGTAGC AGGAGCTCAT	720
GTTGCCTTCA ACGTTATCGG AACAGTTGTC TGCCTATTTT TTCTAGTTCC TTTTACTGTC	780
CTGATTCATT GGTTTGAAGC TACGCTAAAT CTAGCACCGG AAATGACCAT CGCCTTTGCT	840
CACGGAACCT TTAATATTAC CAACACCATT GTCCAATTTT CATTTATCGG AGCTCTGGCT	900
TACTTTGTAA CCAAGATTAT TCCTGGAGAG GACGAGGTTG TCAAATACGA ACCCTTATAT	960

1306

CTTGATGAAC ATTTCATCAA ACAGGCCCCA TCTATCGCTC TAGGAAATGC TAAGAAAGAG	1020
CTCTTGCACT TAGGAAACTA CGCTGCTAAA GCCTTTGACC TTTCTTATAA GTACATCATT	1080
GACTTGGATG AAAAAGTTGC TGAAAAAGGG CATAAAACCG AAGAAGCAAT TAACACCATC	1140
GATGAGCAAT TAACACGTTA TCTCATTGCC CTTTCAAGCG AAGCTCTCAG CCAAAAAGAA	1200
AGTGAAGTGC TTACCAATAT CCTTGATTCC TCCCGTGATT TGGAACGGAT TGGAGACCAC	1260
ACGGAGGCTC TACTCAATCT GACTGACTAT CTTCACGGA AAAATGTTGA ATTTTCTGAT	1320
GCCGCCTTGA AAGAATTAGA GGAAGTTTAC CGCCAACTA GTGACTTTAT CAAAGATGCT	1380
CTGGATAGTG TGGAAAACAA TGATATTGAA AAAGCACGCA GTCTTGTAGA ACGTCATGAA	1440
GCAATCAATA AGATAGAACG TGTTCTCAGA AAAACCCACA TCAAACGCCT CAACAAAGGC	1500
GAATGTTCAA CACAAGCTGG GGTCAACTTT ATCGACATCA TCTCACACTA CACTCGTGTA	1560
TCAGACCACG CTATGAACCT TGCTGAAAAG GTTTTTCAG AACAAATCTA AGAACCAAGA	1620
AGCTATCCAT CATAATTGGA TGGCTTTTTA CTTTTTCCTA AGCAAGACTA GGATGAATGA	1680
AACTGAAAGA GTATTCTGCA GATATATAGT CCCCAATTAT TCACCCCAA TCTAAAAACC	1740
ATCCAGAATC CTTCGCCTAG CTTAGATCCT GGATGGTTTC TTTTTTCACC CAATGGGTGT	1800
TTTTTACTAG ACAAAAAAGA GTTCCCTT TATGGTATAA GTGTAGAAA AAACACAAAA	1860
AGAAAGGAAA CTCACATGAA CAGTTTACCA AATCATCACT TCCAAAACAA GTCTTTTTTAC	1920
CAACTATCTT TCGATGGAGG TCATTTAACC CAGTATGGTG GTCTTATCTT TTTTCAGGAA	1980
CTTTTTTCCC AGTTGAAACT AAAAGAGCGG ATTTCTAAGT ATTTAGTAAC GAATGACCAA	2040
CGCCGCTACT GTCGTTATTC GGATTCAGAT ATCCTTGTC AGTTCCTCTT TCAACTGTTA	2100
ACAGGTTATG GAACGGACTA TGCTTGTAAG GAATTGTCAG CTGATGCCTA CTTTCCAAAA	2160
TTGTTGGAAG GAGGGCAGCT TGCTTCACAG CCAACCTTAT CCCGTTTCT TCCAGAACT	2220
GACGAGGAAA CAGTCCATAG TTTGCGATGC CTCAACCTTG AATgGkCGAA TTCTTTTTAc	2280
AGTTTCACCA GCTAAACCAA CTCATTGTAG ATATCGATTC TACCCATTTC ACAAC	2335

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CGGATTCACCT GTTGTGACT AATCAATAAC ACAGTAGAAA ATCTCACAGC AGTCTATTAG	60
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1307

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TTGCTTTTCA TACTAGGCAA GTGACTGAGG CTTGTACTTG GGTACAGCAA GGGAGCTTAA      120
GGCCGTAGAA GAGAAAAATA GTAGACTGAA AACCCGCAAG ACTTCATCAT TTCGAGAAGT      180
GACGTGGGAG ATGAAAATCG ATTGAACCAC TTACAAGGAG AATAGAAAAT GGCTAAAAAA      240
AGCAAACAAC TTCGTGCTGC TCTTGAGAAA ATCGACAGCA CAAAAGCATA CAGTGTAGAA      300
GAAGCTGTAG CACTTGCAAA AGAACTAAC TTTGCAAAAT TTGATGCAAC TGTAGAAGTT      360
GCTTACAAC TGAACATCGA CGTTAAAAAA GCTGACCAAC AAATCCGTGG AGCAATGGTA      420
TTGCCAAACG GTACTGGTAA AACTTCACGT GTTCTTGT TTTCGACGTGG TGCAAAAGCT      480
GAAGAAGCAA AAGCTGCTGG TGCAGACTTT GTTGGTGAAG ATGACCTTGT TGCTAAAATC      540
AACGACGGTT GGTGGACTT CGACGTAGCT ATCGCTACAC CTGATATGAT GGCTCTTGT      600
GGACGTCTTG GACGTGTCCT TGGACCACGT AACTTGATGC CAAACCCTAA AACTGGTACT      660
GTAACAATGG ATGTTGGCAA AGCGGTTGAA GAGTCTAAAG GTGGTAAAAAT CACTTACCGT      720
GCTGACCGTG CAGGTAACGT TCAAGCAATC AT      752

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(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

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GTCAACATG ATTCAAGGC TGTTGCTTT CTATCTCCCC TTTTTCATAA TGTATAATAA      60
AATGAAATAA TAACAGGACG AATTGATCGG GACAGTCAAA TCGATTTCTA ACAATGTTTT      120
AGAAGTAGAG GTGTACTATT CTAGTTTCAA TCTACTATAT TTTCGTACAG GTGCTTCAAC      180
CATTTGAACG ATTTCAAATC CTTCTTTTGT GTAAAGATTC TGAGCTCTTT GATTTGCCTC      240
GAAGACATTT AGAGAAATAC TGCTATATC TCTATTTTCA AATGCTAAAC TAACAAATTT      300
CCTTAAAGCC TTGCTACCTA AGCCTTGCTC CTGTTTCTGG GGGTTGATAA AAAATCTCCC      360
GATATGAAGA TTGCTGTCTT CTAGCCTGAT TTTCTGGATA AATCCCACAA ACTCTTGTTT      420
ATCAAAGATT GAAAAGACTC CTTCCAAGGC TTGAAGTGTC AGTAGAAAAG GAATCCTTGG      480
TCCCATCCAT TGTCTTGAA AGGATTTGCC TAGGGAGTTG GACCACTGGC ATACAAATTG      540
AGCGTTTCT GTGCTCACCT TTTCTTCAA ACGAATTGTC ATCTTTTCCT CACCACCTTA      600
TCTATGTTTC TCCATTATAC TATTTCTCCC ATTTTCTACG AATAGATAAG TATGATTGAT      660

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1308

TTTTATTTT	TTCTCGTCGG	GAGCATTCTA	GCTTCCTTTC	TTGGTTTGGT	CATGACCGT	720
TTTCCAGAGC	AATCCATTAT	CAGTTCAGCC	AGTCACTGCG	ATTCCCTGTCA	GACTCCCTTG	780
CGTCCCTTAG	ATTTGATTCC	GATTCTCTCA	CAGGTCTTCA	ATCGCTTTTCG	CTGTCGCTAC	840
TGCAAAGTTC	GCTATCCTGT	CTGGTATGCC	CTCTTTGAAT	TAAGCTTAGG	ACTCCTCTTT	900
CTGCTTTACT	CTTGGGGATG	GCTCTCCTTG	GGGCAAGTCG	TCCTAATCAC	CGCTGGTTTG	960
ACCTTGGGTA	TCTACGACTT	TCACCATCAG	GAATATCCCT	TACTGGTCTG	GATGACTTTC	1020
CAGCTAATCC	TAATAGCTTC	CTCTGGCTGG	AATCTGGTCA	TGGTCTCCTT	CCTCATACTT	1080
GGAATTTTGG	CTCATTTTAT	CGATATCCGC	ATGGGTGCAG	GGGATTTTCCT	CTTTT TAGCT	1140
TCTTGTGCTC	TCGTCTTTAG	CGTAACGGAG	TTACTGATCT	TGATT CAGTT	CGCTTCTGCG	1200
ACGGGTATCC	TGGCCTTTCT	CCTGCAAAAAG	AAAAAGGAAA	GACTTCCTTT	CGTGCCTTTC	1260
CTCTTACTTG	CTACTTGT TT	GATTATTTTT	GGTAAGCTAC	TGCTTGTCTG	ATAAAATCCA	1320
ATTTCTGCCA	TATATCCTTC	ATGAAATTAT	TTACAGTTA	AATTATAAAT	TATTTCTTTT	1380
GTACAAAGGG	ATGATGTTAT	CAAATCGATC	TGTTCTTCTA	TCTTCTTGAT	ACTGATCAAA	1440
AAATTT CATT	TCGACTGAAA	ATATTT CGCT	TATAAACTGT	AAACGAATAC	TTTGT TTAGA	1500
CATTATAGTC	GCTAGACTGA	CTAGATGATT	ACTCAAAACG	ACGTCCAGAA	TACTCTTTAC	1560
TTTGCTTGGT	TTTTTAACAA	AAATTTGATC	ATCCAAGGGT	TCAATCATT T	TGTAACCTTT	1620
TTGCGCAATT	TGACGATAAA	AGTAAGAATG	TTGCTTTGGA	GTCAATAATC	CTAACTTAAA	1680
AGCTCGATAC	TCTAAAGCCT	GTATCGAAAC	ATTCAAATCC	GACTTCAATA	AAATATAACT	1740
ATCAGGATTG	CTGACACGCT	TGCCAACCCCT	CTCTTCAAAT	TTGACTAAAA	ACTCTTCTTT	1800
TGGCAATAAA	AAACATGATG	CAAAATAATT	TGCTTCTTGC	TCCAAACGAT	CGCCATCTTC	1860
ATTCATATCT	TTATATTTAT	GTAAAAGAAT	ATGTCCTAGC	TCATGAGCTA	AGTCAAAATT	1920
TCGACGTACA	GATGATTTAT	TCGTTCCTAA	CACAATATAA	GGTCTTCCCA	ATTTTGACCA	1980
TGCGCTATAA	GCATCAGCTT	GGCCATTAAT	TAATCGTTCC	ACGATATAGA	TGCCTGAACG	2040
TTCTAATTTA	TAAAGCAAAT	CATGATTATC	TTTTGAAATA	CCTAATTTTT	CCCTGGCATA	2100
AAGAGCCAAT	TCCTCAATGG	ATTCTCCCTT	ATGATAAGAT	TCACTCACTA	CATTACTTAG	2160
GTCATGAATT	ATAATATTAG	GTATAATTAC	AAAAC TTTCA	AAATAATCAA	TCAAAC TATC	2220
TACCTTATGT	AAATACATAG	TTTGAATATC	TATTGTTTTC	CGTGT TGCTA	GGTCTGCATT	2280
TCTAAAGGCA	ATTACAGAAG	AATCAAATCG	AATGCTCTCT	TCTTCCTGTT	CAAAATAAGT	2340
TAAATCAACA	TGAAATTGGT	TGGCCAAATG	CATTTTGGTT	GATAATTTAG	GTTTCGTTTC	2400
GTGGGACTCA	AACTGCCAAA	TGGCTTGTTT	CGTTAAATTA	ATTCTCTGAG	CTAATTCTGC	2460

1309

TCTACTTAAA CCATTTAACA GCCGTAATTC TTTCAATACC CGACCATTAA ACATTTACAT 2520
ACTCCTTACT ACTTTTGACC TTCTTGTTTT TCTATTCTTG GAATAATTTC AAAATCTTCT 2580
GTTTCCGATA ATTCTGAAAA ATTAGGAATA TCTTGATATT TAGCTTCTTC GAAATGGTAC 2640
GGG 2643

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TGACCAAGTGG CAAAATGGCT ATCCAAATGC AGATGTTATT ATCGATGATA TCATCTCAGG 60
GCAAGCCTAC GTAGCCTTGG AAGAGGGAGA ACTGCTAGCC TATGCTGCTG TGACCAAGAG 120
TCCAGAGGAG GCCTATGAAG CTATTTATGA GGGAACTGG CAAGCTGGAG AGTCAGAGTA 180
TCTAGTCTTT CACCGTATTG CTGTGGCAGC AGATGTGCAG GGAAaAGGAG TTGCTCAAAC 240
CTTCTTAGAG GGCTTGATTG AAGGTTTTGA TTATCTTGAT TTTCGCTCAG ATACGCATGC 300
TGAAAACAAG GTTATGCAAC ATATTTTGA AAAACTTGGT TTAAACAAG TCGGTAAGAT 360
GCCAGTAGAT GGCGAACGCT TGGCCTATCA AAAATTAAAG AAATAATGCA AAAGAAGTAT 420
GTAAAAATCC TCTACTCCTC ACCAATTGGT ATTCTATCAC TTGTAGCTGA TGACCATTAT 480
TTGTATGGAA TTTGGGTCA GGAGCAGAAG CATTTTGAGA GGGGACTAGG AGATGAAACG 540
ATAGAAGAAG TTGTWAGTCA TCCTATTTTA GACCCAGTTA TT 582

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 554 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

CCCAAGCTAC TAAGAGACTA AACTTGCTA GAGAAGCAAG AGAAAGTGTG AATCTTTTTA 60
ATTCATGAT GAATTCCTT TCTGCTACCA ATTTAGAGAA ATTTTCTCTA ACCAGCAATT 120
CCCCTAGTAT AACAAATTCA AAAAATGGAG TCAATTTATC TGCTCACGGT CCAGCAGGTA 180

1310

GCCCCGTACT TCTGAGATAA AATAGAGAGA CCCTGTAACG AACAGCAAGT CTTGAGCGTC	240
TGCCCTTTCT TCAAAATCGC TGATAAATTC TCGGTAAGAA GAAACTATAT CGTAACCTGT	300
CACATCCCTT TCGTCCAAAG CCCCCTGATA GTCAAAGCCG GTCACCTTGA GTTCCACCTG	360
AGGCAATTTT TCAGTCAGAT AACCCAACAT CCCTTGATAA TCCTTACGTT TCAAGGATCC	420
AAAGAGGATT TGAGGTCGAT AGCCTTCCTG CTCTTTTCTT TTGATAAACT CAGCCAAGCG	480
AGTCAAGGCA GGGAGGTAT GAGCACCATC CAAATAAATC TGTGGGCGAA TACGCTCCAA	540
GCGAsCAGCC CAAT	554

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

CCGGTTTTTC AAATGAATTT CTGTTGTG GCTAAAAAAT ATGCTACACT ATCAATATGA	60
AAATTTTAAT CCCAACAGCA AAAGAAATGA ACACAGACTT CCCAAGTATC GAGGCAATTC	120
CTTTAAACC AGAAAGTCAG GCCGTGCTTG ATGCCTTGGC TCTCTATTCT GCCAGTCAAT	180
TGGAGAGTTT CTACAAGTA TCAGCTGAGA AAGCGCGGA AGAATTTCAA AATATCCAAG	240
CTTTGAAAAG GCAAACTGCT CAACACTATC CAGCCTTGAA ACTTTTGTAT GGGCTTATGT	300
ACCGCAACAT TAAGAGAGAT AAGCTGACCG AGCGGAACA AGATTATCTT GAAAATCATG	360
TTTTATTAC CTCGGCTTG TACGGTGTG TTCCAGTCTT GTCACCCATG GCTCCTCACC	420
GTTTGATTT TTTGATGAAA TTAAAAGTCG CTGGTAAGAC TTTGAAGAGC CATTTGAAGG	480
CAGCCTATGA TGAAACTCTG AAGAAGGAAG AAGTGATTTT CTCTCTCTTG TCATCAGAGT	540
TTGAGACTGT ATTTTCTAAG GAAATCAGAG CAAAGATGGT GACCTTCAA TTCATGGAGG	600
ATAGAGGCGG TCAGCTGAAG ATTCACTCAA CTATCTCCAA GAAAGCGCGC GGGGCCTTTC	660
TAACAGCTTT AATAGAAAAT CAAGTACAAA CTGTGGGGG AGCACGTCGC TTGAACTTTG	720
CTGGATTGT TTACCGAGAA GATTGTGAC AACACAGGG GGATGG	766

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 901 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

CCGGCCACGG TTCCATCCAA CTTCACAGGT GTGCACTTGA TTGTGTATGT AATTGTCACT	60
AACGGTAGAA TTTCACCTAT CCCTCCTATC TGCTCGCAGT ACCCGCAGAC TTTCTGAAAG	120
AAGAAGATAA CCTACTTATC CGTTGCTATG ATTATACTAA AGTTTCTACT TTTTGC AAA	180
TAGATTTT TA AATTTTGGC TAATTGTCTG AATCAGGGTC GGAAGTTTGA CGACCTTGTC	240
ATTGCCTAGT TTTTCGCGTG CAATTTTGAG AATGGCACCT GAGTCTTTTG AAGCAAAGAG	300
GAATTTTCCT TTGTCTGTAA AGACTTCGAA GTGGCGGCTG ATTTTGCGTC CAGTGACATT	360
GGCTCCAATC TGATTGATAT GGCTCCAAGG AATCTGGATA AATTGTTTGA CATTGACATC	420
TGGGTAAAT TCCAAAGCCT GATCTCCGAC AAGGAATTC CCAACTTCC CAGCGATAGA	480
GAGGTAGGAA GTGCCTGTCG TACTGAGGAG TACTGTTT TG TTAAGTGATT GGGCCATGCT	540
TAGTCTTCCT TACTTTCTCC AAAAAAGGCA TTGTAGAGGG CTTTAATTGC TGCTTTCTCT	600
TGGTCTTTAT TGACAACAAA CATAATAGAA ACTTCACTAG AACCTTGAGA CATCATCTGG	660
ATGTTGATTT TGTTTTCAGA TAGAGCGCGT GTCGCAGTAG CAGTCACTCC GATATGGCTC	720
TTCATTTTTT CACCAACAAT CATAATGATA GAAAGGTCGT GTTCGATTTT TGCATGATCT	780
ACTTTAGCCT TTTGAACCAA CTGACGAGG ATTTCTTCTT CCTTGATGGG AGTTAGTTGG	840
CGAGAACGGA GAATGATAGA AAGAWCGTCG ATACCTGTTG GCATATGTTT CCAACCGATG	900
T	901

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

CCCTGTTACG TGGATAATAG GGTAAGACTG CTCAGGATTT CCTAACAAAT CCACCGCTTG	60
CTGCATTCGA CCCAAACCTG ATCGAAAATT CAAACCAATC CGACTATGGA GCCATTCTTC	120
TACTTCAAAC ATACACATCT CCTTGACAAA AGTCCAATCA ATTATCGCAT TAAAGTATGG	180
TTACTAATAA AAACAAGGCC AGGATTTTCG TCCCGACCTC TTACCTGGTT AGCTAATAAC	240
TAGCTACTAT GAATGTGAAT ATGGGCTAAA AACATCCACT GGACGTTC CA ACTCTTCCCC	300

1312

ATTTCTGGGA GTTGGGGTAA AAATGTTTAC TGGACGTTCC AACTCTTCCC CATTTCTGGG	360
AGTTGGGCTG ATACAGTCTC CCAGACTGTA TCACTCCTCC ATAAAGCTGT TGAAGACTTC	420
TTCAATCATG TTCCATTCTG CTTCTGAGTC TTCTGGGATT GGTTCGAATT CGCCTTCTGT	480
TCCATCTTCG TTTTCGATGA ATGAGTAAGC TTGGATTTC AACTTGTCCTT CTTCTGCTTC	540
TTCTGCGTTA ACTGGTACTA GAAGAACATA GTTTTACCA AATTCTTCTT TTCCATCAAT	600
TGTCAAAAGG ATTTCAAACA AGGTTTCATT TCCTTGCTCA TCTACTAGTG TGATTAGTTC	660
ACGTTCTTCG TGGTCGTGGT TATGATCGTG TGACATAGCC TCGCCTTTAT ATTAATAATT	720
TCTATCTAAA TAATTTTGTA AAATCAGCTG AGCTGCTAAC TTATCAATGA CTTTCTTGCG	780
CTTATTGCGA CTGATATCTG CTTGTTCAAT CAACATGCGC TCAGCAGCCA CTGTTGTCAA	840
GCGTTCATCC TGATAGTCTA CTGGTAAACC AAAAACTCT TCTAGCTTTG CTCCGTAGCT	900
TGACTAGCTT CTACGCGCGG TCCACTTGTA TTGTTTATGT TTTTAGGCAA GCCCACTACA	960
AATCGTTCCA CCTTGTAAGT ATCAACCAAT TCCTTAACGC GGTCAAAACC AAATTGCCCT	1020
TGTTCTTCAT TTATCTGGAT GATTTCAGC CCTTGAGCTG TAAACCAAG CGGATCGCTA	1080
ATCGCCACCC CTACCGTTTT TGAACGACG TCCAATCCCA TAATTCTCAT AGGTTATAGA	1140
TCGACTCCTT GTCCTTTGAG GTAGTAGCGA ACCAATTCCT CAACGATTTT ATCACGCTCA	1200
TACTTACGGA TTTGATTTCG TGCATTATTA TAACGAGGAA CGTAGGCAGG GTCTCCACTC	1260
AATACGTAAC CTACGATTTG GTTAATTGGG TTGTaaCCCT TATCGTTCAA CGAAGCATAA	1320
ACATCTGTCA AAGTTTCGCT AATTCTTTT TTATTGGAAT CGTCCAATTT AAAACGTACT	1380
GTTCCTTCAG TAAATCCCAT TCTAACACCC TCTTTCCTTA GAATAGTACC ATTATAGCAT	1440
AATTCCTTAC CTTCTACAAT TCAGGCAGTC TATTTATTTG GATTTTCTAT TGTTCTGTCTG	1500
CGCCATTTGC CAATCTATCT GAAATATATT TGCTTGGTTC ATTTTTCAAA AGATTTTCCA	1560
AACCAATATT CTTCAGATGT TCCAACGGG AAGCCTTCTT GACATCCAGA ACTTGAAAAT	1620
CAAACTAGT CGTTGTTTGA AGTTCCGTTG CGCTCAATAG TTTTGTTTCA AGTTTGAAAC	1680
CTGCCAATTT ACGAGCTTCA ATGATAGACT TATCCTTCTC CTCCGCTTCA AGAAGAGCTT	1740
TTTGAGTTTC CTCCACTCCA TGTTG	1765

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

CTTATCCATT CACTTCTTG TCTGTTATTC TATAAATCTT ACTCCTAAGT ATACCACATT	60
TGCCCCTAGA TGTGAACGAG AGAAACGCTC TAGACATTGC CAAGAAGGAA AAAAAAGGGT	120
ACAATGTAAC AAAATCAAGG GAGGTCTGGA ATGAAGAAAC AAAGCAAGTA CAAAGAGGTC	180
GTTTCCTATC TGAAAAATGG TATCGAGTCT GGACGATTTC CGACGGGTAG TCGCCTGCCT	240
TCTATCCGTC AACTGAGCCT TGACTTTCAC TGCAGCAAGG ACACCATTCA ACGAGCCCTG	300
CTGGAATTAC GGCACGAACA ATACCTCTAT GCCAAGCCTC AGAGTGGCTA CTATGTATTA	360
GAACAAGGGC AACATCAAGA CCTAGAAATC GAGGTTACCG ACGAACATGC CAGTGCCTAT	420
GACGATTTC GACTCTGTGT CAATGAAACC TTGATTGGCC GAGAAACTA CCTCTTCAAC	480
TACTATGACA ATCAAGAAGG ATTAGAAGAC CTAAGACAGT CCATTACAA ACTCCTCTTT	540
GAGCAAGCTC TCTACTGCAA GGCTAACCAA CTAGTACTGA CTTCTGGAAC CCAACAAGCC	600
TTGTTTATCC TCTCTCAAAT ATCCTTTCCT AGACAAGCCA AGGAAATCTT GGTGGAACAG	660
CCAACCTACC ATCGGATGAA TCGCCTCTTG ATTGCACAGG GGCTGGACTA TCAAACGATT	720
GAACGAGGCA TTGATGGGAT TGACTTGAG GAGCTGGAAG GCCACTTCAA AACAGGAAAA	780
ATTAAGTTT TCTACACCAT TCCCCGATTT CACTATCCCC TGGGACATTC CTATTCTGAG	840
CAAGACAAAC GATCTATTCT TAACTTAGCT GCCAAGTATG ATGTCTATAT CGTAGAGGAC	900
GATTATCTGG GTGATTGGA CTCCAAGAAG GGCCAAACCT TCCACTATCT TGATACAGAG	960
GAGCGTGTC TTTATATCAA GTCCTTCTCG ACCAGCCTTT TTCCTGCCCT TCGTATTACA	1020
GCACTCATTC TTCCAAATGC TATCAAAGAA GCATTTGTGG CCTACAAAAA TATCCTAGAC	1080
TACGACAGCA ACCTCATTAT GCAAAAGGCC CTGTCACTCT ATATTGACAG TCAATTGTTT	1140
GAAAAAATC GTTTGGCTCG CTTGACCAAT CATGAATCTT ACCAAAAACA AATCGAGGAA	1200
AGGATAACTA AACACCTTG TCCCCTTCCT CATTATTCCC TACACGATGG yTTATTGCTA	1260
GACCTGAGAC AGTATCCTAA AATCGCCAGT CTCAAACACA GTCAACTGGG cTTGGACTTC	1320
TTTGAAGAGG CCTATTTAAG CACCTG	1346

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

CTATATTCAG AATATGCCAA AAATTCGGAA TGGTATAAAT TTGCGGAGGG TTCATTTGAC	60
ATATTTAGAA AACTCCCCCA AAGAATTAAT TTTAAGAAAG ATTTTCTAG AATTTGGCC	120
CCCTTTATTA TTAATTTGCT TAAATTAATC AATAATTATC TAGAGAATAA AGAATACGAG	180
TGGATTGACA AGAATGGAAA TATTTTTTCC TCTCTAGTAT TTTATTTAGA AGATTTAATC	240
TATCCTTGGG TTGTTAAACC TTTGGTTTGA GAGATAAATT CATTCGCTGA AAAAGGTTTA	300
CTTGAAGGGG AATCGGAGCA GCAACGGTAC AAATATTTTA TAACATTGTT TGACAAGGAA	360
GAGAATATAT TAAATTTTGA TAACAAATAT CCCGTTTAC TGAGGCAAAT ATCGGAGTCT	420
TGTCTTCGGT TCTATACTTA TTTTATAGAA ATTTTATCAA ATTTAGAAAA TGATTTTAGT	480
GTGCTAGAAG AAGAATTAGG GCTAAGGGGG AAATTAAATG ATATAAAATT TGGAAAGGGT	540
GATACACACA GCCAAGGAAA AACTGTTTTG ATACTCTTCT TTGATGACGC GAAAATTGTT	600
TACAAGCCTA AAAATTTAAT AATCAATAAC TCACTAAATA CTATTGCTGA GTATATCCGA	660
AAGGTTGATG AAAAAATTAG GATAAGAATA CCTCGAACTA TTGCTTATTC GGATCACAGC	720
TATGAAGAAT TTATTGATTA TCTACCTCTA GAGCAAAAGA AAAATTTACC TGAATATTAT	780
TATAATTTTG GTGTGCTTTT AGCATTTATA TATTTATTTA ATGGGAGTGA TATACATTTT	840
GAAAATTTAA TTTCTATGG AGATATGCCT GTAATAATAG ACTTTGAAAC AATGTTACGG	900

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 862 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

TTATTTAGCA GAGGCAGTTT TAAATGTGAA GGATTTGGTC AGTCAAACAG TTTTTTATCA	60
GCAGATTATT GGTTTAGAAA TCCTATCTCA AACGGATACA GAGGTCGTTC TGGGACTTGG	120
AGGAAAAGCC TTGGTACACT TGATTCAAGC ACAAGAGGGT GGAGAAGTAA GGAACATTA	180
TGGTCTTTAC CATCTGGCTA TTCTTTTGCC GACACGAAAG GCTTTGGCGG ATGTCTTGAA	240
GCACCTGACG GATTACAGA TTCCTCTTGT TGGCGGTGCA GATCACGGTT ACAGTGAGGC	300
CCTTACTTA GAGGACTTGG AGGGAAATGG CATTGAACCT TATCGAGATA AGCCAGTTTC	360
CACATGGGAT ATTCGAGAAG ATGGACGTAT TATCGGGGTG ACTGAAGTCC TTGCGGCTCA	420
GGATATCTAT GAGTTGGGGG AAAGAGTAGA GCCTTTTATC CTAGCAGAGG GTACGAGAAT	480

1315

GGGGCATATT CATCTTTCTG TCAAGGATAG TCGAAAGTCC AGACAGTTTT ATCAAACGGT	540
GTTAGGGCTC GAGGATAAAT TCAGTGTGCC TAGTGCTAGT TGGATCGCAG CTGGGGACTA	600
CCATCATCAT TTAGCAGTCA ACGAATGGGG AGGAAAAGGT CTGGATCCGC GTAAACAAGT	660
CCTACCAGGT TTAGCCTACT ATGTCATCGA AGTCGCACAT AAAGAAGAAC TGTTAACGAT	720
TGCCCCAACGA GCACAAGAAG TTGACGCACC AATCAAATGG ATGACATCGA TCCAATTGGA	780
AATCACAGAC TCAGATGGCA TCGTGACCCG TATTCGTTTA GCTAGATAGA TGGTATGTGA	840
TGAAGGTAGA GCATCAATTG TA	862

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 650 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCGTTTACAA GATCGCTAAA ATGCATCTCA TGATCGCGAC CACGAATTCC AAGATAGCAC	60
GCGCTACCTC AATCATAGAT AGTTCACTTT TTTCTTGCCC AGCAAATACT TCTAATCCA	120
AAGCGTTTCT CCTCATTTAT ACTACTATCG CCAGAGCGAA CAGACTCTGA CCTCATTTTA	180
TCATTTACTC TTTATTTTAC GATAATTTTG CGGAATAGTC AAAGGTTAAG GGGGAGAAAG	240
TGGCAGGATT AGACTAATTC CAATATAAAA CTCATTCCCTT TTTCTGTTGC TCCATTTTCC	300
ACAAATCCAA GCGACTTGAA ACACCTCCTA GAAGCATGAT TGTAGGTGTA GATTTTCTTG	360
ACTCTCAATT CTTTCCATCC TTTTACTCGA GCCAATTCAA TCAAAGCACT TAGAATCTTT	420
TTTCCAAGTC CTCGATGTTG GTAAGCGGAA TTCCCAATCA CAATGGGGAG ATTATCCTGA	480
GATAGTGTA TATCCCAAT TGGAAACCAT TCTCCCTTCT CCTTGACTTC AATCCAAAAA	540
AGCTCACCAT GCCGATyCar ATAGGAATAC ATGGCTTCCA AGGTCGCTtG ACTGTAAGGA	600
AGCTTCACCC CATCTACGAG GtAAcCAAGT TCACATCCGT GATACCAAGC	650

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GATAGCAATC CGCTTCAGAA ACTTCTCGCT TACCTCTAAC TCCGATCGCT AGTTTGGGAG	60
AAGATACTTC CATTCTCATA CTATCTGTTG GCTTTGCAGG CTGTAAAAAC AACTTTTCTC	120
TTGCTACTTC CTGAAAATCT GAATCTTGCA GTTCTTTGCT TTCAAAATAG TCCTGTACTC	180
GCTCCACATC AAAATTCCCA GCTAAAGACA GAGACATGTT TACAGGTTTG TAAAACTTTG	240
TAAAAATTTT TGCAAATTA GTTAGATTGA TTTGGGAAAT GGACTCCTCA CTTCCTCACTA	300
TATCAGTTGC TAAAGGTGTA CCAGGATACA AATTCGCTAA AGTTGAAAAG AATAAACACG	360
AATCTGGATC ATCTTGGTAC ATTTCTCGTT CTGCTGAAT AATATCCTGC TCTGTCAGAA	420
TGGAAGCTTC AGTAAAGTGT GCTGATGTTA CCAATTCATC AAGTAAATCT AAATTTTCTA	480
AAAAATAATC CGTTGCTGAA AAAAGATAGT TTGTTTTTGT AAAGCTTGTA AAGGCATTAC	540
TATCTGCACC TAGACTCGTA AAAGCCGACA TCAAACTACT AGAATCTTCT CTCTCAAATA	600
ATTTATGTTT AAGAAAATGA GCAATTCCTC CAGGATATTG TTTTACATCT CCGTCAACTT	660
CTGTGACAAA CGTATCTACC GAACCAAAT GTACAGTGAC ACTCCCGTAA ACCTCTTTAA	720
ATTCCTTTTT AGGCAAAAGA GCAACTGTCA ATCCGTTGGC CAAACGAGTT CGATAAACCA	780
TTTCTTTTAC AGCTGGATAG TATTTTCTT CAAAAACAAC CTTTGTGATT CTATTCCTTC	840
CATAAAGTAA ATCGCTTGTA GTTTCACATT ATTAGCTACT CTACAAATAG CATCTTTGTC	900
AATTTGTTC AGCTTTGCAA TCCAACTTTT AAAGTCTGCT GAAGATTTTC CAAATAAGGC	960
ATTTTGATAA GCACGTCAA TCAATGAAGA ATGATTATCT TGAGAAAGTA ACAACGACCA	1020
ACGAATCATT TCCTTGGTCT GATTTAACTC AAAGTCTGTA AAAAAACCTT TTTTAAATC	1080
AAGCCGTTGA TTATTCATCA ATTTACGAGC CTGGTTACG	1119

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ACGCCCTCGC GGGGACATGA CGAATCCCC GTTCATCACG AAGGCCGCCG AGGAGTGGGG	60
GGTGCCGTCC AAGTCAAAAG CGGCCCCACA TCGATTCACT TCCCCGACGA ACAGCCCTTT	120
CCCCAGCGT TCCTGGCTTT GCAACCGTTT CACAACAGCC TCGTAAAGTA GGCCGGACAA	180
GGCAGACGGA CTCCAAAGGA GTTCTTCCAT CTGCAAGTGC GCCTGCGTTA TGTGATCCCG	240

1317

GTCTTTTGCA TGTGTGTGGC ATGAATGCTG TTCCCAATCC CACTCCAGAA CATTCTCCTC	300
AAAAGTGCGC AACGTCGCCC TGAATGAATC CTGCCTTGTA GTCGTGACCA TTCCTATGAA	360
GGGTGCGAGA GGATTTTCCC CGAGTGCAAG CGCATCCTCC GGCTCAAATC GGGTGCAATT	420
CACAGTCCCG CTCAACGCTA GCCCAGATCCC TTTTGGGCAT GGTGACTCAA GCGTCCTTTC	480
AAACAAAAGC TCCTCATCCG CTCCAACCGG CCCGACGTAG ACGCGTAGAC CGAAGTCGTC	540

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1949 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGAATTCG ACCAATTCAA GGTGAGGCA TCGAAACTA TGGACTGTTC CCCCCTCAGT	60
TCTGGACAGA AAACGGGATA AGGTTGGCTG TGAAGCAAGC TGGCCTCCTA CCAACAATTT	120
TGGAAAGTAG GCATCAGCTG ACAATTCCTT ACAAGCATAG TCCGTTCCAT AACCTGTTAA	180
CAGTTGAAAG AGGAACTGGA CAAGGATATC TGAATCCGAA TAACGACAGT AGCGGCGTTG	240
GTCATTCGTT ACTAAATACT TAGAAATCCG CTCTTTTAGT TTCAACTGGG AAAAAAGTTC	300
CTGAAAAAAG ATAAGACCAC CATACTGGGT TAAATGACCT CCATCGAAAG ATAGTTGGTA	360
AAAAGACTTG TTTTGGAAGT GATGATTTGG TAACTGTTC ATGTGAGTTT CCTTCTTTT	420
TGTGTTTTTT TCTACACTTA TACCATAAAG GGGAACTCT TTTTGTCTA GTAAAAACA	480
CCCATTTGGT GAAAAAGAA ACCATCCAGG ATCTAAGCTA AGGCAAGGAT TCTGGATGGT	540
TTTGTAGATT GGGGTGAATA ATTGGGGTTT TACAATATCA ACTCCCATGA TAGTCATGAG	600
ATGACTCTTC ACGAATTGAC GTGATGACTG TCCTTCCTTT TGCATAATTA CCTCCGAAAC	660
ACAAAAAAG GGGTAGACAA TCTAGTGTCT ACCCCGAAA GTTTATTAAA AAAAAATCC	720
TGCCAAAGAA TTTTGGCAG GAAACCAAT CAATTTATCA GTTCTATCA ATCGCTTATC	780
GCTCTCAAAG ACTGGTAAAT AGGGATTCCG CAATCAAAT GCGATACTCT ATTATTTAAG	840
AGTAACTGAA GCTCCAGCTT CTCCAATTT AGCTTTGATT TCTTCAGCTT CTGCAGTTGC	900
AACGCCTTCT TTAACAAGTG CTGGTGACC GTCAACAAGT TCTTTAGCTT CTTTAAGACC	960
AAGACCAGTG ATTTCACGTA CAACTTTGAT AACGCCAACT TTTTGTGCGC CTGCAGATGT	1020
CAATTCAACG TCGAATGAAT CTTTAGCAGC ACCAGCATCA GCTGCATCAG CTGCAGCAAC	1080

1318

AGCTACAGGA GCAGCTGCAG TTACACCAA	TTCTTCTTCG ATAGCTTTTA CAAGGTCGTT	1140
CAATTCAAGG ATTGAAGCTT CTTTAATTTT	AGCAATAATG TTTTCAATGT TCAATGCCAT	1200
TGTTATTTCC TCCAAATAAG TTTTAAATTT	TATAATAGTT TTTTTCGTAG CTAGksTACG	1260
CTGTGTAGCT TAAGATTAAG CCGCGTCTTC	TTTGCTTTCT GCAACCGCTT TGA CTGCAAG	1320
AGCAACGTTG CGCACTGGCG CTTGAAGTAC	AGAAAGGAGC ATAGAAAGAA GTCCTTCGCG	1380
GTTTGGAAGA GTTGCAAGTG CAAGAATCTC	TTCTTTAGAT GCGACAGCGC CTTCGATTGC	1440
ACCACCTTTA ATTTCAAGTG CTTCAGCGTT	TTTAGAAAAG TCGTTCAAGA TTTTCGCTGG	1500
TGCGATAACA TCTTCATTAG AAAATGCTAC	TGCAGATGGT CCAACAAATA CAGATGCAAG	1560
ATCTTCAAGA CCAGCTTTTT CAGCTGCACG	ACGCAAGATT GAGTTTTTAA TAACTTTATA	1620
CTCAACTTCG CTTCCACGAA GCTCACGACG	AAGAACTGTA TCTTGCTCAA CTGTCAAACC	1680
ACGAGCGTCT ACAACGACGA TAGATGCAGC	AGCTTTCATT TTTTCAGCTA tACGTCAACT	1740
AGTTCGCTT TTTTAGCAAT AATTGCTTCA	CTCATTAGTG TGTTCACCTC CGTAATTATT	1800
TTGCTTGGGG AATTTTTCOA AAAGAAAAAC	GCGCCCAATC CTAGACACGA AAGTACAATA	1860
CGCTTCTTTT TACATGATAC GTTTTGTCCT	CGGTAGGATA TTTATGAGTC GAGCTCCCCT	1920
ACTGTCTTAG GCAGTTTTTT TAGATACGG		1949

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1023 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GGACTGTTTG ATCTTATACA GTAGCTGCTT	GATCCAAGCT TTCACCGATA GCGGCTAGGC	60
GCTCGATAAC TTCAGCTTGT GTCAATTCAT	TTTTTGAAAC ATAGCGGTTA CGTGGGTGAA	120
CACGGCACTC GTGTGAGCAT CCACGAAGGT	ACTTGTCTTC ATTTTCTTCT GATGTCAAGA	180
TACGACGGTT ACAGAAATGGA TTTCCACAGT	TGACATAACG TTCACATGGT GTTCCATCAA	240
ACCAGTCTTT CCCTACGATA GTTGGGTGTA	CATGGTTGAC ATCAACGGCA ATACGCTCGT	300
CAAAGACGTA CATTTCCTCA TCCCAAAGCT	CACCTTGAAC TTCTGGGTCT TTACCGTAAG	360
TTGCGATTCC TCCGTGCAAT TGGCCGACAT	CTTTGTAGCC TTCACGGACC ATCCAGCCTG	420
AGAATTTCTC ACAGCGAACG CCACCTGTAC	AGTAAACCAC GACACGCTTG TCCATGAATT	480
TTTCCTTGTT ATCACGGACC CATTGTGGTA	ACTCACGGAA GTTGCGAATA TCTGGGCGAA	540

1319

TAGCTCCACG GAAATGTCCT AGGTCGTACT CATAATCGTT ACGTGTGTCA AGGACAACGG	600
TATCTTTTATC AAGAAGCGCT TCTTTGAACT CTTTGGAGA CAAGTAAGCA CCTGTTGTTT	660
CAAGTGGGTT GATGTCATTG TCAAAGTCGT TGTCTTCCAA ACCAAGGTGG ACAATTTCTT	720
TCTTGTAAGC AACAAACATC TTCTTGAAGG CTTGTTTCATT TTCTTCGTCA ATCTTGAACC	780
AGAGTTCTTC CATTCCTGGA AGGCTGTGAA CGTAGTCCAT GTATTTTGA GTTGTTCAT	840
AGTCACCTGA AACTGTTCCG TTAATCCCT CGTCAGCGAC TAGGATACGG CCTTTAAGGn	900
CGATTGATTT ACAGAAAGCC AAGTGGTCTG CAGCAAATG CTCTGCATTT TCAATTGGAG	960
TATAAAGGTA GTAAAGTAAG ACACGAATAT CTTTgkCaw AAGATTTGTA TCTCTTTATC	1020
TAT	1023

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3831 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

ACTATGAACA AGACCCAGAA AAAGTAGCCT TATTTCTTAA GAATTTTAAT AGTTTAAAGC	60
ACCTAGCACC TGTTTAGATT GACGAAACAG GATTCGATAC TTATTTTAT CGAGAATATG	120
GTCGCTCATT AAAAGGTCAA TTAATAAGAG GCAAAGTATC TGGAAGAAGA TATCAGAGGA	180
TTTCTTTGGT TGCAGGTCTA ACAAATGGTG AATTAATCGC TCCAATGACT TACGAAGAGA	240
CGATGACGAG CGACTTTTTT GAAGCTTGGT TTCAGAATTT TCTCTTACCA ACATTAAACA	300
CACCATCGGT TATTATTATG GATAATGTAA GATTCCATAG AATGGGGAAG CTAGAACTTT	360
TATGCGAAGA GTTTGGGCAT AAACTTTAC CTCTCCTCC CTACTCGCCT GAGTACAATC	420
CTATTGAGAA AACATGGGCT CATATCAAAA AGCACCTCAA AAAGGTATTA CCAAGTTGCA	480
ATACCTTTTA CGAGGCTTTT TTATCCTGCT CTGTTTCAA TTGACTATAT TAGAGGCGAG	540
ACATTTTTCG GTTCTTTGTC AACTGTAGTG GGTGAAGAA AGCGAAGATC TAGAAAGGAC	600
AAATTTTCGTC CTTTCTTTT TGAAGTTTTC AAAGTTCCTA AAACCAAAGG CATTGTGCTT	660
GATAAGTTG ATGAGATTAT TGGTGGCTTC CAGTTGGCG TTGGAATAAG GTAATTGAAG	720
GGCGTTGACG ATTTTCTCTT TATCTTTGAG GAAGGTTTAA AACAAAGTCT GAAACAGAGG	780
TGAAAAACCA AGAGCTGATA GAGATTATAG TGGTGTAA AGTCTTCGGA ATAGCTCAAA	840

1320

AGTTTATCTA GAATTTCTTT ATTAGTCAAG TGCATACGAA AAGTAGGGCG ATAAAATCGT	900
TTATCACTCA GTTCTGACT ATCTTGTTGA ATGAGCTTCC AGTAGCGCTT GATAGCCTTG	960
TATTCATGGG ATTTCCGATG ATGGCTTGTG TTCTGCTCTC AAGAACAGTT ATGATATTGA	1020
GTTTATCAAA GTCCTGAGCA ATAAAGCTCA TCTCCATCTC CCGATTGAAA CAGTCACTCC	1080
CCGGACTGTT TCAACsTCCT AGGACATAAT CTCAGGAAGA CGCGAAAAAT CATGCTCAAA	1140
GTGAAAATCA TTGTTCTTGC GAATGACAGT TGAAGTTGAA ATAGACAACT GATGATCAAT	1200
GTCGGTCATA GAAGTCTTTT TAATTAGCTT CTGAGCAATC TTTTGGTTGA TGATACAAGG	1260
AATTTGATGA TTCTTCTTGA CGATAGAAGT CTCAGCGAGC TCCATTTTTG AGCAATGATA	1320
GCACTTAAAA CGGCCTTTTC TAAGAAGAAT TCTAGTTTGA ATTTTTTTAT ACTAGAAAAT	1380
CAGAACCATA ATACCTATAT AAAAATATTA TAGTCTAAT AGGATTTACC CAAAAGTTTT	1440
AAGGCGGTCT TTTTAGAACT TTAATTGTTT GAAATTTAGG TAGCAAATTT GTTCTATTT	1500
TGTCAACTTT TCCTATTTTT ATCTTGTTGA GGCTGGTATT TTAACAATTC AGGAATTGAT	1560
AGTGAATGTG TAAAATTTTT TGTTAGAATA AGTTTATAAA AAAGAAAAGG AGTATTTGAT	1620
TATGTTACAA AAAATTTATG AGCAGATGGC TAATTTCTAT GATAGTATTG AAGAAGAGTA	1680
TGGTCCTACA TTTGGTGATA ATTTTGA CTG GGAACATGTT CATTTTAAAT TTTTAATTTA	1740
TTATTTAGTG AGATATGGCA TTGGTTGTCG TAAGGATTTT ATTGTTTACC ATTATCGTGT	1800
TGCTTATCGT TTGTATCTTG AAAAATTGGT AATGAATCGG GGTTTTATTT CTTGTTGAGG	1860
TAATTTTAGT AAATTTCCGA ACTAATTTAC TCTTTTATGG AAAGATGATA GTAAATAGCT	1920
AGTAATTTTT CTAAATCATT TTTTAATAGT TGGAAATAGC AAATCTTTCT ATTGTTTCTT	1980
CTTGATAAAA AGGCGATTTT TTATTATAAT AAATTGTAAG ATATAATTGC AGGTGAGAGT	2040
CCTGCCATGT ATGTGAGAAA GGAAGAGCCT GATGGCTCAG ACAAGATTAT GACTTCAGTT	2100
GTGTTGTAG GTACCCAATG GGGTGATGAA GGTAAAGGGA AGATTACAGA CTTCTTTTCA	2160
GCGAATGCAG AAGTGATTGC ACGTTACCAA GGTGGTGATA ATGCTGGTCA CACGATTGTG	2220
ATTGACGGTA AGAAATTTAA GTTGCACCTG ATTCCATCTG GGATTTTCTT CCCTGAAAAA	2280
ATATCTGTCA TTGGGAATGG TATGGTTGTA AATCCTAAAT CTCTTGTAAG AGAGTTGAGC	2340
TATCTTCATG AGGAAGGTGT AACAACTGAT AACTTGCGTA TTTCTGATCG TGCGCATGTT	2400
ATTTTGCCCTT ATCATATCGA GTTGGATCGC TTGCAAGAAG AAGCTAAGGG CGACAATAAG	2460
ATTGGTACGA CAATTAAGGG AATTGGTCCA GCTTATATGG ACAAGGCTGC TCGTGTGGA	2520
ATTCTGATG CAGATCTTTT AGATAAAGAT ATTTTCCGTG AGCGTTTGA ACCTAACCTT	2580
GCTGAAAAGA ATCGTCTTTT TGAAAAATTG TATGACAGTA AAGCGATTGT TTTGATGAT	2640

1321

ATTTTGAAG AATATTACGA ATATGGTCAA CAAATCAAGA AATACGTGAT AGATACATCT 2700
 GTTATCTTGA ATGATGCGCT TGATAATGGC AAACGTGTGC TTTTGAAGG TGCACAAGGT 2760
 GTTAGCTAG ATATCGACCA AGGTACTTAT CCATTGTGTA CGTCATCAAA CCCTGTAGCT 2820
 GGTGGTGTGA CAATTGGTTC TGGTGTCCGT CCAAGCAAGA TTGACAAGGT TGTAGGTGTA 2880
 GTAAAGCTT ATACGAGTCG TGTAGGAGAT GGTCTTTCC CAACTGAGTT GTTTGATGAA 2940
 GTGGGAGAAC GTATCCGTGA AGTGGGTCAT GAATATGGTA CAACAACTGG TCGTCCACGT 3000
 CGGTAGGTT GGTGTGACTC AGTTGTGATG CGTCATAGCC GTCGTGTTTC TGGTATTACT 3060
 AACCTTCTT TGAACCTCTAT TGATGTTTTG AGCGGTTTGG ATACTGTGAA AATCTGTGTG 3120
 GCCTATGATC TTGACGGTCA ACGTATTGAC TACTATCCAG CTAGTCTTGA ACAATTGAAA 3180
 CGTTGCAAGC CTATCTATGA AGAGTTGCCA GGTGGTCAG AAGATATTAC CGGAGTTCGC 3240
 AATTGGAAG ATCTTCCTGA GAATGCGCGT AACTATGTTC GTCGTGTGAG TGAATTGGTT 3300
 GCGGTCGTA TTTCTACTTT CTCAGTAGGT CCTGGTCGTG AACAAACAAA TATTTTAGAA 3360
 AGTGTGTTGGT CCTAAGAGAT TTTAAGATT TGTTAAGAT AGGTCGGTA TACTATAGAC 3420
 GGTACAAGA AGACCTCCTA ACTTGTGTA ACAAATATCC TAACTTTTC TTTTCATAA 3480
 TAATCTCCCT ATAGAGTCAC CGCATTCGGT GGCTTTTTT GTGTGGGAT TCATGATATA 3540
 ATAATAAAT CGATAAGTAG GAAAAGAGAA AAGAGATGTA TTATACGCTT GAAGAAAAAG 3600
 AAGTCTTTAT GAGGGAGGCT TTGAGAGAGG CTGAGATTGC TCTTGAACAC GATGAAATTC 3660
 CAATTGGTTG TGTGATTGTC AAAGATGGG AAATCATTGG TCGTGGGCAT AATGCGCGTG 3720
 AGGAATTACA GCGAGCGGTT ATGCATGCGG AAATTATGGC TATAGAGGAT GCGAACTTGA 3780
 GTGAGGAGAG TCGGCTTGCT GGATTGCACA CTTTTGTGA CCATTGAACC G 3831

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CCGCTGTTCC AACCGCAACA TACCATAGTC CGTACGGGAT TCGAACCCGT GTTACCGCCG 60
 TGAAAAGGCG GATGACTTAA CCCCTTGACC AACGGACCTG AGTTGTTATT TTCAACTCTT 120
 ACTATTATAC AGTCTTTTCA AACTTTGTCA ACTACTTTTT CTAATTTTGT TTTATTTTTT 180

1322

CAACTTATAG TAAAAAAGC CAGAATTATA CTGACTCTTC TATCGCTCAT TAACTTAGA	240
AGCACGTTCT TTTCCCCACC AATAAGGGAT TAGTTCTGCG ACTTTAACTG TTTTCTTAT	300
ATTATAGTCC ATCATGAATT CTGCATCTTT ATTTTCAGCA TTAAGCTCTA AAAGGAATTC	360
TCTACAAGCA CCGCAAGGCA TGGCTGAAC TCCACCATAA GGTGGTTTGT CTCGAAAGGC	420
TAATACTTTC TTAACCTTAG TTTGTCCTGA AAATGGTAC ATATTGAAGA GGGCCGCCCCG	480
TTCTGCGCAG AGATGGAAAA CACCACAGGT TCCCTCCATA CAGAATCCTG TAAATATTTG	540
TCCATCTCCT GCTTCTACTG CAGCTACAAC ATGATTGGCA TAAACAAAGT CTGATACTTC	600
ATGTGGATTG TATAGTTTCT GTGCTTCTTC GTACATCTTT TCCCAGATGT CCATTATTGT	660
ATCCTCTTTA TTTAGAGATT TCTTTTAGCA TGTTCGAT ATGCTGAAT TATTTTTCAC	720
GTCCAAGCAA GAAAATTGTA TCTGGTAATT CTGGCCCATG CATTCGCCT GAACTGCGA	780
TACGAATAGG CATGAAAAGA TTTTCCCTT TAATACCTGT TTCTTTTGG ACTGCTTTAA	840
TTTGTGGGAA GATATTTTCT GTCACAAAT CATCATCTGT CATCGCTTCA AGTTTGTCT	900
TGAATGCTTC AAGAACTGTT GGAAGTGT T CACCCGTCAT GACTTCGCGC TCTGCTTCTG	960
TCAATTCTGG GAAATCTGAG AAGAAAAGAT CTGTCAATGG GATAATCTCA TCTACTGATT	1020
TCATTTGTGG TTTATAGAGC TCAACTAATT TTTCAGCCTT GTCAGTCAA CGGCCTGCTT	1080
CCTCTAAGAA TGGTTTTGCC ATTTCAAAGA TGGTTTCAAG GTCTGCATTC TTGATATAAT	1140
CATTGCTCAT CCAGTCTAGT TTTTCTGAT CAAAGGCTGC TGGTGACTTG CTGAGGCGGT	1200
TTTCATCAA AAGTTTAATG AATCTTTCAC GAGAGAAAAT CTCATCCCCA CCACCTGGGT	1260
TCCAACCAAG AAGAGCAATA AAGTTAAAGA CTGCTTCTGG AAGGTAACCT TTCTTTCGGT	1320
AATCTTCGAT AAATTGAAGT GTATTAGTAT CACGTTTGA TAACTTCTTA CCAGTTTCAG	1380
AGTTGATAAT CAAGTGTCAT GTGACCGAAC TCTGGAGCTT CCTCAACCTA AGAGCGGGTA	1440
T	1441

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

CGGCTTATGT AGTGGCAATC TTTCTACGTA AGCGAAACGA GGGGAGATTA GAGGCGCTAG	60
AAGAAAAAAA AGAAGAACTA TACAATCTTC CAGTAAATGA TGAAGTAGAA GCTGTAAAAA	120

1323

ATATGCACTT GATTGGACAA AGTCAAGTGG CTTTCCGTGA ATGGAATCAA AAATGGGTCG	180
ATTTATCTCT CAACTCTTTT GCCGATATTG AAAATAATCT CTTTGAAGCA GAAGGCTATA	240
ACCATTCATT TCGTTTCTC AAGGCCAGTC ATCAAATTGA CCAAATTGAG AGTCAAATTA	300
CTTTGATTGA AGAAGATATT GCGGCAATTC GCAATGCTTT GGCAGACTTA GAGAAGCAAG	360
AATCTAAAA TAGTGGTCGT GTTCTTCATG CTTTGGATTT ATTTGAGGAA CTTCAGCATA	420
GAGTTGCTGA AAATTCAGAA CAGTATGGTC AAGCCTTGA TGAAATTGAA AAACAATTAG	480
AAAATATCCA ATCTGAATTT TCACAATTTG TAACCTTGAA TTCATCGGGT GACCCGTGTGG	540
AAGCCGAGT GATTTTGGAT AATACAGAAA ATCACATTTT GGCCTTAAGT CATATTGTGG	600
ATCGTGTTC AGCCTTGGTT ACGACGCTTT CTACAGAATT GCCAGATCAA TTACAGGATT	660
TGGAAGCCGG TTATCGTAAA CTAATTGATG CTAATTATCA TTTTGTGAA ACGGATATTG	720
AAGCGCGTTT CCACTTGCTT TATGAAGCAT TCAAGAAAA CCAAGAGAAT ATTCGTCAGT	780
TGGAATTGGA TAATGCCGAA TATGAGAATG GACAGGCACA AGAGGAAATC AATGCCTTGT	840
ATGATATTTT TACTCGAGAA ATTGCTGCTC AGAAAGTAGT GGAAAATCTA CTTGCAACTC	900
TTCCAACCTA TCTTCAACAT ATGAAAGAGA ATAATACTTT ATTGGGAGAA GATATTGCAC	960
GTTTGAACAA GACCTATTTA CTTCTGAGA CAGCTGCAAG CCATGTTCGT CGTATTCAGA	1020
CAGAATTAGA GAGTTTGGAG GCAGCTATTG TTGAGGTAAC TTCAAATCAA GAAGAACCAA	1080
CCCAAGCTTA TTCAGTTCTT GAAGAAAATC TTGAGGATTT ACAAACTCAA CTAAAAGATA	1140
TTGAAGATGA GCAAATTTCA GTTAGTGAGC GCCTGACACA AATTGAGAAA GATGATATTA	1200
ATGCACGTCA AAAGGCCAAT GTTTATGTCA ATCGTCTCCA TACTATCAAG CGATACATGG	1260
AAAAACGCAA TCTGCCAGGT ATTCCACAAA CTTTCTTGAA GTTATTCTTT ACGGCAAGCA	1320
ATAATACCGA GGATTTAATG GTTGAGTTAG AACAAAAAAT GATTAACATT GAATCTGTTA	1380
CCCGAGTTCT TGAAATTGCA ACGAATGATA TGGAAGCTTT AGAAACGGAA ACTTATAATA	1440
TTGTACAATA TGCAACTTTG ACAGAGCAAC TCTTGCAATA TTCTAACCGC TATCGCTCAT	1500
TTGATGAACG CATTCAAGAA GCATTTAACG AaGCTTAGA TATTTTGA AAAGAATTTG	1560
ATTATCACGC TTCATTTGAC AAGATTCTC AAGCATTGA AGTGGCAGAG CCTGGTGTA	1620
CCAATCGCTT TGTTACCTCA TATGAGAAAA CACGTGAAAC GATTCGTTTT TAATAAAAGA	1680
AAAAGATTTT ATTGTGTGAG GAGCAGAATC AAATCTTTTT CTATAGTTGT GGGGAGATTT	1740
ACTTCATTTT CTCCTGAGAT TGAGTTTTTG CCCAGCCGAT TTATCCACTA CCTCAAAACA	1800
GTGTTTTATA CTCTCGAAA ATCTTTTCAA ATCACGTCAG CGTCGCCTTA CCGTACTCAA	1860

1324						
GTACAGCCTG	AGGCTAGCTT	CTTAGTTTGC	TTTTTGATTT	TCATTTAGTA	TTAAAGTGAT	1920
TTCGCCAGTC	TTATCTGCAG	CTTCAAATCT	GTACTTTGAG	TAACTTGGA	ACCGTCCAAT	1980
AACGAAGTCT	ATTGAAAAAT	CTCCAGACTA	GAGAACTCAC	GGATAGTTCC	TAATCTGGAG	2040
ATTTCTTATT	TGCACTTTTC	TTGTACAAC	TTAGTCCACG	GTAAATAGAC	CTCTAAAACC	2100
TCTTTGTTTA	CGAGAGTTTC	CTCGTTTGGA	AGACATTCTA	GAAGATAGGA	TAGATATTTT	2160
TCGCTATTTA	TACTAGACTA	AAATCAAAAA	GCATTATATA	ATAGTGATAT	GAAATCAACT	2220
AAAGAAGAAA	TCCAAACCAT	CAAAACACTT	TTAAAAGACT	CTCGTACAGC	TAAATATCAT	2280
AAACGCCTTC	AAATCGTTCT	ATAGTAAAAT	GAAATAAGAA	CAGTACAAAT	CGATCAGGAC	2340
AGTCAAATTG	ATTTCTAACA	ATGTTTTAGA	AGTAGAGGTG	TACTATTCTA	GTTTCAATCT	2400
ATTATATTTT	GTCTGATGGG	CAAATCTTAT	AAAGAGATTA	TAGAACTTTT	ATAGTAGATT	2460
GAAATAAGAT	GTGAACAAC	CTATCAGGAA	AGTCAAATTA	ATTTATAGAA	ATATTTTAGC	2520
AGCCAAGGTG	TACTGTTATA	GATTCAATAC	ACTATAGACT	GTAATCAAAC	AACGATTTGG	2580
CGAAATGTAA	AAAAATATGA	GGAGTTCGGA	CTCGACTCTC	TCCTTCAAGA	AACACGTGGT	2640
GGTCGTAACC	ATGCATATAT	GACAGTTGAG	GAAAAGAAAG	TCTTTCTTGC	CCGCCATTTG	2700
AAGGCTGCAG	AGGCAGGAGA	ATTTGTTACA	ATTGATGCCT	TATTTCAAGC	TTATAAAAAG	2760
GAGTTAGGTC	GTTCTTACAC	ACGTGATGCC	TTCTATCAAC	TGTTGAAGTG	CCATGGTTGG	2820
CGAAATATTA	TGCCACGTCC	AGAACATCCT	AAGAAAGCAG	ACGCTCAAAC	CATTGTGCGG	2880
TCTAAAAATA	AAATCTCAAT	TCAAGAAGAA	AAGAAAGCGC	TTTAAAACCA	GTAGACGTTT	2940
TCGTAAGGTT	CGCTTGATGT	ACCAAGATGA	GGCTGGTTTC	GGTAGAATCA	GTAAACTGGG	3000
ATCTTGTTGG	GCTCCAATAG	GAGTAGGTCC	ACATATCCAT	AGTCACTATA	TACGAGAATT	3060
TCGCTATTGT	TATGGAGCTG	TTGATGCCCA	TACAGGCGAA	TCATTTTCT	TAATAGCTGG	3120
TAGATGTAAT	ACTGAGTGGA	TGAACGCCTT	TTTAGAAGAG	CTTTCACAAG	CTTATCCAGA	3180
TGATTATCTT	TTACTCGTTA	TGGACAATGC	TATATGGCAT	AAATCAAGTA	CCTTAAAGAT	3240
TCCGACTAAT	ATTGGTTTTA	CCTTTATTCC	TCCATACACA	CCAGAGATGA	ACCCCATTTGA	3300
ACAAGTGTGG	AAAGAGATTC	GTAAACGTGG	ATTTAAGAAT	AAAGCCTTTC	AAACTTTGGA	3360
AGATGTCATG	AATCAACTCC	AAGATGTTAT	ACAAGGATTG	GAGAAGGAGG	TGATAAAGTC	3420
CATCGTTAAT	CGGAGATGGA	CTAGAATGCT	TTTTGAAAAC	AGATGAGTAT	AAAAGAAAAG	3480
TCCTCATTTT	AATAGAAATC	ACGACTTTCT	GATGGATTTA	TAGTAAAATG	AAATAAGAAC	3540
AGGACAAATC	GATCAGGACA	GTCAAATCGA	TTTCTAACAA	TGTTTTAGAA	GCAGAGGTGT	3600
ACTATTCTAG	TTTCAATCTA	CTATATTTTT	GGAGTGATAG	AAAAGCCCTT	CATAAGCTAG	3660

1325

TCTACTTGTT	CAGGTGCGAG	AGCTTTGACA	TCTTTTCTG	TACTTAGCCA	AGTCAGTTT	3720
CCGTTCTCAA	AGCGTTTATA	TAGTAGCCAA	AATCCTTGAC	CATCCCAGTA	AAGGGCTTTA	3780
AAGCGGTCTT	TACGTCCACC	ACAAAAGAGA	AAGACTTGAC	CGGAGAAAGA	ATCCAATTCA	3840
AAGTGGGTTT	TAACTACATA	GGCTAATGAG	TCTATTCCCT	GCCTCATATC	TGTCTTGCCA	3900
CAAACAAGGT	GAACCTGACC	TAAATCACTT	AGTTGAATTA	TCATAGTACA	ATACCTTTCC	3960
TCCGATAATT	ATTTTTTATC	TAGTATACTG	GAAGTTGGGG	AATTAGGATA	GATACCTTGT	4020
TATGACGCGC	TTACGTAACT	TGTAAC TAGC	TGCCTAGTTT	GATCTTTGCT	TCTTCATTGA	4080
TTAGCAGTAG	ATTTCAAAAT	GATAAAAACG	CATAGTATCA	GGTATTGAAA	TGTACTGCCC	4140
CAAAAGTTAG	ACAGAAAAAA	TCTAACTTTT	GGGGTGTTTT	TGTTATGAAA	TTAAGTTATG	4200
ATGATAAAGT	TCAGATCTAT	GAACCTAGAA	AACAAGGATA	TAGCTTAGAG	AAGCTTTCAA	4260
ATAAATTG	GATAAATAAT	TCTAATCTTA	GGTATATGAT	TAAATTGATT	GATCGTTACG	4320
GAATAGAGTT	CGTCAAAAAA	GGAAAAAATC	GTTACTATTT	TCCTGATTTA	AAACAAGAAA	4380
TGATTAATAA	AGTCTTAC					4398

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 718 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AGATTTT TAG	ACTTTGTCTT	TAATCGTTTC	TTTTTAGGGA	TGATTGCGAC	ACCTTCTTTT	60
GGCTATTAAC	TTTAGCAGGA	GGGATTATCC	TTGGTCTAGC	GCCGGCTAGT	GCCACCTTGA	120
TGAGCTTATA	TGCAGAACAT	GGTTATAGCT	TTCCGGAATA	CAGTTTGAAG	GAGGCTTGGT	180
CTCTTTACAA	GCAAAATTTT	GTCTCAAGCA	ACCTGATTTT	CTATAGCTTT	TTAGGTGTGG	240
GTCTAGTTTT	GACCTATGGT	TTGTATCTCT	TGGTGCAATT	GCCTCATCAG	ACCATTGTTC	300
ATTTGATTGC	GACCCTTTTG	AATGTCCTAG	TAGTTGCCCT	GATCTTTTGT	GCTTATACAG	360
TATCTTTAAA	ATTACAAGTT	TATTTTGCCT	TGTCCTATCG	AAATAGTCTC	AAATTATCCT	420
TGATTGGCAT	CTTTATGAGT	CTAGCAGCTG	TGGCTAAGGT	TCTCCTTGGG	ACTGTGCTAC	480
TTGTAGCAAT	TGGTTATTAT	ATGCCTGCCC	TGCTATTTTT	TGTAGGAATT	GGGATGTGGC	540
ATTTCTTTAT	CAGTGATATG	TTGGAACCTG	TCTATGAAAT	CATCCATGAA	AAATTGGCGT	600

1326

CAAAATAGAA TGAAGCAGTT TTGGCTACAT ACGCTTCTAA GAACCTATAG TTCAGTGATG	660
ATCATTATCA TTGCGAGTTT TGCAATCTTA CTCTCTTACG CTGTCTGGGA TTCACGTG	718

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 718 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

TCGGTACCAA AATTCTGGAT TTATACTAGC AAAGATCCAA GAGCAAATTA TTAAACAGAT	60
TTAGGTCTAG TTTTCCTGA ATCATTAATA GAATTTGAGA GTGAAGATAG TTTTGCAAAG	120
GAAATTTCTG CAGAAGAAGC AAATAAGATA AATGATGCTG ATGTAATCAT AACTTATGGT	180
GATGATAAAA CTCTTGAAGC TTTACAAAAA GATCCTCTTT TAGGTAAAAA AAATGCAATT	240
AAAAATGGTG CCGTTGCTGT AATTCCAGAT AATACACCGT TAGCAGCCTC ATGCACTCCA	300
ACACCACTTT CAATAAACTA TACTATTGAA GAATACCTAA ATCTTTTAGG AAATGCATGC	360
AAAAATGCGA AATAAAAAAC AAATAAACCT AGGCATAATT TTTATAATCT GCCTAGGTCT	420
TCTTATTACA ATATTTTGT CATTAAAGCT TGGAACAAAA GAAATTAATA TCAGAGATTT	480
TTTAGCAGCT TTTGGAATGG GTAATACAAA TGATGATTTT ATTAATCAAA TTATATATAA	540
rAGAATACCT AGAACTATTT TTGCAATTTT AGCAGGTTCT AGTCTTGCCA TAAGCGGTGT	600
ATTGATGCAA TCAGTTACTA GAAACCAAT AGCTGATCCA GGTATACTCG GTATAAACAC	660
AGGAGCAAGT CTTAGTGTAG TAATTGGTCC TTCTTTTAG GGAATTCATC AAGCATAA	718

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GAACTAATCA TTTTACAGG ATGAGATTTA CAGCAGAGAG TTTGAAGGCT TTATCAAAGG	60
TTTTTCTGG CATAATGACT TTTCTCGTT TCCACTTAAT TTTGTGTCTA CTTTATTATA	120
CCAAGTCCAC sCTTAAGTTA GATAATAAAT CTAACCTAAG GAAGCTAGAA GGATGAGAAT	180
CCAGGTGGTC AAGAGTCCCA AACTTAAGCT GATGGGGACA CCCAGAATAA TTTGCTTTTT	240

1327

GAAGGCAAGG CCACGTTCCCT CTATATTGGG AAGTGAGAGT TGAATGAGAG AACCAGCTGA	300
TGAAAAGGGT GAGATATTAG TAGATAGAGC GCCAATAACG GTGGCTGTTG TGAGTAAGTG	360
AATATCAATC TGAGGATTTT GAGCACTGAT GATAGCAATG ATGGGAAAGA GGGCTGGAGC	420
TACAACGGAT AGGGTGGAAC TAAAGAGTGA CATCACTCCG GCTATCACAC AAAAGAACAG	480
AGGTAACCAG AAATGAGGAA TGGTTGTTGT CATGAGGTGC CCTATCAGTG TGAATAAACC	540
TGACTTGACC GCTAGAGACA TTAGTAAGCT CATGCCGAG AGCATGATAA TTGTAGCCCA	600
GGGAACCTTA GCTAAAATGG CTTCTTGCTT CCCTAATTG AGCCTTAAGG CGAGGCAGAC	660
CATGAGTATT GAGACAAAGC CAATATCAAA TGTTTTTTGA TAAGTAGCTA TCCAGGCGAT	720
GTTTGGGAAA ATGAGATGCA ACAAGGAAA AAGCCAAACC AAAACCATGC TGCTGATCAT	780
GAGCAAGGTG GTTTGTCTTT GAACCTTGCT GAGGAGTGGT GGTGGGTCAA TAGTCAAGGA	840
TGAGTTTGT CTTCCCTTAC TATAGTGACT GTAACAGGAT AATAAAAGCA AGACGATGAG	900
TGGGTAGATA ATGCTGACGA TAAAGATATG ATTGCCAAGT GAAAAAGCTT GCTCTTCCCA	960
TCCCATTGTC TTAAACAGGC CTTGAAAGAC AATGCCTGAG CTAAGGTTA TCAAATTAGC	1020
CCCTCCTGAA GCTCCCAAT TGACGGCTTG AGCTCCAATC AAAGGGTGT TGTCCGCTTT	1080
TTGACAGAGG GTAATCGCTA GAGGACAGCA AACGGCCATA GTAGTGAAAA ATCCAGCACC	1140
TAAAGCAGAC AAAAGGGTTG CCATCAGGTA TAAATCATG TAGAGGGCGT TAGGGTGGGT	1200
GCGTGTGCGG TAGAGAATGT GTTGAAGCAA AACATCAAGA GTACCGTTAG TTGTTGCAAC	1260
GTTATAAAG AGAGAGACGC TAAAAATGGT AAAAAAGAGT GAGGTTGGCC AAAAATGAAG	1320
AAGTTCTTTG GGGCTTAATC CCATGAGAGT GGTGCGATG AGGTAAGAAA AAGCAATAGC	1380
CAGCAGGCCA ATATTGATTT TGGTGCGGTA ACCAATTCCA ATGGCTAGAG CAATGG	1436

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1696 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

CCATTTGGGA AAGAACGTAA GAGTTTGCAG GGTGAGATTC CAGAAGAATT TTCAATGTCA	60
GCCGTTGACA TGTCTATGAT TGACCACATT CCAGATATGA TTGAAAATGG TGTGGACAGT	120
CTAAAAATCG AAGGACGTAT GAAGTCTATT CACTACGTAT CAACAGTAAC CAACTGCTAC	180

1328

AAGGCGGCTG TGGATGCCTA TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC	240
TTGGTGGACG AGATGTGGAA GGTGCCCCAA CGTGAAGTGG CTACAGGATT TTACTATGGT	300
ACACCATCTG AAAATGAGCA GTTGTTTGGT GCTCGCCGTA AAATTCCTGA GTACAAGTTT	360
GTCGCTGAAG TGGTTTCTTA TGATGATGCG GCACAAACAG CAACAATTCG TCAACGAAAT	420
GTCATTAACG AAGGGGACCA AGTTGAGTTT TATGGTCCAG GTTTCCTGCA TTTTGAAACC	480
TATATTGAAG ATTTGCATGA TGCCAAAGGC AATAAAATCG ACCGCGCTCC AAATCCAATG	540
GAACATATGA CTATTAAGGT GCCTCAACCC GTTCAATCAG GAGATATGGT TCGTGCATTA	600
AAAGAAGGAC TCATCAATCT TTATAAGGAA GATGGAACCA GCGTCACAGT TCGAGCTTAA	660
GAAAGGAAAA GGAAATGATA GAGGCACAGG GTTCTTAGT GGATAAGCAA ACAAGATGCA	720
TTCATTACCA TAGCAAGCTG GATATTATTG CTTTACAATG CTATGATTGT AAAAAGTATT	780
ATGCTTGTTA TCGGTGTCAT GATTCATTAG AACATCACCC TTTTGAGCCG TATCCCTTAT	840
CTTTGATACA GGATAAGCCT ATTTTATGTG GTGTTTGTCT AAAACTACTA ACATATAAGC	900
AATATAAAGA AAGCTTAAGT TGCCCCTTTT GTTTTCTCG CTTTAATCCA GGTGCCCCAA	960
ATCATAAGGA ACGCTATTTT AAATAGCAA TCATCTAGTT TTGAAGTAGG AGAAAACCTCA	1020
ATTTCAAGAG AAAATGAAGT AAATCTTCCC ACAATAAAC GCATAATATC AAGATTGTTC	1080
AATACCTGAT ACTATGCGTT TTTAAGATTT TAAAGACTTT TTTCCTTTAT CTGGTATTTT	1140
GACTACTTGT TAAACTGGG TTAATTTTCG ACTGTTAAT AGTTATTATG CAAAGCTAA	1200
AAGGTTAGAA TTGTCAAAAC AATCCGTCTA GAGTATGCGT GATGCCAACC GTGGTGGATG	1260
TTCTCAGTCA TGCCGTTGGA AGTACGACCT TTACGATATG CCATTGCGGA AAGAACGTAA	1320
GAGTTTGCAG GGTGAGATTC CAGAAGAATT TTCAATGTCA GCCGTTGATA TGTCTATGAT	1380
TGACCATATC TCAGATATGA TTGAAAATGG TGTGGACAGT CTAAAAATCG AAGGACGTAT	1440
GGAGTCTATT CACTATGTAT CAACAGTAAC CAACTGCTAC AAGGCGGCTG TGGATGCCTA	1500
TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC TTGGTGGACG AGATGTGGAA	1560
GGTTGCCCAA CGTGAAGTGG CTACAGGATT TTACTATGGT ACACCATCTG AAAATGAGCA	1620
GTTGTTTGGT GCTCGTCGTA AAATCCCTGA GTACAAGTTT GTCGCTGAAG TGGTTTCTTA	1680
TGATGATGCG GCGGTA	1696

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1022 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

CCGAGTTTAT TATGGTTTCT TCGGAATTTA TCTCAAAGAT TGAATTTGCT TGCAATAAGA	60
AAGAAAGTCT TTATAGTCAA AGCAAATTTA AGTATGCGAT TCGTTTCGATG TTCGCAGGTG	120
CATTTTTAAC CTTCAGTACT GCTGCAGGTG CAGTTGGGGC TGACTTGATT AATAAAATTG	180
CACCAGGTAG TGGACGCTTC CTCTTTCCAT TCGTTTTTGC TTGGGGCTTG GCCTACATTG	240
TTTTTTTGAA TGCCGAGTTG GTCACTTCAA ACATGATGTT CTTGACTGCT GGTAGTTTCT	300
TAAAAAAAT CTCTTGGAGA AAAACAGCTG AGATTTTACT ATACTGTACC TTGTTCAACC	360
TTATCGGAGC CTTGATAGCA GGGTGGGGCT TTGCTCATTC GGCAGCCTAT GCGAATCTGA	420
CACACGATAG TTTCATCTCA GGTGTTGTTG AGATGAAGTT AGGCCGCTCA AATGAATTGG	480
TCTTGCTTGA GCGGATTTG GCAAATATTT TTGTAAATAT TCGGATTC TGTCATTTATTT	540
TGGTCAAAGA TGGTGGTGCC AAACCTTGGC TTGTGTTGTC AGCTATTTAC ATGTTTGTAT	600
TCTTAACAAA CGAGCACATT GCGGCGAACT TTGCTTCTTT CCGGATTGTG AAATTCAGTG	660
TTGCTGCGGA TTCAATTGCC AACTTCGGTG TTGAAATAT GCTTCGCCAC TGGGGTGTGA	720
CTTTCATCGG AAACCTTTATC GGAGGAGGCC TCTTGATGGG TCTTCCATAT GCCTTCCTCA	780
ATAAAAACGA AGATACTTAT GTAGATTAAG AAAATGAGCA CGATTGAGTC GTGCTTTTTT	840
CATTTTCAAA ATAAGGTAAT AGCTATTTCT TATATCAAAA TATAGAAAAC TGATATTTGT	900
AaACTATAAC TCAAGGTGCT ACAATATCCT TAATAAAATA ATATGGAGGT CACCTTATGA	960
CTGTGATTT TAAATnTGAA ACTCTACAAC TACATGCTGG TCAAGTTGTG GCTCCAGCTA	1020
CT	1022

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 663 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

CCTTAAGTAA TCTCTGATAA TATTTTCTTT ATTAGCATAG GGGAATATCG ATATAATGGC	60
TCATTATGA GTGGCAGGAA TATCCAATAT GGCAACTTTT CCAATAGATA ATTTAAACT	120
CATTAATAAA GTTCCTTTAG GTGAAATGTC TATTTTCTTT GATTTTAATG CTAATTTAGA	180

1330

AATAGATTCT CTCGCATTAG TTACATAACC AGATATAGGC ATATCTGATA TAGATACCCA	240
AGGTATTTCA GTTCCCCAAA AAGTAGCTTC ACTGCGTGGA GGAGTTTTC CTATTCTGAA	300
GTTAACTAGG CTAGCAAATT TAATATATCT CCATGCTTCT GGGATTTCAT ATATAGGATA	360
AGAGGTGTGT TCGTCTTTGT TCCCATAATA AGAGTTATCA TCTCCTTGGG AAACAATAGA	420
AATGTCCAAA TCTTCTTTT TAATCTTGCC TTCTTCAAAG AGTTTTTGTT TTTCTGCTCG	480
TATTTTTCCTA AGTAAACTT CGACTGATTC ATCATTTGGG TCTTGTTCAA CTAATTTTCC	540
TTGCATAGCA TATTGAAGAA TAGATTTTTT TAGTTTATCT GGAAATTCCT TATCTAGCTG	600
TTCTAGTCTA TTATAACTTT CAGCATATTC ATCTACTTTT TCTAAAGCTG ATTCGATTGC	660
TTC	663

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 881 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

CGTCGCTGAA CATGTCAACA GCAAATTAAA CTAAACAAAC TAAAATTATG TGATACTTCA	60
CATAATTTTC TTTAGAAAAT ATTATCAGAA GAAAGTTGAG AAAAATGGCA GAAAAACAT	120
ATCCTATGAC CCTTGAGGAA AAGGAAAAAC TTGAAAAAGA ATTAGAAGAA TTGAAATTGG	180
TTCGTCGACC AGAAGTGGTA GAACGCATTA AGATTGCCCG TTCATACGGT GACCTTTCAG	240
AAAACAGTGA GTACGAAGCA GCTAAGGATG AACAAGCCTT TGTCGAAGGA CAAATCTCTA	300
GCTTAGAAAC AAAAATCCGC TATGCTGAAA TCGTCAATAG CGACGCAGTT GCCCAGGACG	360
AAGTAGCGAT TGGTAAAACA GTCACCATCC AAGAAATTGG TGAGGACGAA GAAGAAGTTT	420
ATATTATCGT AGGTTAGCT GGTGCAGATG CCTTTGTAGG TAAGGTTTCA AATGAAAGCC	480
CAATTGGGCA GGCCTTGATT GGCAAGAAAA CAGGTGATAC AGCAACCATT GAAACGCCTG	540
TTGGTAGCTA TGATGTAAAA ATCTTGAAGG TTGAAAAAAC AGCCTAAAAA CAGAAAAAGG	600
AGTGGGGAGG CGATGTGCTT CACTCACTCC TTTTCCATT TTGCTACTCT TCGAAAATCT	660
CTTCAAACCA CGTCAGCGTC GCCTTGCCGT ATGTATGGTT ACTGACTTTG TCAGTTTCAT	720
CTACAACCTC AAAACAGTGT TTTGAGCTAA CTTTCGTCAGT TTCATCTACA ACCTCAAAAC	780
TATGTTTGA GCTGACTTCG TCAGTTTCAT CTACAACCTC AAAACCATGT TTTGAGCCGA	840
CTTCGTCAGT TTCATCTACA ACCTCAAAAC TATGTTTGA G	881

1331

(2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 949 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

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CCTTTTTTAA TACAAGTTAT TTTGATTTAA CCGGCTTGTC TTGAGCTGTC TGCAAAGCTG      60
TGGCAATCGT ATCTGCATAC AATTTTGCTC CTGCTTCGAT AGTGCTACTC TCACTCCCGA      120
AATGAACCTG GTCTGTTCCA GCCCAAATTT CTGGATGCTC TTTCGCAACT TGATTCCAAT      180
CTGTATCGT AATGTAAGGT GTCTTCTCTG CCAATTCTCT CATATAGGCA GCAGCCTTCT      240
CAACGATGGC ATAGGTCTCT TTTGTCTTAT CTCCCTCATA AGGAGTCACC AAAATCATAT      300
GGTGTCCTT AGGAAGATTT TTCACGATAC TGTCCAGTC ATCCTTGTA TTCTCAGGAT      360
TATTTACCCC AGTCGCAATG ACCACCGTCT TAGGTAAAAA TTTATTCTGG CTATTATTTA      420
GCATGATTTC ATTTGCGGTC TTGGTTGTTA CGCTGACCTG CGCGTTAATC TGTGCTCCAG      480
GAAGAGCTGT CTGTAGTGCT GTATTTGCCC TTAAAGCCAC TGAGTCACCA ATTAACATAG      540
TGCCATCAGC AATTCCCAAA CTGTTTGCACT CTGCCCCTTC TGCCATCACC TTGGTCTGGC      600
CAATATTTGT TGCAGCTTGC TTCAAGCCAT TGACAGTCAA GTCTGTCTCA AACGCTCCCA      660
CTTGTGGTGC CAACAAGGTC ACCGTGCAGA CAATGATGGT CAAGATTCCT GTACCTGCTG      720
CAAGAATTGC GTGAATATAA GGCAGGGGAC GAAsGGTTT GACAATAGGT GTGTTCTTGC      780
CTGCAATCCA AGGTTCCAAT ACATAAAATG ACAGACTGGC AAAGCCATAA GAACAAATCA      840
GAGTCAGTAA TACAGCAAGA AGATTTGATG TCAACTGTGA GAAAATGATA TAGAAAGGCC      900
AATGGAAGAA ATAAACCGCA TAGCTAGTAT CCGCTAAAAA GCTGATAAT      949
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(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 622 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

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AAGATATATT TTTTACACAG AAGTATGCAA AAGTAAAGAG TGCAAAAAAT GGAATTAAAG      60
```

1332

CGAAAATAAA AGCCGTGTAC AGGCGACCAA ACCAACGTAC ACGGCTAAGG AAAAATAACA	120
AAACTCAAGC AAAGGCAAGG CGCGTGGTTT TGTTAGGTAT TTAGCAAGGG GACAAACCCC	180
TTTGTAATA ATCTCCTCTT ATTTTATCAA AATTAGAGGA AAATGACAAC TTAATTTATA	240
AAAAGGAAAA ATGGAGGATA TAAATGAAA TTCTGTCTAA AGAAATACAG TTACAGGGCT	300
TACAACCTTCT TAAACAGACT CTTGAACTT TAGTTGAGCT AGAAAAACAA CGATCTAGTA	360
AGTTAGATTT AATTCTCTCGT AAAGAATTAA TGGATCTGCT AGGTATAAGT GCTACAACCC	420
TTGATACTG GGAGGATCTT GGTCTTAAAC GATATCAGAC TCCGATGGAT GGAGCTAAGA	480
AAGTATTCTA TCGTCCGTCA GATGTGTATT TATTTTATAG AATAAAATAG GAGTTATGAA	540
ATGAAAATG TTAACCTTCAA ACCAACTAAA CAAATAGACG ATGGGTTTTA ACTGCCAGGT	600
ATTGACATTC TATTTGTCTC AG	622

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1929 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

CGCTAAGTTG CAAACAAAAG AAGAACGCAA ACTCCACAAA TCCTTTACGC AGAAACTCAA	60
TTCTCATCTAC TTACCTTGCT GACTTGGTAG AGTATGTTGC AGACAAAGAC TTCTCAGTAA	120
ACGTAATTTC TAAATCAGGT ACAACAACCTG AACCAGCGAT TGCTTTCCGT GTCTTTAAAG	180
AACTCTTGGT TAAGAAATAC GGTCAGAAG AAGCTAACAA ACGTATCTAT GCAACAACCTG	240
ACCGCCAAAA GGGTGCTGTT AAGGTTGAAG CAGACGCTAA CGGTTGGGGA ACATTTGTTG	300
TTCCAGATGA TATCGGTGGA CGTTCTCAG TATTGACAGC CGTTGGTTTG CTTTCAATCG	360
CAGCATCAGG AGCTGACATA AAAGCTCTTA TGGAAAGTGC GAATGCAGCT CGCAAAGACT	420
ACACTTCAGA CAAAATCTCT GAAAACGAAG CTTACCAATA CGCAGCTGTT CGTAACATCC	480
TTTATCGTAA AGGCTATGCA ACTGAGATCT TGGTAAACTA TGAGCCATCA CTTCAATACT	540
TCTCAGAATG GTGGAAACAA TTGGCTGGTG AATCAGAAGG AAAAGACCAA AAAGGTATCT	600
ACCCAAGTTC AGCCAAGTTC TCAACTGACT TGCACTCACT TGGTCAATTT ATCCAAGAAG	660
GAAGTCGTAT CATGTTTGAA ACAGTTGTCC GTGTTGACAA ACCTCGTAAA AACGTGCTTA	720
TTCTACTTTT GGAAGAAGAC CTGACGGAC TTGGTTACCT TCAAGGAAAA GACGTTGACT	780
TTGTAAACAA AAAAGCAACT GACGGTGTTT TTCTTGCCCA CACAGATGGT GATGTACCAA	840

1333

ACATGTATGT GACTCTTCCA GAGCAAGACG CTTTCACTCT TGGTTACACT ATCTACTTCT	900
TCGAATTGGC AATTGCCCTT TCAGGTTACT TGAATGCTAT CAACCCATTT GACCAACCAG	960
GTGTTGAAGC TTATAAACGT AACATGTTTG CCCTTCTTGG AAAACCAGGA TTTGAAGAAT	1020
TGAGCAAAGA ACTTAACGCA CGTCTATAAT AGAAGAAAAG AGTGGTTTGC CCACTCTTTT	1080
TACTCTCTTT ATCCATAGAA ATTGGACTCA GCCAAGACTT GTGATATAAT ATAGAAAGCA	1140
AAAAGGCAGA CGCCTAGATA ATAGGAGAAA CTATGTCAA AGATATCCGC GTACGTTACG	1200
CACCAAGTCC AACAGGACTA CTACACATCG GAAATGCTCG TACAGCATTG TTTAATTACT	1260
TGTATGCGCG CCATCATGGT GGAACATTTC TCATCCGTAT CGAAGATACT GACCGTAAAC	1320
GCCATGTCGA GGATGGTGAA CGTTCACAAC TTGAAAACCT TCGCTGGTTA GGCATGGATT	1380
GGGATGAAAG TCCAGAATCA CATGAGAATT ATCGCCAGTC TGAGCGTTTG GACTTGTATC	1440
AAAAATATAT TGACCAACTA TTAGCTGAAG GAAAAGCCTA TAAATCTTAC GTTACAGAAG	1500
AAGAGTTGGC AGCTGAACGC GAACGCCAAG AAGTAGCTGG CGAAACACCA CGCTACATCA	1560
ATGAATACCT TGGTATGAGT GAAGAAGAAA AAGCAGCTTA CATCGCAGAA CGTGAAGCAG	1620
CAGGGATCAT CCCAACTGTT CGTTTGGCTG TCAATGAGTC AGGTATCTAC AAGTGGCATG	1680
ATATGGTCAA AGGCGATATC GAATTTGAAG GTGGCAATAT CGGTGGTGAC TGGGTTATCC	1740
AAAAGAAAGA CGGTTACCCA ACTTACAACT TTGCCGTGT TATCGATGAC CACGATATGC	1800
AAATCTCTCA TGTTATCCGT GGAGATGACC ATATTGCTAA TACACCAAAA CAGCTTATGG	1860
TCTATGAAGC TCTTGGTTGG GAAGCTCCAG AGTTCGGTCA CATGACCTTG ATTATCCACT	1920
CTGAAACTG	1929

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AAATTTAAGA AAAAGGAGAC ACATCATGTC TAAAAAGTA TTATTTATCG TCGGATCACT	60
ACGTCAAGGT TCTTTCAACC ACCAAATGGC GCTCGAAGCT GAGAAAGCAC TTGCTGGTAA	120
AGCGGAAGTT AGCTACCTTG ATTATCAGC CTTTCTCTC TTCAGCCAAG ATTTGGAAGT	180
TCCAACACAT CCAGCTGTAG CTGCTGCTCG TGAAGCAGTT CTCGTTGCGG ATGCTATCTG	240

1334

GATTTTCTCT	CCAGTCTACA	ACTTCTCTAT	CCCTGGTACA	GTGAAAAACT	TGCTTGACTG	300
GCTATCTCGT	GCCCTTGACT	TGTCTGATAC	ACGTGGCGTT	TCTGCCCTTC	AAGACAAGTT	360
TGTCACAGTA	TCATCTGTAG	CCAATGCAGG	GCACGATCAA	CTTTTCGCTA	TCTACAAAGA	420
CCTCTTGCCA	TTTATCCGTA	CACAAGGCGT	TGGTGATTTC	ACTGCTGCAC	GTGTTAATGA	480
CTCTGCCTGG	GCAsACGGAA	AATTGGTTCT	TGAAGAAACA	GTCTTAAACT	CACTTGAAAA	540
ACAAGCTCAA	GACTTGGTCTG	AAGCTATCAA	GTAACATAACA	CTCAATAAAA	ATCAAAAAGC	600
AAACTAkGAA	GCTArCCGCA	AGCTACTCaA	gCACTGCTTT	GAGGTTGTAG	ATAGAAGTGA	660
CGAGTGThnA	ACATATATAC	GGTAAGGCGA	CACTGACGTG	GCTTGAAn		708

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 781 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

CTCTTTTCT	TGGAAATAGG	TGTATAATAC	GTTTATTAAA	TTTTTGAGGA	GTTGTCTATG	60
AAGAAAAGTT	TTATCCATCA	ACAAGAAGAA	ATTTCCTTTG	TCAAAAACAC	TTTTACCCAG	120
TATTTGAAAG	ATAAGCTAGA	AGTTGTCGAA	GTTCAAGGTC	CTATCTTGAG	TAAGGTCGGT	180
GACGGAATGC	AGGACAACCT	GTCTGGTGTG	GAAAATCCAG	TATCGGTCAA	GGTTCTCCAA	240
ATCCCTGATG	CTACTTATGA	AGTGGTGCAC	TCACTTGCTA	AATGGAAACG	CCACACCTTG	300
GCTCGTTTTG	GCTTTGGTGA	AGGAGAGGGT	CTCTTTGTCC	ACATGAAAGC	CCTTCGTCCA	360
GATGAGGATT	CCTTGGATGC	AACCCACTCT	GTTTATGTTG	ACCAGTGGGA	CTGGGAGAAG	420
GTTATCCCAA	ATGGTAAGCG	TAACATCGTT	TATCTAAAAG	AAACAGTTGA	GAAGATTTAT	480
AAGGCTATTC	GCCTGACTGA	GCTAGCTGTT	GAAGCCCCT	ATGACATCGA	GTCTATCTTG	540
CCAAAACAAA	TTACCTTTAT	CCATACAGAA	GAATTGGTAG	AACGCTACCC	AGACTTGACA	600
CCGAAAGAAC	GTGAAAATGC	GATTTGTAAA	GAATTGGAG	CCGTCTTTTT	GATTGGTATC	660
GGTGGCGAGT	TGCCAGATGG	TAAACCGCAC	GATGGACGTG	CACCAGACTA	TGATGACTGG	720
ACAAGCGAGT	CTGAGAATGG	CTACAAGGGT	CTAAATGGTG	ATATTCTTGT	CTGGAATGAG	780
T						781

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:

1335

(A) LENGTH: 846 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

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CCCGCATCTT GTAGGGTTTT AACGGGCACG ATTTTCATAT CCGTCTTGAT TGTTTTAGCC      60
GCTTCTAGGG CTGTTTGGTA GTTGTTTTTC GCGTCCGAT GCGCCTTTTG TTCTTCTTCG      120
CTAACAGGGT TATCAGGAGC AAAGAAAATA GCAGCACCTG CCCTAGCCGA AGCTACAACC      180
TTCTTATCAA TACCTCCAAT GTCTCCACA TTACCATCGC GGTCATGGT ACCTGTACCG      240
GCAACAATAC GACCATTACG AAGATCTGGG TGAGCTATTT GAGTATAGAT AGCTAGACTA      300
AACATGAGAC CAGCACTTGG ACCGCCAATA CCAGCTGTTG AAAAGCTAAT TGGGACATTG      360
CTGATTACCT CTGTACGGTC AATCAAGCCG ATTCCAATTC CATTTTGGCC ATTTTCCAAG      420
GTGATGATTT TTCCTTCTGC AGACTTGGTT TGCCCATCCT CTCATAGGT GACCTTGACG      480
GAATCCCCTA ATTTTGTGAGA ACTGACGTAA TCAATCAAGT CTTTGGAAT ATCAAAGGTC      540
TGATCATTGA CTGCTGTGAC TGTATCAGAG ATATTGAGAA TCCCTTTAAA GGTGAATTA      600
TCCGTCACAT TCAAAACATA AACTCCAAAG TACTTGAGTT CGATATCCTT ACCAGCTGTT      660
TTTAGTCCTT GATACTTGGC CATATTTTGC GATGTTTGCA TGAGAATTG ATTGATTGCG      720
ATAAATTCAT CATCGGAAGA ACCACCTGTA GTCTCCTGAG CACTACGAAT ATCTGTAAAA      780
GGTGTCAACC AAGCATAAAT CATATGAGCT AAAGTGGCAT GTTGAACACC AACCGTAACG      840
AATTGT                                           846

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(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

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GCGATCTGCT TGGGCTTTTC CTATTACCTT ATCTAATAAA TAGGTACGCA GACTCATAAC      60
CATATAAAGT CCACCCCCCA TGGCACCGAC AAGAGCTACA TAAAAGAAGC TCCACAAACG      120
TCCACTTGGT TGGAAGAAAA ATCCTAACAG CCACTGGATG GTTCCTATTA ACAGAAACAT      180
GACTAGGGTC AGCAAACTGA TTAAATGGT TCGCTTCAAA ATCACCTTGC GCTTGACACC      240

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1336

AGTTACTTTA CAAATATCCC GATACATCAA GACGTTAGGA ATGATGAGAG CAATGGTTGT	300
TGAAATCAAA GGACCATAAC TGTGGAAGAG GGCGATGGTA GGTAGTTGCA AGACTAGCTT	360
GGCAATAGAA CCATAGATAA AATAGAGAAC GGCCTTGCGG TTGCGGAACA TGGCCTGAAG	420
CATTGGAGAC AAGACCATGT ACAAGCCTAA AATAATAGAC TGCAAACTG CAAAGACAAA	480
TAAGCCCAGA GCCAACTAT CTGGCTTACC ATAGAAGACC GTATAAAGAG GTTCTCCTAC	540
CATAACCACT CCAACCGTTG CTGGTAGCAA GAACATAAAG AGTAGGGTGA GACTGTCCTG	600
AACGAGACGA GAAGCTGCTT TCAAGTCCCC CTTGACATAG TTTTCCGTCA AAAGTGGCAA	660
ACCAACACTC CCAATCGAAA CCCCTACAGA AATCAAAATC ATCGTGATTT TATTAGGATT	720
GGCTGAGAAA TAAGAAAACA TGACAACCAA GTCCTCATTG CTGTAGTTGG TAAACCAGCT	780
CATACTATTG ATAAAGGTCA GCTGAGTCCA AATCTGGAAG AGCTGGATG	829

(2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CGAACATCTT GCTGGCTGAT TCGTCTGCCG CCATCGCAGC CCCGAACACA TTGCGACCCA	60
TGGCAAGCGG GCTCAATCCG CACATGGGAT CCGTGCCAAA GCCCCGCGTG TGCATCATTT	120
GCTCATCTAG TAACGTATGA GGTTCGCCTT CGCTGTCGAT AAACCGATAT TCAATCGCAC	180
CACTGCTCGT TCTCCGCGGA GGGGAAACCG ACTGCGGTAG GATGAACTCC AGAGAAGAGA	240
GATCACGACC TACCAGGTGC GGCTCGTTGA AGCTGTTGCC GCTTAGCAGC AGGCTCGCCA	300
CCACGCATTC CCAGAACTCA ACGGGGGTTT GATCGGCGTT CGGTTGCTGA CTAATAACTC	360
GGTGACAGGG ATGCGAAGTG GCCACTTCTG GCACACCGTT CTTGTCTTCG TAGAGAGCAA	420
TTGGGAGGGT GGCCAGCGTT TCGGCGATGA GCGCACGCA GGCC	464

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 982 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

1337

CCGTCTATAA TGGTAATAGA TTTTATTTGG AGGTTTTTAT GTCATTTCTA TCAAAAAATG	60
GAGCAGGTAT CTTGGCCTGC CTTCTCATTT CCATCCTATC TTGGTACTTA GGAGATTCT	120
TCCCTGTGGT TGGCGCGCCC GTTTTGGCCA TTTTCATAGG CATGCTCCTA CATCCCTTTC	180
TCTCGTCTTA TAAACAACCTG GATGCTGGTT TGACCTTTAG TTCCAAGAAG TTGCTCCAAT	240
ATGCCGTTGT CTTGCTTGGT TTTGGTCTCA ATATCTCGCA GGTCTTCGCA GTTGGCCAAT	300
CTTCACTCCC TGTTCATCTG TCCACTATCT CAATAGCTCT GATTATTGCC TACCTCTTCC	360
AGCGTTTCTT TGCCCTGGAT ACAAACCTGG CTACCTTGGT TGGAGTAGGT TCTTCTATCT	420
GTGGGGGTTC TGCCATTGCA GCGACAGGCC CGTTATTGAT GCTAAGGAAA AGGAAGTAGC	480
CCAAGCCATT TCCGTTATCT TTTTCTTCAA TGTCTTGGCT GCGCTCATCT TTCCAACCT	540
CGGCACCTGG CTTTCATCTAT CCAATGAAGG CTTGCGCCCTC TTGCAGGGA CTGCGGTCAA	600
CGACACTTCC TCTGTAACGG CTGCCGCCAG CGTTGGGAC AGTCTTTACC AAAGCAATAC	660
CCTCGAGTCT GCAACCATTG TTAACTCAC ACGTACTTTG GCCATTATCC CTATCACGCT	720
CTTTCTATCC TACTGGCAAA GTCGCCAACA AGAAAACAAG CAAAGCCTGC AACTGAAAAA	780
AGTCTTCCCA CTTTTTATCC TTTACTTTAT CCTTGCCTCT CTCCTACTA CACTACTCAC	840
CTCTCTAGGT GTGTCCAGTA GTTCTTTTAC TCCTCTCAA GAACTCTCTA AATTCCTTAT	900
TGTCATGGAC ATGAGTGCTA TCGGTCTCAA AACCAATCTG GTCGCTATGG TCAAATCCAG	960
TGGAAAATCC ATTCATCATG GA	982

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CTAGCTGCCA ATATGATTGG GGTGCAGAAG CGCGTGATTA TCTTTAATCT TGGCTTGGTT	60
CCTGTGGTCA TGTTTAACCC AGTGCTTCTG TCCTTTGAAG GATCCTATGA GGCAGAAGAA	120
GGCTGTTTGT CCTTGGTAGG TGTGAGATCA ACTAAGCGTT ATGAAACCAT AAGGCTTGCC	180
TATCGTGACA GCAAGTGGCA GGAACAGACC ATTACCTTGA CAGGCTTCCC AGCTCAGATT	240
TGCCAGCATG AGCTGGATCA CTTGGAAGGA CGAATCATTT AGGAGGAAAG CAAATGAAAC	300
GAATAGTCTT TGAACCTATT TTTATCGCAA CGACCTGGTA TATCTTTTTC CCGCCCCCTTA	360

1338

ACCTGACCAG CTGGGAATTT CTCTTCTTCC TCTGTGGGCA TTTGTTAGTT GTGGCAATAT	420
TATTTGGCTT TGGCAAGGGG ATAAACCTTG TCAAAACGGT TCATGTGCGC CACGGTAAGG	480
CGGAAGCTGC CTAAATCTT GAGGGTTTCA AAATCAATCG GTTAGGGAAA ATTCTGTTAG	540
CTTCGATTGG AGGAATCTT CTCTTGGCAG CTTTGGTTTc CTTGGTAACT TCCAGCATGT	600
TCAGGCTAA AAATTATGCC AATGTAGTCA CGGTTACGGA AAAAGACTTT ACTGAATTTC	660
CTAAGAGTGA CACCAGTAAG GTTCCTATCC TAGATAGAAG TACTGCTGAA AAAATTGGAG	720
ACCGCTACTT GGGTTCCTTA ACCGATAAGG TGTCGCAATA CGTAGCGGCA GATACCTATA	780
CCCAATTGAC AATTGATGGG AAACCTTATC GGGTCACACC ACTAGAATAT GCAGACCCTA	840
TCAAATGGTT TAACAATCAA GCCAAGGAA TCGGTGAGTA TATTAAGGTG GACATGGTAA	900
CTGGAATGCG GGATTTGGTG GACTTGAAGA CACCAATCAA GTATTGAGAC TCGGAGTATT	960
TTAACCGTGA TGTCAAACGT CACCTGCGCT TGAAGTACCC GACCAAAATC TTTAAAACTC	1020
CATCTTTTGA GGTGGACGAT GAGGGCAATC CTTTCTATGT AGCAACGGTT TACCAAAAGC	1080
AATTTGGACT TGCTGTTCTT CGTCCTGCTT CAGTCATTAT CTTGGATGCT ACAAATGGAG	1140
AAACCAAGGA ATACAGCTTA TCAGATGTTT CAGAATGGGT GGACAGGATC TATCCAGCAG	1200
AGGAAACCAT TGAGCAAAATC AACTACAACG GCAAGTACAA GGACGGTTTC TTGAATGCCA	1260
TGATTTCCTA GAAAAACGTG ACCCAGACTA CCAATGGCTA TAATTACTTG TCTATCGGTA	1320
ATGACATCTA TCTCTACACA GGTGTGACGT CGGCTAATGC GGATGAGAGT AATCTTGGTT	1380
TCATCTTGA AAATATGCGA ACAGGAGAAA TCACTAAGTA TAGCTTGGCT TCTGCGACAG	1440
AAGAATCAGC CCGTGAATCA GCAGAAGGTG CTGTTGAGGA GAAATCCTAC AAAGCAACCT	1500
TCCCAATCCT CATCAACCTC AATGACAAGC CTCTCTACAT CATGGGCTTG AAGGACAATG	1560
CTGGCTTGGT CAAAGAGTAC GCCCTGGTAG ACGCAGTCGA GTACCAAAAT GTTATCGTTG	1620
CTACTACAGT GGAAGAGATG CTCAGCAAGT ATGCCAATAA AAACGACCTT GAAATTGACA	1680
ATGCAACGAC AGAAAGCATC AATGGAGTAG TAGCAGACCT CAAATCAGCT GTTATCAAGG	1740
GAGACACTGT CTACTTCTTT AAAGTTGATG GCAACATCTA CAAGGTCAAG GCTTCAGTAT	1800
CCGATGACCT TCCTTACCTT GAAAATGGTA AAACCTTCGA AGGTCAAGTA GGAAAAGACA	1860
ATTATCTCAA GACCTTTAAG CTACGGTAAA AATAGGTTTT TTTCAGAAAG TATATGTTAT	1920
AATAAGGTAA ATTAAGCCG	1939

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 907 base pairs
 - (B) TYPE: nucleic acid

1339

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

CCTGCTAATA GAGAGAAAGA CTAGGAGTAG AAGTAAGCCA ATTAAATAAT GAGAAAGTTT	60
CATACCCCGT CCTTTCATGT AGATTTGGTA TCGAAAGATA TCTGCGGATA TAAATGTAAC	120
ATTATTTTTC TAATCTGTCA ATAAAATTTC TGACAATTTA ATAAATACAA CAAGGAGAGA	180
GCAACAAGAC TTTCTCCTTT GTTATCCTAT TCTAAAATGT TTTTACCTTA ATCTGATAAA	240
ATAATATCTT CGAGGGAGTA GCTAGCCGTC CAATCAAGAT ATTGTTTAGC TTTTGAAGCA	300
TCTGCTAGGA CACTGGCTGG GTCACTAGCA CGTCGAGCAA CAATCTCGTG TGGGATTTTT	360
TAATTTAGTA ATTCTTCAGC AGTTTTAAAG ATTTCTTTGA TAGTATAGCC TTTTTTAGTT	420
CCTAAGTTAA AGATTTGAGA AGAACTGTCT TCTTGAAATA GGTAGTTCAI TCCTTTAACA	480
TGAGCCTATG CAAGGTCCAA GACATAAATG TAATCTCGAA TACATGAACC GTCACGTGTA	540
TCGTAGTCAT CTCCAAATAT TTTTAAGCTA TCATTTTGTC CCAATGCGGT CTGTGTGATA	600
TTTGGAATGA TGTGAGTTGG ATTTTTCACA CGCAGACCGT TTGAAGCATC CATTTCAGCC	660
CCAGCAACAT TAAAGTAACG GAAAATAACA TATTTCCAGT CGTAGCGATT GGCCATCCAG	720
TAAATCATTC GTTCGCCCAT CAGTTTTGTC TCTGCATAAG GGTTGACAGG GTCGAGCAGG	780
GTATCTTCAG TCACCGGCTT GTCAATACAG TTATTTCCAT AGAGAGAAGC AGTCGAAGAG	840
AACATGATTT TTTGAATGCC AACTTCAGAT AAGACTTTGA GAACTTGGTT CATACCAGCA	900
ACGTTGG	907

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CCACATAAAG GTAAATATCT TTTGTACTAT CTTGGGCATC CAAGAAAAGC AATTGGGCAA	60
TAACAGAGTT AGCCATATTG TCTTCAACCG GACCTGTCAG CATAATGATG CGGTCTTTGA	120
GAAGACGTGA GTAAATATCG TAAGAACGTT CTCCACGGCT TGTTTGTTCA ATAACTACAG	180
GAATCATTC A TTTCTCCTTT TGAGTTTFAA TTTTGTGGT CAAATGACTG AAGATAAGAC	240

1340

TATTATAATA	TCTTGGTCAA	AAAAGGTCAA	ATTTTGGCTC	TGCTTTCATT	AGACAGAAAC	300
AAAAACCCAA	CCTCCTTTCG	TGACTGGAAA	TACTTTTCCA	AGTCATTCTT	CTTTTCGATC	360
TTATTTTGTA	CCGAACAAGC	GGTCTCCAGC	ATCTCCAAGA	CCTGGAACGA	TATAACCGTG	420
TTCGTTCAAA	CGTTCATCCA	AGGCTGCTGT	AAAGATTTCT	ACATCTGGAT	GAGCTTCTTG	480
AAGGGCTTTT	ACACCCTCTG	GAGCAGATAC	AAGGCAGACA	AATTTGATAT	TTGATGCGCC	540
ACGTTTTTTA	AGAGAATCAA	CAGCCAAGAT	TGCTGAGCCA	CCTGTGCCA	ACATTGGGTC	600
TACTACAAAA	ATTTGACGTT	GGTCAATGTC	CTCAGGCAAT	TTCACCAAGT	ATTCAACTGG	660
TTGAAGTGTT	TCTTCATCAC	GGTACATACC	GATGTGGCCA	ACTTTAGCAG	CTGGAACCAA	720
GTTCAGAGA	CCATCAACCA	TCCCGATACC	TGCACGCAAG	ATTGGGACGA	TGGCCAATTT	780
CTTACCTGCC	AATTGTTTTT	GAAGTGTGTT	TGTAATTGGT	GTTTCGATTT	CCACATCTTC	840
TAGTGGAAGA	TCACGAAGTA	CTTCATACCC	CATCAACATT	GCAATCTCAT	CTACTAGCTC	900
ACGAAAAGCT	TTTGTAGAAG	TATCTGTACG	ACGCAAGATT	GACAATTTGT	GTTGAATCAG	960
TGGGTGATTA	ATAACTTCAA	TTTTTCCCAT	TTTTGGAATT	CCTTCTTTCA	ATTTATTTCTT	1020
CTTATTATAC	CAAAAAACGG	TTTAAAAATC	TTTCTAAACC	ATTTATTTTT	GATAATTTTT	1080
ACATTAGATC	AGCCTCTTTA	AGAGCTGTCT	GTACTGTCTC	AAGTGGTAAA	TGGGTCAATT	1140
CTGTCCCTTT	TTCTTGATAA	AGGTATTGGG	CGTAGTCGTC	CATTCGGTAC	TGGTTGATAT	1200
AAACCACGCG	CTTGCAGCCG	ACCTGAAGCA	ATTGTTTTGT	ACAGTTGAGA	CAAGGAAAT	1260
GGGTACATA	GGCTGTAAAG	CCTTTGGGAA	CACCACGCTC	AGCACCTTGA	AGGATAGCAT	1320
TGACCTCAGC	GTGAAGGGTG	CGAACGCAGT	GGCCTTCAAT	GACCAAACAT	TCGTGATCAA	1380
TACAATGCTC	AGTCCCTGAC	ACCGAACCAT	TGTAACCAGT	GGAAATAACC	TTATTATCTT	1440
TTACCAGAAT	CGCGCCCACT	TTAGCACGTT	TACAAGTGGA	ACGATTCGCA	ATTAGTAGAG	1500
CTTGGGCTGC	AAAATACTCA	TCCCAGGCCA	GTCTTTTTTC	AGTCATCTCT	TTTCTCCTTT	1560
TTCTCTATTT	TTTAAAAAAT	GGTAAACCTA	AATCTGCAAT	CTTTTCAGCT	GGTACCTTCA	1620
TGCCATCCTT	GATCCATTTT	AGAAGGACAG	AGACGATGGC	TGAGCTCCAG	AAGGAATGAA	1680
GATAAGAGCT	GACACCTTTT	GATTTCCCAT	GGTATTTTTT	TAGAAATTCC	TGCATGGCTT	1740
GGACAAAGAT	TTTTTCCAGA	TGGTAATCCA	AGGCCAATTG	AATTACTCTA	GCTTCCTTTC	1800
TGGCCTCCCG	GAAAAGGTGA	ACCCAAACCA	AATAAAGGTC	TGCTTTTAAA	TCGTAATGAT	1860
GCAGCTGTTT	CATAATATTG	TGGACAGTTC	GTTTAAAGAC	GCTCTCTAAA	ATTTCTCTTT	1920
TGGAGTCATA	ATTGCGATAA	AAGGCCGCAC	GCGAAACACC	TGCACGTTTG	ACCAATTCAG	1980
AAATACTAAT	CTTGGTCAGT	TCCTTTTTTT	CCAAGAGTTG	CAAGAGGGCT	GTTTCAATGG	2040

1341

CTTCTCTGGT TAATAAATG GATTCTTGGT TTGATTTTCT GAGATTTTCA AGAGACTTTT 2100
 CAGAGATTCT ACGTTCAGAC ATAACATTTT CTTTCTACTT GTCACAACAG ACGGATGATG 2160
 CTTTGTGTTT 2170

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

ATCTGCACGA ATCAGGGCTT TCTAAGTGAC TATTTCCACC GAAATATTAT TTATATCAGG 60
 AGGACATTCA TATGTCACGT TATACAGGAC CATCTTGGA ACAAGCTCGT CGTCTTGGCC 120
 TTTCACTTAC AGGTACAGGT AAAGAATTGG CACGTCGTAA CTACGTACCA GGACAACACG 180
 GACCAAACAA CCGTTCTAAA TTGTCAGAAT ACGGTTTGCA ATTGGCTGAA AAACAAAAAC 240
 TTCGTTTCAC TTACGGTGTA GGTGAAAAAC AATTCCTGTA CTTGTTTCGTA CAAGCTACAA 300
 AAATCAAAGG CGGAATCCTA GGTTCACACT TTATGCTTCT TTTGGAACGT CGTTTGATA 360
 ACGTTGTTTA CCGTCTTGGT CTCGCGACTA CTCGTCGTCA AGCTCGTCAA TTCGTAAACC 420
 ACGGTCACAT CCTTGTGAC GGGAAACGCG TTGATATCCC ATCATrCCGC GTAACCTCCAG 480
 GTCAAGTGAT CTCAGTTCGT GAAArATCAT TGAAAGTTCC AGCAATCCTT GAAGCAGTA 539

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 667 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CCGGTTTTGC TCCTTCTCTA CGGCTACGAC GTGATGTATC TCTGATGATA TCCACTGTTT 60
 CTGTAGCAGG CGTAGGTGTT TCTGGACCTG CTTGTTCTGC TTTTCTCTCT GCCGTCGTAT 120
 AGGAAACAGC TACCCTTGTT GGGGTTTCAT TGTATTCTCT TTCAAGTTTC TTAGGTCTAA 180
 CAGGACCTGG ACCTGGTCTT GATCCACTTT CTCCCGCTGG AGAAGAAGGT ACATCTTGAC 240
 TTGGATGACT TGGAACACCA GGAGTTTCTC TTTGAATCTC ATCTGCTGGA GAAGCTGGTA 300

1342

CACCTTGACT TGGGTGAGTA GGCACGGTAG GAGCTTTTCT CATAATCTCC TCTACCGTTG	360
ACAAGGAATC AGCCATGAGT TCTTCAGTTG AAGGTTTCATT TGCAGGAGTG CGAACTACTG	420
CCTCATCTTC TTTCAGAACT TCATCATAGC CTTTACTTTT TTCTAAATCT CTCAGAATCT	480
GCTCTTTTAA GCGTAATTTC TCTTCTGCTC TTGACTTTTC ACTCAAAAGT TTTTCCTCCT	540
TGTTGAGAAT CCATAATATT AGAGCTGAGA AGTCCAAAAA AAGCAATCTA TGATACTTTT	600
CCTAACGGAT TTTGTCATTT CCCAGACCAT ATCATACCAT GTTTCCTCTG CAAAGGTTGA	660
CTGGGAA	667

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GGGAAGCCAA GGTATTTTAT CGGATGAAGT TGTTACTAGT TCTTCACCGA TGGCTACAAA	60
AGAGTCTTCT AATGCAATTA CTAATGATTT AGATAATTCA CCAACTGTTA ATCAGAATCG	120
TTCTGCTGAA ATGATTGCCT CTAATTCAAC CACTAATGGT TTAGATAATT CGTTAAGTGT	180
TAATAGTATC AGCTCTAATG GTACTATTTC TTCCAATTCA CAATTAGACA ACAGAACAGT	240
TGAATCTACA GTAACATCTA CTAATGAAAA TAAGAGTTAT AAGGAAGATG TTATAAGTGA	300
CAGAAATTATC AAAAAAGAAT TTGAAGATAC TGCTTTAAGT GTAAAAGATT ATGGTGCGGT	360
AGGTGATGGG ATTCATGATG ATCGACAAGC AATTCAAGAT GCAATAGATG CTGCAGCTCA	420
AGGGCTAGGT GGAGGAAATG TATATTTTCC TGAAGGAACT TATTTAGTAA AAGAAATTGT	480
TTTTTTAAAA AGTCATACAC ACTTAGAATT GAATGAGAAA GCTACAATTC TAAATGGTAT	540
AAATATTAAG AATCACCCCTT CCATTGTTTT TATGACAGGT TTATTTACGG ATGATGGTGC	600
GCAAGTAGAA TGGGGCCCAA CAGAAGATAT TAGTTATTCT GGTGGTACGA TTGATATGAA	660
CGGTGCTTTG AATGAAGAAG GAACTAAAGC AAAAAATCTA CCACTTATAA ATTCTTCAGG	720
TGCATTTGCT ATTGGGAATT CAAATAACGT AACTATAAAA AATGTAACAT TCAAGGATAG	780
TTATCAAGGG CATGCTATTC AAATTGCAGG TTCGAAAAAT GTATTAGTTG ATAATTCTCG	840
TTTTCTTGGG CAAGCCTTAC CAAAAACGAT GAAGGATGGG CAAATCATAA GTAAGGAGAG	900
CATTCAGATT GAACCATTA CTAAGAAAAG TTTTCCTTAT GCCTTGAATG ATGATGGGAA	960
AAAATCTGAA AATGTGACTA TTCAAAATTC CTATTTTGGC AAAAGTGATA AATCTGGGGA	1020

1343

ATTAGTAACA GCAATTGGCA CACACTATCA AACATTGTCG ACACAGAACC CCTCTAATAT	1080
TAAAATTCAA AATAATCATT TTGATAACAT GATGTATGCA GGTGTACGTT TTACAGGATT	1140
CAC TGATGTA TTAATCAAAG GAAATCGCTT TGATAAGAAA GTTAAAGGAG AGAGTGATACA	1200
TTATCGAGAA AGCGGAGCAG CTTTAGTAAA TGCTTATAGC TATAAAAACA CTAAAGACCT	1260
ATTAGATTTA AATAAACAGG TGGTTATCGC CGAAAATATA TTTAATATTG CCGATCCTAA	1320
AACAAAAGCG ATACGAGTTG CAAAAGATAG TGCAGAAaTwT TTAGGAAAAG TATCAGATAT	1380
TACTGTAACA AAAAATGTAA TTAATAATAA TTCTAAGGAA ACAGACAAC CAAATATTGA	1440
ATTATTACGA GTTAGTGATA ATTTAGTAGT CTCAGAGAAT AGT	1483

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

CCTGAACGCT TTTTATAAAA TATCATAAAG CCAATCTGAT TTATCAAGTG TGTCTAAGCG	60
ACGCGAATTA AAATTCATTG CATACTCCAT CGCTTCTAAA AAATCATTT TTGAAAAGAC	120
GTAAAAATCA TCTAAATTCT GACTCCAATA TAATAACAAA ACCAATCCCA TAATATCCTC	180
TGGTTGATTA TTCAATAAAT TTAAGTTGGT TTCATAAAAC CCTGGAGTTC CAAATAGAGG	240
CAACTTTTTT TCTCAATTT GAGTTTCTTT CCTTAGGGCA TGCTCAAAGT CTATAATATA	300
AATATTATTT CTATTATCAA TAAGTATATT ATTAAATGAT AAATCTCTAT AGGAAAGATT	360
ATATTTGGAG TTTATTATCT CCATATAATC AATTAATGTT AAAAACCAAT CATACGAGCC	420
ACTAACCATA TTATACTCGC TTAATTTATC TGCAATAATA AACTCAAATT CCACAAAATA	480
CGAATTC'TTT ATGTAAAAAT CGTTAAAAAC TTTTGGAGTA AATTCCTCCT TTTCCAATTC	540
TACTAATATT TCTCTTTCAT TTATTAAACG ATTCACAGAA TCTCTATTG TAAAATCAAC	600
CAACGATAAA TCACTAGCTT CTTTAAATAA AGAATAAACT CGCTTTTGAG TATTAAATAC	660
TTTATAAACT CCACCTTTGG CATTTT TAGA AATCACTTCC AAAATAATAT ATTGATCAGG	720
AATAGTGTTA TATCTTGGA TATAGTAATC CCTATTGGA ACATTCACAT TTGAAGGGAT	780
TTTCTTATCT CTTTATCCT TGAAAGTGCT ATCTTTTACG AACTCCCCAT ATCTGTAATA	840
TACAACCTCG CTAAGTTGAA ATCTGAAATC TGATGGTATG TTTACACCCT TTACACCTTT	900

1344

ATACAATATT TCTAATTGT GTAACAAACG TTGAAACTCT TTATTATCTT TTGGATAAAT	960
TGTAATGAAT TTCCCGACTT GTGAATAACC ATTAAGCCCT GTATTTTGCA AAGAAAGTTC	1020
TTTAATGCTA ACCAAAATTT TGAAATTTAT CTCTCTCTCT CTAGAAAATA TAAAATCAAA	1080
GAATTTTTTA GCAACCAAAT TAGCATTTAA TATTGAAGCG CTCAGGTGTA TTTTAAATCC	1140
CTTAGATTGG GTGATATTAG ACGGCAAATT ATATAACCAA TGTTTCATCAC TAAAATTATC	1200
ACTAATTTTA TATTCTAATA ATAAATTATG GTATGCGTCT TCTATTTTCAG TTTCATAGTC	1260
CAAATAGTTT AAATACTTTT CGTAATTCAT ATTAAGAAAT CTCTCCATA AATTTTGTAGA	1320
CCATCATTTA AAGCCAAACA ATTTAAAGCG TGATAATAAA TGTTGATAAT CAATGTAACT	1380
TTCAGTCCCT TATTTTGTA TCCCTTCACC AATAATTTTA TGCTATATCT ATTTTCTCGA	1440
GGCAATTTAT AGGACTTCAA GATAAAACCA TAAAAGAGAT AAGTATTATA ATCTGACAAT	1500
CCAGTTTCAG AATAATTTT TAGAAAAATA TCTAGTGATT CTGATAATTC ATCCGGAATA	1560
ATTCCTTTAA CATCGTATTT ATTTTTCATA TCGGCCACTC TTCCTTAAAA AGCTCACAAT	1620
AAAATTTTAA ATTTCTATAC AACAAATCCG GAGTAGTCTC ACAATTTGAA CATTTACAT	1680
CACTCTTAAT ATATAAAAA TGAATTAATC AGAAACCTCT GACTAAGATT TCCTAATTAA	1740
TTCACCTTCT ATATCATAGT AAGGAATTCT ATTATCCCTA ATTGAAAATT GAAATTTTAT	1800
GTTTTATATA TTAACAATTA TGCGGATTGT AAATCTTGTC TAACAAAATG GCAAGTGCTA	1860
CTATGTGCCC CAGAAGCGA TGCAACGCTA TTTTGAATTG AAAGAGCATA ATCATCCATA	1920
TCATTTAAGT CACGGATTAG CAATGCTTCC TTCTCTCTC CGACAATTCC AAATTTTCTA	1980
ATTACCTTTT CAGGATTATC AAAAAATTCT CCAACAACCT CCATATTTC TTGAAGTTCA	2040
TTCAAGAAAG CTTTCATTTG ACTACTCATT ATATAGCTCC TTTTCTATTA CTTTATTTGG	2100
AATCAAAACT TACTTGTACA TTGGAAACAC CTCTATTCTA CGCTTTCATA TTGCTGCATG	2160
ACACTTTCAA AATCAAATTG CTAAAAATA TTTTAAAG CTTAATTTAG ATTTAATTAC	2220
ATATATCTCA AAAAATTGTT TTGAAATTAG TAAATAAAA TAGGTTTCTG TACTTATAGG	2280
AACTAGTTAT AAAAAGCTCG CCCATCATAA AATATCTATT TAAGTAAAAC AAAAATTTTA	2340
TAATTTTTTG ATTTTAAAGT GACTATAATC TCCTATCTAT AAATACCATT CGCAGGACCT	2400
GGATCAATCC CTCTAGCCAT CTTATGAACT TGAGTTCCTC CAGACAGTCC CGG	2453

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1049 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CCAATTTGAA GGCTCTAAAA CAATGGAAAA GTGCTACACA GATGTGACAG AATTGCCAT	60
TCCAGCAgTA CTCAAAAACCT TTACTTATCA CCAGTTTTAG ATGGCTTTAA CAGCGAAATT	120
ATTGCTTTTA ATCTTTCTTG TTCGCCTAAT TTAGAATAAG TACAAACAAT GTTGAACAG	180
GCATTCAAAG AGAAGCACTA TGAGAATACG ATTCTCCATA GTGACCAAGG CTGGCAATAC	240
CAACACGATT CTTATCATCG GTTCCTAGAG AGTAAGGGAA TTCAAGCATC CATGTCACGC	300
AAGGGCAACA GCCCAGACAA CGGCATGATG GAATCTTTCT TTGGCATTTC GAAATCGGAG	360
ATGTTTTATG GTTATGAGAA GAACTTTAGA TCTTTAGAAA ACCTTGAACA AGCTATTGTG	420
GACTACATTG ATTATTACAA CAACAAGAGA ATTAAGGTAA AGCTAAAAGG ACTTAGCCCT	480
GTGCAATACA GAACTAAATC CTTCGGATAA ATTAATTGTC TAACTTTTGG GGTGCAGTAC	540
ATTTTTGGTA TATATAAAAT TTGTAGGAGC TATATCTACA ATTTTATATT CCCAGTTTAT	600
GGATGTAACT TACTATATTC ACAATGTTAT CCAGTGTTTT TTCTCTAATA TTTAAGGAGT	660
GTTCTGTTTC TCGAATAAAT TCTTCAAAGT TTAACCCGTC AACTTGTTCC TGAACAAGAA	720
AATAATCATC CACGATATAA AATTCATCAG TTAAATTAGT AGTATAACTT TTATCGGCTA	780
ATTTTTTTAG CATGTGAGCT TCATTTTTTA TATCATCAAG AGCTGTCCAT TCTCCTTCAG	840
CATCATAATT CACAAAAGGT CTTGACTGCT TGATGATTAC TTTTGGCCCG TCCGATTTTC	900
TAATTGCCCC ATAAACATTT CCTTTATTTG ATCTCTTAAT AATTTTTTCC ATTTTGTATT	960
TATTTATTGC AGAGTCCTTA CTGAAACTT CACATGTGGT TTGAAAATAA ATCCTTTTTT	1020
CTTCTTCTGA AAATAAATCC ATTTTCCGG	1049

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 776 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

TTAGTTGGTT AGAATCAGAA AATCGCCGAA GTGGTTATTT ATTTTGAAT AAATTTAACG	60
AACCAATTAC AGCAAGAGGA GTTGCTCAAC AGTTAAAAAA TTATGCTGAT AAATACAAAA	120
TGAATCCTAA AGTAATTAC CCTCATCTT TAGGCATTT ATTTGCTAAG AATTTTTTAG	180

1346

CGAAGTATAA TGATATTGCC TTGCTTGCAG ATTTGATGGG ACACGAAAGT ATAGAAACTA	240
CTCGAATTTA TCTAAGGAAA ACAGCTACTG AACAAACAAA TATTGTAGAT AAAATTGTTA	300
ATTGGTAAAA AATAACAGGT GGTCAAACCTG ACTACCTGCT ATTTTGTGA TTATGGCTCT	360
TATTATGGGA ATATACCTAT GAATTGGGTT GTTATAAAAA TAAAAGATAT TTTTCAATA	420
AATACAGGTC TTTCTTACAA GAAGGGCGAT TTAAGCATTA ATAATAAAGG TGTTAGAATT	480
ATACGTGGTG GTAATATTAA GCCTTTAGAA TTTTCTCTGT TGGATAATGA TTAACATT	540
GATACACAAT TCATCTCCTC TGAGCAAGTT TATTTAAAC ATAATCAGCT AATAACACCT	600
GTATCAACCT CTTTAGAACA TATTGGAAG TTTGCAAGAA TCGAGAAAGA CTATGATGGT	660
GTGTGGCTG GTGGATGTAT TTTCCAATTA ACACCATTTC AAAGTGCAGA GATGATGTCA	720
AAATGTCTAT TATGTAACCT GTCCTCTCCG TTATTTTATA AACAATTGAA AGCAAT	776

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC CCATTCGACC ACCAAGCGAA	60
ACATCGCATC GAGCGAGCAC GTACTCGGAT GGAAGCCGGT CTTGTCGATC AGGATGATCT	120
GGACGAAGAG CATCAGGGGC TCGCGCCACC GAACTGTTCG CCAGGCTCAA GCGCGCATG	180
CCCACGCGC AGGATCTCGT CGTGACCCAT GGCGATGCCT GCTTGCCGAA TATCATGGTG	240
GAAAATGGCC GCTTTTCTGG ATTCATCGAC TGTGGCCGGC TGGGTGTGGC GGACCGCTAT	300
CAGGACATAG CGTTGGCTAC CCGTGATATT GCTGAAGAGC TTGGCGGCGA ATGGGCTGAC	360
CGCTTCCTCG TGCTTTACGG TATCGCCGCT CCCGATTTCG AGCGCATCGC CTTCTATCC	420
CTTCTTGACG AGTTCTTCTG AGCGGGACTC TGGGGTTCGA TGTCGACAGC CCGCCTAATG	480
AGCGGGCTTT TTTTTCCTGA GGCTGGACGA CCTCGCGGAG TTCTACCGGC AGTGCAAATC	540
CGTCGGCATC CAGGAAACCA GCAGCGGCTA TCCGCGCATC CATGCCCCCG AACTGCAGGA	600
GTGGGGAGGC ACGATGGCCG CTTTGGTCCC GGATCAATTC GCGCGACCGG ATCGATCC	658

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1475 base pairs
 - (B) TYPE: nucleic acid

1347

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

CCGGCTTAAT TTTTAGAAAA CGTGGGCAGG GAACCTTTGT TCTCTCTCGT GGCAGCTCAA	60
AAAGAAAATT AATCGTTCCA GAAAGAGATA TCCGGGGACT GACAAAAATA TCTGAAGATG	120
CTCATTCTAC AATTGACTCG AGGATTATTC ACTTCAAATT AGAATTTGCA AATGAATTTT	180
TAGCAGAAAA ACTACAGGTC GCTTTGCAGA GTCCAGTTTA TAATATTTAC CGCCTGCGTA	240
TTATTGACGG TAAACCTTAT GTTCTGGAAC AAACCTTATAT GAGTACCGAT GTTATTCCAG	300
GTATTACTGA AGATATTTTA CAAAAATCGA TTTACAATTA CATTGAAGGA AAGTTAGGAT	360
TGCATATTGC CAGTGCTACA AAAATCTTAC GAGCTTCTTC TAGTTCAGAA AATGAGCAAC	420
ATTACTTGCA GCTCCTTCCA ACGGAACCGG TATTTGAAGT AGAACAAGTG GCTTATTTGG	480
ATAACGGAAC TCCGTTTGAG TACTCGATTA GTCGTCATCG CTATGATTTA TTTGAATTTA	540
ATTCTTTTGC ATTACGACAT TCCTCCTAGG AGAAAATGTG AAAATGAAGC CAATCTTTTA	600
CAGACTCTAG TTTAAGAAAA ATTTAAACA GGGCAAGAAG GTCCCATCTA TGCTTAAATG	660
GTTTCTCTTT TCTAAATAAG ATGGCTTTAA AAGAGTGATC GTTGATCCA TCATGTTGAA	720
AAATATCTTC GTATAGCTTA TAGAGTAGGT ACTGAAATG TTCACCTGAT CTACTTCTTA	780
TAGTTATTTA GTTTTAAATA GTGTTTCAAA CATTCTTACA CTGACGAGAA GTTTTTGAGT	840
CTTTTCTTGT AACACATATA GTATACTGTG GTTAGAATAG TAGACTGTGA CTTCTAACAA	900
ATTGCTAGAA ATGAATTTCA ATCTCCAAT TTATTTGTTC ATATCTTCTT TTAATATATT	960
AAATAAATTC TAAATCATAA TCATTTAAAA AAATTTTATT TTTTATTTT CATTACGAAT	1020
AATATAGATG AAGGGGAAAG AGTATGAAAA CAGAACTGTT TCTTTTGCTA TTAGTTCAAA	1080
AGGAGAAAAA ATGAAAGTAG AAAATATTTT GTATAGGGTG GATCATCGTA AATTGTTTGA	1140
TAATATTTCT TTTGATACTT CGAGTTCAGA CGTGACATTA ATTACTGGTA AAAATGGTAC	1200
AGGAAAGTCA ACTTTACTAT AGTAGATTGA AACTAGAATA GTACACATCT ACTTCTAAAA	1260
TATTGTTAGA AATCGATTTG ACTATCCTGA TCTATTTGTC CTGTTCTTAT TTCATTTCAC	1320
TATATCTCAA ATTGAGTATG ACGAAGTGCG TCCCCATGTC CTGGGAACGC ACTTCTTCA	1380
TATTTTTCAT ATTCCTGAAT CCATCGATAA AGACTATTGG GATGAATTTT TAAAGTTGAA	1440
CTAATCATTT TTACAGGATG AGATTTACAG CAGAG	1475

(2) INFORMATION FOR SEQ ID NO: 321:

1348

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GAAATATATA TACTTCATCT TAATAGTGAG CAAGCTAAAC TTAGCATTTC ATGCCCTCAT	60
ATGGGATGTT CTTTGACTAA ATAATATGAT TATCGAGATA TATCTGGATA AATGAACTAA	120
TAAGTCTGAC GCGTAGACTT ATCAAAGTCA TTGGCATACA CCACTATGAA CTCGTTGGTC	180
TGTTCAAATC CCAACACATT ACCTGAGAAG AAAGTTGCAA TGTGTGTTTT GGTGCGGGTT	240
TGAATTAA AAATTTGTTA TGTAGTACCT AATCTAAGGA ATTAGAACAA TGCCTCTAAT	300
TTTTCTTTAA TACACTGAAA CATTGATGAT TCTGGCTGTA TTTTGGAAAC AGCTCTCTTT	360
TGCTCCTGGA AAATATCTTC AGAAGTTATA TTCTCTATTC CTAACGCTAC TTGAGTTTTT	420
TTTCTAAAT ATTCTTTTCC GTTGCCATCT TTAGAAAAAT CATAACCTTC CCTATCTACG	480
CTGTTACACA AATTAGCTAA AAAAaACTCT GGGGTTGGGA AAGGAAGATA AGAAaCGTAT	540
TTAGCCCATATA ATCTATAAAG	560

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CCGCCCGGCC ACCGCTGCCT ATCCTCGGGA GAGGGTCACC TGGAGTGAAC CTAGAACGAT	60
AGACACGGTG CGGTACGACC TCGTACTACT TTCGCCGACG GCCTCGTCCG TTGTCATCCA	120
CGAACTGATC GGACATGGGT GCGAACACTT CAGAGAAAAA ATCGTTGGAC TGCGTGTCGG	180
GCCTGAGGAA CTACGGGTGG TGGCTTTTCC GAAGAACGGC TCCGGGTTTG ATGACGAGGG	240
TACACCCTCC GAAGAGATTG TACTTGTGGA GAACGGCATT GTGAGGCACG CTGTCAGGGA	300
TCGGGCGACT GGAGGAATGG CGCCTTTTTC CGGTTTGACC AAAGTGGCAT CACATGGTGT	360
CAAACCTGGC TCAAGATGTA CGCATCTCAA GGCGGAAGGG GAATCGTCAC AGGAAGGAGT	420
TACCGGAGTA CCCGCCGAAC GCACCGTTTG GATAGAGCAT TTTTCTGCAG CGAACTACCA	480
TTCAGGTCGA GCCTTTTTC GGTCTGGCCT TGCCTGGGTA GGCAGCCGAG AAGAACTCTT	540

1349

ATATCCCTTA ATGCCTTTCA CCATGTCAAT TGATATCTAC GAACTGGCCA GCTTATTGTG 600
GCATTTAGAC GGTCAAACGG AACGAGCACG TAGGGTACTG TGC 643

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GGTACCCACT CATTCTTGAT GAATTGTGAA CAGTTGCCCT TGGGTCGTTT TCGGAGTTGA 60
AGTCAAGAAG AGGAAAAAAA CAAAAGGAG AAATACTCAT GGCAGTAATT TCAATGAAAC 120
AACTTCTTGA GGCTGGTGTA CACTTTGGTC ACCAACTCG TCGCTGGAAT CTAAGATGG 180
CTAAGTACAT CTTTACTGAA CGTAACGGAA TCCACGTTAT CGACTTGCAA CAACTGTAA 240
AATACGCTGA CCAAGCATAC GACTTCATGC GTGATGCAGC AGCTAACGAT GCAGTTGTAT 300
TGTTTCGTTGG TACTAAGAAA CAAGCAGCTG ATGCAGTTGC TGAAGAAGCA GTACGTTTCA 360
GTCAATACTT CATCAACCAC CGTTGGTTGG GTGGAACCTCT TACAACTGG GGAACAATCC 420
AAAAACGTAT CGCTCGTTTG AAAGAAATTA AACGTATGGA AGAAGATGGA ACTTTCGAAG 480
TTCTTCCTAA GAAAGAAGTT GCACTTCTTA ACAAACAACG TGC GCGTCTT GAAAAATCT 540
TGGGCGGTAT CGAAGATATG CCTCGTATCC CAGATGTGAT GTACGTATG ACCCACATAA 600
AGAGCAAATC GCTGTTAAAG AAGCTAAAAA ATTGGGAATC CCAGTTGTAG CGATGGTTGA 660
CACCAATACT GATCCAGATG ATATCGATGT AATCATCCCA GCTAACGATG ACGCTATCCG 720
TGCTGTTAAA TTGATCACAG CTAAATTGGC TGACGCTATT ATCGAAGGAC GTCAAGGTGT 780

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 624 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGGAAAAAT CAGATTGTGG GTTCAGATAT CGAATTAGCC AAGGCTATCG CAACAAAAT 60
AGGTGTCGAA TTGGAATAT CTCCCATGAG TTTTGATAAT GTACTGGCTA GTGTTCAATC 120

1350

AGGAAAAGCC GACCTTGCCA TATCAGGTGT TTCTAAGACA GATGAACGGA GCAAGGTGTT	180
TGACTTTTCC ATTCCCTACT ATACTGCAAA AAATAAACTC ATTGTCAAAA AATCTGACTT	240
GACTIONTAT CAGTCTGTAA ACGACTTGGC GCAGAAAAAG GTTGGAGCGC AGAAAGGTTT	300
GATTCAAGAG ACGATGGCGA AAGATTTGCT ACAAATTCCT TCCCTCGTAT CTCTGCCTAA	360
AAATGGGAAT TTAATCACAG ATTTAAATC AGGACAAGTG GATGCCGTTA TCTTTGAAGA	420
ACCTGTTTCC AAGGATTG TGGAATAA TCCTGATTTA GCAATCGCAG ACCTCAATTT	480
TGAAAAAGAG CAAGATGATT CCTACGCGGT AGCCATgAAA AAAGATAGCA AGAAATTGAA	540
AGAGGCAGTT CGATAAAC ATTCAAAAGT TGAAGGAGTC TGGGAATTA GACAACTCA	600
TTGAGGAAGC CTTATAAGCA TCCA	624

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TCTTATGAAG CCGAAGCGTG ATTTATGGCG GATAGGTTTG GTCTGCAGAA AGTGACAAAT	60
CTAGTGCCAT CAGCGTATAT GGAATCTnTG GCTGAGAAAC AGTCCCGGGG TGAAGTACT	120
TATGAGCAGG TTTATGAGGA TGCAACGGCT TATCATCATA CCATTGATGC GAGTACAGAG	180
GAGGCAGACT TGGTTTCTCT ACGTATTGTA GAACTATTGT CTCGAAGAGG CTTTAGCTTC	240
AGTCCTGCGA TCTTACTTGC TATTCATAAG GAGTTGTTTC AAGATATATT TGAACCTCG	300
ATCCCGGTAG GTCAATTTTCG TCAGACTAAT ATCACAAAGA ATGAACCTGT TTTGAATGGT	360
GAAAGTGTG TGTACTCTGA TTAATCCATG ATTCAAATGA CCTTGGATTA TGATTTTAAT	420
CAGGAAAAAC AAGTGCATA TGCAGACTA ACCCAGGCGG ATATGGTTAA AAAAATCCAG	480
CATTTTATTT CAGGAATCTG GCAGATTCAT CCATTTGCGG AAGGAAACAC TCGGACGGTA	540
ACGGTATTTT TGATTCAGTA TCTTCGTGAG TTTGGTTTTC ATATTGATAA TACACCATTT	600
CAGCAACATT CCAAGTATTT TCGTGATGCC TTAGTGTTAG ATAATGCAAA GATTTTACAG	660
CGACGTCCTG AGTTTTTAAC AGCTTTTTTT GAAATCTCT TGCTCGGTGG TCAAAATGAT	720
TTGTCTTCAG AAAAAATGTA TCTAGATTTA GACCTCGATC TTTCATAATC CTAATACTGA	780
GTAAACATTG AATTTTAGGA AAAAATGAAG TAAATATTCT CACAAGAAAA CGTATATCAT	840
CAAAGTTTGG CTCTTTGTCA ATTGTAGTGG GTTGAAGAAA AGCTAAGTTC GAGAAAGGGC	900

1351

AAATTTCGGC CTTTCCTTTT TGATGTTTCAG AGCGATAAAA ATCCGGTTTT TTGAAGTTTT	960
CAAAGTTTCG AAAACCAAAG GCATTGCGCT TGATAAGTTT GATGAGATTA TTGGGCGCTT	1020
CCAGTTTGGC ATTAGAATAG TGTAGTTGAA GGGCGTTGAT AACCTTTTCT TTATCTTTGA	1080
GGAAGGGTTT AAAGACAGTC TGAAAAATAG GATGAACCTG CTTAAGATTG TCCTCGATAA	1140
GTTCGAAAAA TTTCTCCGGG TCCTTATTCT GAAAGTGAAA CAGCAAGAGT TTGAAGAGCC	1200
GATAGTGATG TATCAAGTCT TGTGAATAGC TCAAAAG	1237

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TTTGATTTTT CTGAATTAGA AGAGATTGAA TTGCCTGCAT CTCTAGAATA TATTGGAACA	60
AGTGCATTTT CTTTGTAGTCA AAAATTGAAA AAGCTAACCT TTTCCTCAAG TTCAAAATTA	120
GAATTAATAT CACATGAGGC TTTTGCTAAT TTATCAAATT TAGAGAACT AACATTACCA	180
AAATCGGTTA AAACATTAGG AAGTAATCTA TTTAGACTCA CTACTAGCTT AAAACATGTT	240
GATGTTGAAG AAGGAAATGA ATCGTTTGCC TCAGTTGATG GTGTTTGTGTT TTCAAAAGAT	300
AAAACCCAAT TAATTTATTA TCCAAGTCAA AAAATGACG AAAGTTATAA AACGCCTAAG	360
GAGACAAAAG AACTTGCATC ATATTCGTTT AATAAAAAAT CTTACTTGAA AAAACTCGAA	420
TTGAATGAAG GTTTAGAAAA AATCGGTACT TTTGCATTG C	461

(2) INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

TAACATTTAG GTACCTCTTC TTAACAAAGT TCAATAGTAA CAATTAATAT TTAAACAAT	60
ATATCAAACA TCAATGACTA GAATACTTGC ATCATCCTTC TTCCATAGA TTGGATCAAT	120
AGCAGAAGAA TTAAATCTCA TCTTAATTAA CTCTCAAAA GTTTTATTTT GATTATTTTG	180

1352

ATAGAATTCA TAAAAGCCAT CGCTCATTA	AACAATTTGT TCACTAGTAA CATCTATTTG	240
ATTAATAATA GCATGGTCTA AAAATCTCTC	ATCCAACGAA CCTATCCAGT ACCCACTCGG	300
TTGATTAGAT AATTTTCTGA TTTTTTGTA	AATAATTTTT TTATTTAAAA CACTATTTGT	360
ACCAATTGAA TCTTTTATCT CATTTTTC	TTTTTCAAAT AAGTTATCTA CTCTATGATC	420
AGTTATTTCC ATTTTCGTTA CTAACATGAC	GCAGTCACCT AGCATCATAT ACTCCAAC	480
TTTTTCTGAA AGTTTAGCAA ATATTGGTAA	GCGATAATAT AGTATATTGA AACTAGAATA	540
GTACACCTCT ACTTCTAAAA CATTGTTAGA	AATCGATTTG ACTGTCCTGA TTGATTGT	600
CTATTATTAT TTCATTTTAC TATACTCTGT	TAATTTATAT GAGTTTAAAC CGATTTCATC	660
TTTAACCTCG AGTAAAGCAG TTTCAAATAT	TTGTTTAAGA GTTTTGTGATT CTTTACAATT	720
AACCGACAAA CTTTCTGATA AAATATGTAC	AACTTCTGAG ACTGAATAAC CTATCTCCTC	780
TTTAGAATTA TATAAATCTG TAGCTCCACC	AATAATCCAA AAATACTGAT TTTGTGAACC	840
TACAATATCC TCATTTTCTA CGGAACCTCC	TTGTATCGAA CAAATTTTAT TTATCTTTAC	900
CATAATACTT CAACCCTTTT AGTGTCAAAA	GTAACCAAT TCCTGTCAC	960
GTTCATAAT CTTATTCGAA CCAGTCTTTG	GTAATTTTTG TTTKACATCT ACTATyTCTT	1020
TAGATTTATT AATATGATTT TCAGTTTCTC	TGCCATCTCC AACTATTTTA TAGTTTACTT	1080
CTTCTGTCTT ATTATCTTGT TTATTGTCGA	TCTTGTCATT CATTGTGCTA TTATCTTTAC	1140
TTGAGTTAAA CTCTCCGTTT TTCTGGTTAC	TATCAATTAC ATTATTTGAA TTAGATTGTT	1200
TTTCCTCTTT GTTTTTTCT TTTTCGTTTT	TATCACTTAA ATTATTTGTT ACAATTTTGT	1260
AAAGCCCAT CTCCGTTACA ATATTGAAAT	TACCATCGCT ATCACGTATA ACAGGTTCTT	1320
TCCCATTTGC ATTAGATTTG ATGAATGATA	TATACTTACC GGATAAATTA TAAATTTGGT	1380
TATTTAAAAC GGTATTTTA CCCTTTGAAT	CCTCAATAAC AATTCCTTCT TTACCC	1436

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

CCGGCAGACA GGAGAAGGTG TTAAATATCA	ATCTCAAATG GTTCGTCAAT GGTTCCTGAT	60
ACGTATTTTC CGTCTTTCTT CCGTTGCTTG	ACACACTCTG TGAGGAGATA TTCGATTTGC	120
CCATTGACTG AACGAAAGTC GTCTTCTGCC	CATGATGCGA GTGCAGCGTA TAACTTTGTT	180

1353

GAGAGTCGAA GGGGGATCTG CTTTTTTTTA GCTTCAGCCA TCTTTAGTAA AGGCTTCCTG	240
TGTTGACAAAT TGGTTGTGCA TCATGATTGC CACAAAGAAC GACAAGGAGA TTTGAAACCA	300
TGGCAGCTTT TCGTTCCTCG TCAAGTTCTA CCAATTCCCC TTCATTGAGC CGTCTAGTG	360
CCATTTC AAC CATTCCTACA GCACCATCTA CAATCATCTT CCGTGCATCA ATAATGGCAG	420
ATGCTTGTTG GCGTTGAAGC ATAACGGCAG CAATTTCTGG AGCATAAGCT AGGTAAGTGA	480
TACGTGCTTC AAGGATTTC AAGCCAGCAT CCTCAACACG ACTTTGGATT TCTTCACGAA	540
TACGGGTAGC AACAAATTCG CTAGAGCCAC GGAGACTACC TTCATCTGCG TGCCCATCAC	600
CCGGAGTATC CACATTAGGA GACACATCGT AAGGATAGAT GCGGAC	646

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1653 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

GTTGCAGGTG CAGTAGGTGT TACTTCAGAT ACATTTGAAC GTGCAGAGGC TCTTTTGTAG	60
GCAGGAGCGG ATGCGATTGT TATTGATACT GCACATGGTC ATTCTGCAGG TGTCTTGCGT	120
AAAATTGCCG AGATTCGTGC TCATTTCCCA GATCGGACTT TGATTGCTGG AAATATTGCT	180
ACTGCTGAAG GTGCACGTGC CCTTTATGAA GCGGGTGTAG ACGTTGTTAA GGTGGTATT	240
GGACCAGGTT CTATCTGTAC TACTCGTGTG ATTGCTGGTG TTGGTGTTC GCAAGTAACA	300
GCTATCTACG ATGCTGCAGC TGTTGCGCGC GAATATGGTA AAACGATTAT TGCTGACGGT	360
GGGATCAAGT ATTCTGGAGA TATTGTAAAA GCACTTGCTG CAGGTGGAAA TGCTGTATG	420
CTTGGATCTA TGTTTGCTGG AACTGATGAA GCTCCAGGCG AAACGAAAT CTTCCAAGGA	480
CGTAAATTCA AGACTTACCG TGGTATGGGA TCAATTGCTG CTATGAAGAA AGGTTCAGC	540
GACCGTTATT TCCAAGGTTG TGTCAATGAA GCAAACAAGC TTGTTCCAGA AGGAATTGAA	600
GGTCGTGTTG CTTATAAAGG AGCGGCAGCT GATATTGTTT TCCAAATGAT TGGTGGTATT	660
CGCTCTGGTA TGGGTACTG TGGTGCAGCT AACCTTAAAG AACTACACGA TAATGCTCAA	720
TTTATTGAAA TGTCTGGTGC TGGTTTGAAA GAAAGCCATC CTCATGATGT GCAAATTACT	780
AATGAGGCAC CAAATTATTC TATGTAAAA ACAATGAAAA GAACTCCAGT GAAAACAGGA	840
GTTCCTTTAC AATGTTGTCA ATTTCCATTT ACAGCAGCTT TACCATCCTG AATAGTGAAG	900

1354

ATACTTAGAT TTTCTGGCAG ATTTTGAAGA TGGTCTAAGC TGTTTGTGT GATAAAGGTT	960
TGGATTGATT GAGAAATCGT TTCTAATAAT TTAACTGTC TAGTGTGTC AAGTTCACCTC	1020
ATCACATCGT CAAGCAGTAA TATAGGAGAT TCTGTGGTAA TGCTTTCCAT TAATTCGATT	1080
TCTGCTAATT TTATCGAGAG GACGAGACTA CGATGTGAC CTTGGCTTCC GAAACTAGCA	1140
TCCATCCCAT TTATATAAAA AGAAATGTCA TCTCGATGAG GACCGACACC AGTATTCTTT	1200
TTAAATAAAT CTCTGGATCT ACTTTTTTCT AAAGCAATTT TGAAAGATTC GGATAAGTTT	1260
TGTTTGTGAG TTATATTGAC AGAAGATTGA TAGGATATTG ACAACTCTTC GATCTGATTA	1320
GAGAGTTCAA AATGTTTCTT ACGCCCAAAT GATTCTAGTT TTTTATGAA ATCTAAGCGG	1380
TGATTCATTA CACGACATCC ATAATCAACT AGCTGATCAT CTAACACAGA AAGGAATGTT	1440
TCATCTATTT TTTGAGCTGA TTTTAGGTAA GTGTTTCTTT GCTTTAGGAT GTGGTTATAA	1500
TTGGTTAAGT CAGATAAATA GATTGGCTTA ATTTGCCCAA GTTCCATATC AATGAATTTT	1560
CGTCGAATCG AAGGTGCTCC TTTAATTAGT TGTAATCTT CAGGAGCAAA TAAGACAACA	1620
TTCATGTGTC CTACATAATC TGAAAGGCGT GCC	1653

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GAAACACTGT ATTTCAAAGC ATTTTTTGTT AGTTTAAAAT TACTCCCATT CTTCTTTTCC	60
AAACGTACAA TATATCCAAA ACCATTCAAA ATACTAGATT CTATTTTTTA TAATATCACT	120
AAATCCACCT AATTATAGGA CGTTTTCAGA TTTTtagtcc CAGTCCCAGT ACCGGAGAAA	180
TATTGTTTTA ATATAATATC TCTTTTGTG TTCTAAGCTC TTAAAAGCAA AAGAACAAGT	240
AAAGAGTCAA GACAAGGATA AAAAGTCCAT ATTAGGGCAA ATAAAAAGCT TTAAGACAGA	300
TGACAAATCT AAGTCAAATA AGAAAGACCA TAGCAAAGGT GCAGAGAGAT AAATATTGGC	360
GGTCTTCGGA CTGCCTTTAT TTTTtTATCC ATTTTTCAAA TCAAATTTAT TCAGACTATA	420
TATGCACATA TACACTTAAA TTCATATAAA AACATGGCTT GTAAAAAATT ACTTTAATCA	480
CAATAATCGC ATTTAAAATT GTGATGTTTG CAAGCTAAAT TACGGACTTC ACTTGAAGT	540
TTCCCTTGT ATCTTTTATA ATAGATAGAA AATTGCTGG CAGATGAATA TCCAACAGAT	600
TCTGCTATCT CTTTtATAGG TAGTTCAGTG TTTAAAAGAA GAGTTTCAGC TACATTCAAT	660

1355

CTTTTCTTT GAGTGACTC TGTAATGCTT TGACAATATT TTTCCTTAAA TAAATTTTTT	720
AATTTAGTAC CACTCATTTT AGATATTTTT TCAAGCGTGC CTTGATTAC ATTCGTTGCA	780
AAATGATCAT CTAAGAATCT TGCTACATCT TCAAGTGCTT TATCATCATC AATTTCAATT	840
TTATATTTTT TTCTATTTAA GTATGTGTCA ATTACTATAC TTATCCATTC ATTTGCCTTT	900
GCTTTAAAGA AAAAATCAGC GGCAGGAGCG TCCATCTTAC AATTTAATAT TTCCATTGCC	960
ACTCTTTCTA AGGCCTTTGT AAGTATTATT TGATTCGGTT GAAGCAAGGT TGAATAAAAA	1020
GATTCCTGGAT TAATGTTAAT AGATGCTAAA TGTTTTTCTA TTAGCTCTTT TTTAAAACcm	1080
ATGGAAACAG CAAGATAACA ACAATTCTCG TGAATAAAAA AAACAAAATT ATCTTTTATA	1140
TTATCAAAAT CAAAAGTACA TAGAGAGTTT GCGGTAATAG TTTGATACGG ATTAACTTT	1200
TCTCCGTTTG CACTGACAAT GTAACCTGAA TAAATTGAAA CATAGTCTGA CATACTATAA	1260
GTGCTATTTT GAACTACTTC CTCTTTGATA TAAAAATCAT GTATATCGAT AATGAAGATG	1320
CCTCCTTCAT AAAACCGGTA	1340

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 607 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

TATGTTTCGTG ATGAGTTTTT AAGTAGGAAA AACGTGCTAA CCTCTCAGAT TTTGGAAGTT	60
GTAAAAGAAA CTCTTTTTTC ACCCGTAGTA GTTGATAATG GGTTCGATCC GGCCTTATTT	120
GAAATTGAGA AAAACAATT GCTAGCAAGT TTAGCAGCTG ATATGGATGA TTCTTTTAT	180
TTTGACATA AAGAATTGGA TAAATTGTTT TTTCATGATG AACGTCTTCA ATTGGAATAT	240
AGTGATTAC GAAATCGTAT TTTAGCTGAA ACTCCACAAA GTTCTTATTC TTGTTTCCAA	300
GAATTTTTCAG CCAATGATCG AATAGATTTC TTTTCCCTAG GTGATTTTAA TGAGGTTGAA	360
ATTCAAAATG TATTAGAATC ATTTGGCTTT AAAGGTCGAA AAGGAGATGT GAAGGTTGAG	420
TATTGTCAAC CTTATCTTAA TATCCTTCAG GAAGGTATGG TTCGGAAAAA TGTGGGACAA	480
TCCATTTTGG AATTAGGTTA TCATTACTGT TCTAAATATG GTGATGAGCA ACATTTACCC	540
ATGGATTGAA TGAATGGTTT ACTTGGTGGA TTTGCTCACT CTAAGCTCTT TACAAATGTC	600
CGGGAAA	607

1356

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

TTAAAATACC GAATTTTGTT TTGTCCCTCTA TTTCAACATT GTGAATCGCC TCAGGCAGAG	60
AACCGATACT AAAGATATAA CCAAAATAGT TGTCATTGTC TTTACCGATA TCAATCTTAT	120
TGGTTAAATC AAAATCCAGT TCGTCAATTG CGCCATCGAT GTCTTGATTG ATTTCCAAAA	180
GTTTTGTAAT GAGGTTACCC GTACCGCCTG GGATAATCCC TAACTTAGGA ATGTAGTCTC	240
TCTCATCAAT ACCTGAAATG ACTTCATTGA CAGTTCCATC TCCACCAAAC ACAACCACTG	300
CATCATACTG CTCACGAGAA GCTTCTTCAG CAAAATGTGT TGCATCCAGC GCTTTTTCGG	360
TAATTTTGGT TTCAACATAT TCAAAGTATT CTTTGGCTTT ATTCTCCAGC TTTTCTTTGT	420
AATCCAAAGC CTTCTCGCCA CCAGAAGTAG GGTGATAAT TACCATTGCT TTTTTCATTG	480
ATTTTATCCT TAATTTTAAA CAGAAATGTT TACATTTCGT CGTATGCAAG TAAATGTAAT	540
CCTATTATAC AATGAAAATA CAGAAAAGAG AAATCTGACG TACTGGAGAT TAATACGCTT	600
TTATTCTATT TTCCCATCGC CTAACATACAT CCTTTAAGGG TTCATCCAAG TAAGAATAGG	660
CCTTATCCTT GATCCAATCA GGAATACCGT AAGCTGCCTC TGCTAwGCTA CAAGTGATTG	720
CTGCGAGAGT ATCACTGTCG CCACCAAGTG AGATGGCATT TCTTATCGCA TCTTCGAAGT	780
CTCTACTTTC AAGAAAGGCG ATAATGGCTT GAGGGACAGT TTCCTGACAT GTTTCGTTAA	840
AACGATAGTT AGGACGGATT TCATCTAAAG TTTGAGATAG ATTGTAATCG TATTCTTTTT	900

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCTTTCTGGC ACCTGGTCT TGGAATACGG CAAAACCTCT GAAAATATCT ATGCTGGAAT	60
GGACGAGGAA TACCGTCGTT ATCAGCCTGC CATCATCACT TGGTACGAAA CAGCCAAACA	120
TGCTTTTGAT CGCGGACAGA TTGGCAAAAT ATGGGTGGAA TCGAAAACGA CCTCAAGGGC	180

1357

GGTCTCTACA GCTTTAAATC CAAGTTCAAT CCGACCATTG AGGAATTTCG TGGTGAGTTC	240
AACCTGCCAA CTAATCCTCT TTACCACCTC TCCAATCTGG CCTACACTCT CAGAAAGAAA	300
CTGCGCAGaA GcATTAACAG AAAGGAAGCC TATGACCTTT AAACCTTCTCA GCCAAGAAGA	360
ATTCATCCAG CATACTCAG CTAGATCCCA ACGCTCTTTT ATGCAGACCG TAGAAATGGC	420
AGAGCTGCTG AGCAAGCGTG GCTTCAGTAC CCAGTATGTC GGCTACACTG ACCCACAAGG	480
GAAGGTAGTG GTGTCAGCTG TCCTCTACAG CATGCCTATG ACTGGTGGCC TTC	533

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CCAGCAAACCT AGGAAGCTAG CCGTAGTTGC TCAAAGCACA GCTTTGAGGT TGTAATAAG	60
ACTGACGAAG TCATGTACAA AACACTGTTT TGAGGTTGCA GATAGAACTG ACGAAGTCAC	120
TCAAAACACT GTTTTGAGGT TGCAGATAGA ACTGACGAAG TCACTCAAAA CACTGTTTTG	180
AGGTTGCAGA TAGAACTGAC GAAGTCAnnA ACCACACCTA CGGCAAAGTG AATCTGAAGT	240
GGTTTGAAGA GAGTACAACT TGTCTTTTAG AAAAGGAGCC TATAATGAAA GTCTTTCAGC	300
ATGTAAATAT CGTGACTTGT GATCAAGATT TCCATGTTTA TCTTGATGGA ATCTTAGCAG	360
TCAAGGATTC TCAAATCGTC TATGTCGGTC AAGATAAGCC AGCGTTTTTA GAGCAAGCTG	420
AGCAGATTAT AGACTATCAG GGAGCTTGGA TTATGCCTGG TTGGTCAAT TGTCACACCC	480
ATTCTGCAAT GACAGGTCTG AGAGGGATCC GAGATGACAG CAATCTCCAT GAATGGCTCA	540
ATGA	544

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

CCAGGAACTC AAATGTAAGT AGGGGTTCCCT TTTTGTATA TTTTCAAAT AACGCCTCTA	60
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1358

CACTATTGTG	AGCAAATTCA	CCAACTACAG	TTGTATCTTA	GTAAAAATAA	GTAGAATAT	120
GTAAGTGAGT	ACCAGATATA	CCAAGACATC	GTCACCATCT	AAGGTATATT	CAAAATACAA	180
AAGTTGACCA	ACTAGATTTC	TGAATATCCT	TATATATCCA	TTCTTAAAAAT	TGGTTTAAAT	240
AGCGTAGTCT	TTTAAACTAG	TTTTGAGAAT	CCAAAAAATC	TTCCCTACATA	TGTAAGAAGA	300
TTTTTTAGTT	CAGAATGATT	AGaTTTAGCT	AATGGATACC	TATCCTACC		349

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

CTCCGATAAC	CACACCAGCA	ATGGAAATAA	TTCCATCGTT	AGCATCAAGA	ACACCCGCAC	60
GCAGGATATT	TAAACGACCT	GCAAAATTG	AATCAATTTC	GTGATTGTGTT	TCTGACGCTA	120
AATTTCAAGT	TCAAGTTAGC	CATCAAGAAG	TCTTCTCTGG	GTGACTTGTA	GTCCAAGCAT	180
TTTTTAGGAT	AGTTGTAAAT	CCACTTTTCG	ATGAATGCGA	CTTCTTTGGG	AGTCATTTTC	240
TTGGTTCCT	TAGGTAACCA	TCTACGAATG	AGCCTGTTGT	GATTCTCATT	AGTCCCCTGG	300
ATCCTCTAGA	GTCGACCTGC	AGGCATGCAA	GCTTGGCACT	GGCCGTCGTT	TTACAACGTC	360
GATGACTGGG	GAAAACCCCTG	GCGTTACCCA	ACTTAATCGC	CTTGACGAC	ATCCCCCTTT	420
CGCCAGCTGG	CGTAATAGCG	AAGAGGCCCG	CACCGATCGC	CCTTCCCAAC	AGTTGCGCAG	480
CCTGAATGGC	GAATGGGGCC	TGATGCGGTA	TTTTCTCCTT	ACGCATCTGT	GCGGTATTTC	540
ACACCGCATA	TGGTGCACTC	TCAGTACAAT	CTGCTCTGAT	GCCGCATAGT	TAAGCCAGCC	600
CCGACACCCG	CCAACACCCG	CTGACGCGCC	CTGACGGGCT	TGTCTGCTCC	CGGCATCCGC	660
TTACAGACAA	GCTGTGACCG	TCTCCGGGAG	CTGCATGTGT	CAGAAAGTTT	CACCGTCAATC	720
ACCGAAACGC	GCGAAACGAA	AGGGCCTCGT	GATACGCCCTA	TTTTTATAGG	TTAATGTCAT	780
GATAAGGATG	GTTTCTTAGA	CGTCAAGTGG	CACTTATCGG	GGAAATGTGC	GCCGAGACCC	840
TATTTGTTTA	TTTGTCTAAA	TACATTCAAA	TATGTATCCG	CTCGTGAGAA	AATAAACCTG	900
ATAAATGCGT	CAATAATATT	GAAAAATGAA	GAGTATGAGT	ATTCTACATT	TCCGTGTCGC	960
CCTTATACCC	TTTTTTGCGG	CATGTTGCCT	TCCTGTTTTT	GCTCACCCAG	AAAACGCTGG	1020
TGAAAGTTTA	AGATGCTGAA	AAATCATTTG	GGTGCACAAC	TGGGGTTACA	TCCAACCTGA	1080
ATCTCCAnCA	GCAGTTAAGA	TCCTCTGACA	GTTGTACACG	CCGCAAGAAC	TATTCCCAGT	1140

1359

GAATGAGCAA CTTTTAAAAG TCCTGCGAAT GTTGGGGCGG TAATAATCCC CGTGTGTAG 1200
GCCCCG 1206

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTGCTCAACT CAGACAGTCA AATTTCTGAC TTTACCAAAA GAACCATCAA AAAAGTTGCT 60
GAAAAAGGCC ATCAGGTTAT TATTACGACA GGTCGCCCTT ACCGTATGTC AAAAGATTTT 120
TACCGTGAAC TGGGCTTAGA CACTCCTATG ATTAACCTCA ACGGATCCCT TACTCATTTA 180
CCAGACCAAG TTTGGGATTT TGAAAAGTGT TTGACTGTAG ACAAAAAATA TCTGCTAGAT 240
ATGGTTCAAC GTTCAGAGGA CATTCAAGCC GATTTTATCG CTGGAGAATA TCGTAAAAAA 300
TTCTACATTA CAAATCCCAA TGAAGAAATT GCCAATCCCA AACTATTTGG TGTAGAAGCT 360
TTCCAGCCTG AAGATCAATT CCAGCCTGAA TTGGTGACCA AGGACCCTAA CTGTATCCTC 420
TTGCAGACTA GAGCCAGTGA CAAATATTCC TTGGCAAAAAG AAATGAACGC CTTCTACCAG 480
CATCAACTTT CTATCAATAC CTGGGGAGGT CCGCTCAATA TCCTTGAATG TACCCCAAAA 540
GGTGTCAACA AGGCCTTTGC TTTGGACTAC TTGCTCAAGA TAATGAATCG TGACAAAAAA 600
GATTTGATTG CCTTTGGAGA TGAACACAAT GATACCGAAA TGCTCGCTTT TGCTGGGAAG 660
GGTTATGCCA TGAAAAATGC CAATCCAGAG CTACTCCCTT ATGCAGATGA GCAAATTTCC 720
CTTACCAACG ACCAAGATGG GGTGCCAAA ACCCTACAAG ACTTATTCTT ATAACCTATA 780
CTGATACTCA ATGAGGGGCA AAGAGCGAAC TTA 813

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 683 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

CCTAGATAAA TGATATAATT CTATTATTGT TCGTAAAAAT TAAAAGGAGA TTGATGATGG 60

1360

ACAAATTATT TAAACTAAAA GAGAACGGTA CAGACGTTTCG TACAGAGGTT CTCGCTGGTT	120
TAACAACTTT CTTTGCAATG AGCTATATTC TCTTTGTAAA CCCACAAATA CTTTCACAAA	180
CAGGAATGCC TGCTCAGGGC GTCTTCCTAG CGACGATTAT TGGTGCAGTA GCGGGTACCT	240
TGATGATGGC TTTTATGCT AACTTACCTT ATGCCCAAGC GCCAGGTATG GGACTCAATG	300
CCTTCTTTAC CTTTACAGTT GTATTCGGGC TTGGTTATTC TTGGCAAGAA GCCCTAGCTA	360
TGGTCTTCAT CTGTGGGATT ATTCATTGA TTATTACCTT GACAAATGTT CGTAAAATGA	420
TCATTGAATC GATTCCCAAT GCTCTTCGCT CAGCTATTTC AGCTGGTATC GGTGTCTTCC	480
TTGCCTATGT AGGGATTAAG AATGCTGGAC TTTTGAAATT CACGATTGAT CCAGGCAACT	540
ATACTGTTGT AGGAGAAGGG GCTGACAAAG CTCAAGCAAC GATTGCAGCA AACTCTTCAG	600
CAGTTCCAGG ATTGGTCAGC TTTAATAATC CAGCTGTTTT AGTGGCTCTT GCAGGACTTG	660
CCATTACTAT CTTCTTTGTC ATC	683

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CTACTTTACA TGGAAGTAGT CACTGAATTC CAGTTAGAAA TTACTTTGTA ACTACGTTTT	60
GAGGAGGAGT AAAATGCTTT CCTACGTTTCG ATATTACCCA CTAGCGATAG CTAAATTAAT	120
GTGTCTGTGC TCTCCTAAAA TCTGCTGATT TATTACTGAC TAATACAGGA GGTTTTTTTT	180
ATGgACAGAC AATCATATCT GCTATTGGTG TTTATATTTT CACCAGTATC GATTATTTAA	240
TTATTTTAAT TATTTTATTT GCACAGCTAT CACAGAATAA ACAGAAATGG CATATTTATG	300
CGGGGCAATA TCTAGGCACA GGCTTACTTG TAGGGGCGAG TTAGTTGCT GCTTATGTCG	360
TTAATTTTCGT GCCTGAAGAA TGGATGGTTG GATTGCTTGG TTTAATCCCT ATCTATTTAG	420
GGATTCGCTT TGCAATTGTT GGAGAAGATG CGGAAGAAGA AGAGGAAGAA ATTATTGAAA	480
GATTAGAACA AAGCAAGGCA AATCAACTGT TTTGGACAGT TACATTGCTG ACAATTGCGT	540
CTGGCGGAGA TAATTTAGGT ATCTATATAC CTTATTTTGC TTCGTTAGAT TGGTCACAGA	600
CCCTCGTGGC CTTGCTTGTG TTTGTAATCG GCATAATTAT CTTTTCGCGAG ATTAGTCGGG	660
TGTTATCCTC TATTCGGTTA ATATTCGAGA CAATTGAAAA ATACGAGCGA ATCATTGTGC	720
CCTTAGTATT CATTCTACTT GGACTATACA TCATGTATGA AAATGGCACG ATAGAGACTT	780

1361

TTCTGATCGT GTAGATTTTT TTGTTTCACT AGGGATTAG CCCGAGCTCA AATCAGCTCT 840
 CTGATTTTCA GA 852

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

CCGCACAAAA GCGCATAGTA TCAAGATTCT ATAAAGCCTT GATACTATGC CTTTTTAATG 60
 GATAAATAGT TAGTCTTTTT TAAAGACCGG ATCTTTCAAA CTCTGCATAC TGGCATTGAT 120
 CACCGCGCCT AGGATAACAA TTTTAGCAAT CAAGATAAAC CAAAACATCA TAACAACAAG 180
 AAGAACGGAA CCTAAAATTC GGACATCCAC CAAATGATGG ACATAGTAAT TGAGATAACT 240
 AGAGAACAGA GTTAGTAAAC CTAAATCAC TAAGAGAACA AAGGCACTGC CTGGTAGGGT 300
 ATAGCTAATT TTCCTGTTAG ATAGATTGGG AAGAAAATAA TAAAGCATGA CCAAGATAGC 360
 AAAGAGGAGG GCGTAAATCA GAGGACCTGC CAACCCTTGT AAAGCCTGAT AGATAATGCC 420
 ATCTTTTGTC CAATAATGAG CAAGTAAAGC CAAAATCATC TGACCAAATA AGATCAAAAA 480
 CAAGGCAAAC GCAAAGAGGA GCTGCAACCA AAACCTGACTA GGAGACTTAG CATCTGATGG 540
 GAAATAAGTC CACGACTCTT TCGACGCCA TAAGCCTTGT TAAAAGCTTT TTGCAAGAAA 600
 TTCATAGATT TTGAAAACT CCATAACGCC GATAAACAG AAAAAGCTAA TAAACCTGTT 660
 GAAGGTGCG TCAAGACTTC TCTGGCTATT TTTCCACAC CTTCATAGAG GCTTGGGGGG 720
 CAGACGTCTT TCATAAAGCC CAAAATTCT CCCA 754

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 707 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GGGGATAACT CTAGGAGTAC CGCTATTACT CGACTTAATG AGTGACAAG AAGTCAGGAT 60
 TTTTATGCAG GTTGGGCGCT TCATCAGACA GGGAAGATTT ACAGCGACTA TTATGGAAGT 120

1362

CAAGGTTTGC TTTATTATTT GCTGACTTAC GTGAGTCAGG GCGGATTTT CTTTGCCATC	180
TTTGAGTGGT TAGCCTTGGT AGCAGGAGGA TTTTTCCTTT TTAGATCAGC GGACACCTTG	240
ACAGAGCAAG GAGACCAAGC TGGACATCTG GTGACTATTT TTTACATGCT AGTTACAGGT	300
CTTGCTTTTG GTGGAGGCTA TGCGACTCTT TTAGCGCTTC CTTTCTTATT CGCAGCCTTT	360
AGTTTAGTTG CGGCTTACCT AAGCAATCCA AGCCATGATA AGGGATTTGT ACGGATTGGG	420
CTAGCTTTGG CAGGCGGATT TTTCTTTGCT CCCTTATCAT CGCTCCTGTT TATTGCTGTA	480
GTGAGTTTAG GCTTGTGGT CTTTAACCTT GGGCATAGAC GCTTTGCGCA TGGGTTTTAT	540
CAGTTTCTTG CAGTGGCTTT AGGTTTTTCA CTTGTCTTTT ATCCAACCTGC CTACTATAGT	600
GCTGCAACAG GAAGTTTGG GGATGCGwTT AGTGGTATTC GTTATCCTAT TGACAGTATT	660
CGCTTTGATT TTACTTCTAA AATTTTAGAG AATATGTTTT TTTAAGG	707

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GGATTTTGAA AAACCATACC GATTTGACGA CGTATATTCC AAACATTTTC CTCAGTCAAA	60
CGTTGGCCAT CAATTACAAT CTCTCCGGAT TCTGCTTCCA GTAAGCCATC AATTAATCGA	120
ACCGTCGTTG ATTTACCACT ACCATTATGC CCTACAATCG AAAGCCATTC TCCACGTTTC	180
ACGTGAAAgT AATATCCTTC ACATCGTAGT AGTTCTGATT TTCTTTATAG CGAAAAGAAA	240
GATTTTTTAC ATCAATTATT GATTTCATTT CGAACCAAAT GTCCCTTTAA ATACATAGGC	300
ACTACCCTTG AAATAGTCAT AGCCAGAGTA GATAGTGAAA AATAAGGCTA CATAAAGTAG	360
AACTTGACCA AGCAAAGTCC AATGTAATAG CAAGAAAATA ATGGCAAACA TCTGACTAAA	420
AGTTTTAATT TTTCCAGGCA TTGCTGCTGC TAAAAATTGTT CCACCAGTTT CAACCAATAA	480
AAGCCTTAAA CCTGTCACAG CTAACCTACG ACAGATAATC ACTGCAACAA TCCAAGCCGG	540
AGCCATACCT AACTCAATCA ACATAATAAA AGCCGACATA ACTAGTAACT TATCCGCCAT	600
AGGATCTGCA AATTTACCAA AATTACTGAC CACATTCCAT TTACGAGCTA AATATCCATC	660
TAAATAGTCG GTAATACTGG CAACAGCAAA GATAATAGCT GCAACTATAT GACTCTCTAT	720
CGAATTTCTT ATCGTTAAAA TAAAGATAAA AATAGGTATA AA	762

(2) INFORMATION FOR SEQ ID NO: 343:

1363

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

CTTTTGATAC ACTTAACTA TGAATACAAA TCTCAAGCCC AAACCTCAGC GTTTTGCTTC	60
TGCGACTGCC TTTGCCTGTC CTATCTGTCA AGAAAATCTG ACTCTGTAG AGACTAATTT	120
CAAGTGCTGC AACCGTCATT CTTTGTACTT GGCGAAATTT GGCTATGTCA ATCTAGTCCC	180
TCAAATCAAG CAATCTGCTA ACTACGACAA GGAAAATTTT CAAAACCGTC AACAAATCCT	240
AGAAGCCGGC TTTTACCAAG CTATCTTAGA TGCTGTATCT GACTTGCTTG CAAGCTCAAA	300
AACTACCACA ACAATTTTGG ATATCGGTTG TGGTGAAGGA TTCTATTCTC GCAAATACA	360
AGAAAGTCAC TCTGAAAAA CTTTCTATGC CTTTGACATC TCCAAAGATT CAGTCCAAAT	420
CGCGGCTAAA AGTGAACCCA ACTGGGCAGT CAATTGGTTC GTTGGCGACT TGGCACGACT	480
TC	482

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TTTATTTTAA TAAAGTCAAT ACCTGTCTTT ACTTTTCTT AAAAAAGTT TATTATGTTC	60
TTTAAGGAGG TGTA AACAT GAAAATAAAT AATAAACTCG TTGGAGAACG TATTCAAAT	120
ATCCGTTTAA GCCATGGCGA CTCTATGGAA AAATTTGGAG AAAAATTTAA TACTAGCAAA	180
GGTACAGTTA ACAACTGGGA AAAAGGTCGC AATTTACCAA ATAAAGAAAA CCTACTAAA	240
ATTGCATCTA TTGGAAAAAT GAGTGTGAA GAGTTACTCT ACGGCGATTA CAATACTTAT	300
CTACACTTAA AGATTATGGA TTTAGCTCCT GAATGTATAA AAAATTATGA TGAGTATAAC	360
TCTTTACACG ATGATATAAC AAATAAAGCG TTACAGATCG CTCAAATAC CATTTCTAAG	420
ATTGATTATC AAATTTTACA CGAAACGATC AAAAAATTTA TTGATTTAGC TATCGAACAA	480
TCGAGAGATT TGCAAGGAAA TTGTGTGAAA AATAACGGGT	520

1364

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

GCATCAAATC GCCCATCAAA GAAGTTCTCT GGATTTACCA AGACCAGTCA AATAGCTTAG	60
AAGTGCTTAA TGACAAGTAC AATGTTCACT ACTGGAATGA CTGGGAAGTT GGAGACACGG	120
GAACCATGG TGAGCGCTAT GGTGCCGTTG TTAAGAAACA CGACATTATC AATAAGCTTC	180
TCAAACAGTT GGAAACCAAT CCTTGGAACC GCCGCAATAT TATTTGCTC TGGGATTACC	240
AAGCTTTCGA AGAAACAGAT GGGCTGCTCC CGTGCGCCTT TCAGACCATG TTTGATGTTC	300
GGCGTGTTGA TGGGGAAATC TATCTGGATG CGACCTTGAC CCAGCGCTCC AATGATATGC	360
TGGTGGCCCA CCACATCAAC GCTATGCAGT ATGTGGCTTT GCAGATGATG ATTGCCAAAC	420
ATTTTGGCTG GAAGGTTGGG AAGTTCTTCT ACTTCATCAA CAACCTCCAT ATCTATGATA	480
ATCAATTGTA ACAAGCTCAG GAATTGCTCC GTCGGGAGCC GTCAAAGTGC CAACCACGCT	540
TGGTTTAA TGTTCCTGAT GGGACTAATT TCTTTGATAT CAAAGCAGAA GATTTTGAGT	600
TGGTGGATTA TGACCCTGTT AAGCCACAGT TGAAGTTTGA CCTAGCTATT TAAAAGAATA	660
GAAAAAAGAA GTTGAGAATA ATCCCAACTT CTTTGTGTTT TTAACGTGAT ACGCGGCGAC	720
GAGCTGCTTT TTTACGGTTT TCTTCGATGA AAGCTGCTTT TTGCTCTTCT GGTTTCGATTA	780
CTTTCCTTTT AAATGCGTAT ACTGCACCTG CAACGGCAGC GACAGTTCCT GCGACACCTG	840
TTACAAGACC TTTAGCGAAT CCTTTAGCCA TGAGTCTTCC TCCTTTATAT TCTCAATCAG	900
CCAGCCTCCT CAAGAGGTCA CATTTTCTG ACTGACCTTT TTGTGTTATA ATAATAGTAA	960
CGAAAAAATG GGAATTTTTC AAGGAAAAAA GATGAGAACA AAA	1003

(2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

CCGCACGTAC TATTCCAGAT GCCGAGGAAG TGGACCTCAT CCTCGTTGGC GCAACTGGTC	60
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1365

TCAACGCCTT TGAACGCCTC TTGGTCGGCT CTTTCATCTGA ATACATACTC CGCCATGCTA	120
AGGTCGATTT GCTGGTTGTG AGAGAACAAAG AAAAAACCTT ATAATCACAA AGAAAAGGAG	180
CCCCTAGCTC CTTTTTGTTT ACGATTATT TCTCTCTTTA TGGCGTTCGT AAGCCTTGAG	240
CTGGCGCTGC AGTTCCTTTT TAATAGCAGG TTCTGGAGCA TATTTTCTT CCCAATTATC	300
TGGTTTTAAG ATTTTATGGG TCACTGGATC AAAATGAGCC TTGCCATCTG GAAAAATTTT	360
CCCCATATTG GCCTGATGGA CAATATCAAA AATACGTTCT GGGTCCACCC CCATCAAGAC	420
AAAAC TGCCG TAGGTGAAGT AAAGCGTGT C AATCAAGGCA TCCACTTGCC CTATCAAATC	480
TTGCTGAGCA GGTGTCTTCT TGGCTACTTT ATCTGCTGCC TTATCAAGGG CCTGATGAAG	540
TTGCGATACA GCTTGACCAA AATCTTCTTC AGAAGGACTG GCTGCTCGAA CAAACTCCAC	600
CAATTCTTCT ATTTTAAAC CAGCCCTATG GGTGACCCC TCTAAATCCC AAGCTCGAGG	660
TTCTTCTTGG GTTCGTTTCAT CCATCATGTG GTGAAAGTC TTGACCTTAT TGAAATGATA	720
GTCACGGCTG ACAAAGACTT TTTCTGAAGA	750

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 596 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

CGCAACATAC GGATAACCTC CAAAGAATAT TTTTATATTA TAGCAAAGCT TTAAATTGAA	60
TGTTAGAGTC TTGTTCAAAA CAATCATCAA AACCACGTGG ATGATGGTAT TCTACTAAGT	120
GTTGATCTTG AGGATAAGTG TACTTACCGC CAACTTCCCA GATAAATGGA TGGAATCGT	180
ATTGCAAGCG ATCTTTTCGC ATTTTCCAAA GTTCTAGAAT CTCATTAGTA GAAGCCATGA	240
AGTTAGACCA GATATCATAG TGAAC TGGA TAATGACTTT GGTACGCAGA TTTTCTGCCA	300
TACGAAGAAG GTCGATAGAT GTCATTTTGT CTTGGATACC TACCGGATTT TCACCATAGT	360
TATTCAAAGC AACATCAATT TTAAAGTCTT TACCATGTTT TGCAAAATAG TTTGAGAAGT	420
GAGAATCTGC ACCATGATAG ATGGTTCCAC CTGGTGTTC AAAGATATAG TTAACAGCCT	480
TTTGAGCCAT TTCTTCATCT GTAACAGCCA AGCCAGCAGT TCACCGCCTG TCTCATCAGC	540
ACCGTTCACT GGGAGAGTTA CCAAGCAAGT ACGGTCAAAT GATTCTACTG CATGAA	596

(2) INFORMATION FOR SEQ ID NO: 348:

1366

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

CAGAGTCAAC AGCCTGAGTT GAAGGCAACT TTAGACACAG CAGTTACGAC AGCTGAATGA	60
GCTCCTCCAT CAGTTTTTTC TTTAATGAGT CCAGCTACAT CTTCAACTTC GAGGCCGTTA	120
ATCACAATGT CAGCGCCTAC TTCTTTTGCA AGGGCAAGTT TGTCATTGTT GATATCGACT	180
GCGATAACAT GAGCATTGAA TACTTTTTTA GCGTATTGAA CAGCGAGGTT ACCAAGTCCA	240
CCAGCACCGT AAAGAACAAC CCATTGGCCT GGTTCAACTT TTGCTTCTTT GATAGCTTTA	300
TAGGTTGTTA CTCCAGCACA TGTGATAGAA GAAGCTTGGG CTGGATCAAG TCCGTCAGGA	360
ACTTTGACAG CATAGTCAGC AGTTACGATA CATTGTTTCA CCATACCACC GTCTACTGAG	420
TAGCCAGCAT TTTTCACTGT ACGGCAAAGG GTTTCGCGAC CAGTTGTACA GTATTCGCAA	480
GTGCCACATC CTTCAAAGAA CCAAGCAACG CTGACGCGGT CACCGACTTT AAGGCTTTTC	540
ACATCTGGAG CAATCTCTTT AACGATACCG ATACCTTCGT GCCCAAGAAC ACGTCCTGGG	600
ACTTGACCAA AGTCACCATG AGCAACGTGG AGGTCGGTGT GGCAAACGCC CACAGTATTC	660
ACTTCTACAA GTG	673

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GTACCCTACA AATGCTTTAC AGTATGGGTT GAGGGTGGTC AATGGAACTA TGGAGTAGGT	60
TGGACAGGAA CTTTGGGATA TTCTGATTAC TTACATTCTA CTCGATATCA TACAGCAACT	120
GTTAGACATG GGGGTAGAAC CTCTAAGGAT TATGCAAAAC CTGAGGCATG GGCTAGAGCT	180
TCCCTCACCA AGATTCCG	198

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

GCTTCTTCTA TAGACAAAAA TATCATGGGT AAAATAATCA AGGCTATAGC TAGAAGGAGG	60
GACCAATCCA CTACTAATCC TAAGAACAAA ACACTCAAGA GAGCAGAAGA GAGAGGTTCA	120
CTGGCACTGA TAACGGCAAC CACCAAAGGA GAAACCAAGG ACACAGCCTT CATGGAAATG	180
AAAAAAGCAA AAGCCGTTCC AAAGAAAGCG ATAATGAGGC AAATCAAGAT ACTCCAAATA	240
TCAAGAGTAA AGGAAAGCTG ATAAACCGGC GAGAGGACAT TGCTAAACAA ACCTGCCAAA	300
ATCATCCCCC ACCCAACCGT AGGAACAAAA CCATAACGCT TAGCAAAAGG TTGGGGCAAG	360
ATAACATTAA ACATAACACC CATGGCACTC AGCAAACCTG TTATAAGAGC TAGCGGCGTC	420
ATGGATAACT GAGAGAGGTC TCCCTTTGTC GCCATCAAGC AAACACCCAG CATGGCAACC	480
AAAACATAGA AAACAGCGCT TTTTGACGCT CGTTTTTGAT AAACCAAGCG ATTGTAAAAG	540
AGGATAAAGA CAGGGCTAAT AAAGTGTAAA ATAGTTGCTG TCGTAGCATT TGAGTATTCT	600
ACACAGAGAT AGAAAAATA CTGAAGTAA AAAATCCCCA AAATAGCATA GGCTAAAAAG	660
GGCAGGTAAT TTTTCTTGTC TCGCCAAATA TCTAGCACTT GCGATTTTAA TTGTATTGCA	720
GACCAATGA GTACAAGACT CCCTGCCAGT GTCAAACGCA TAGAGGTAAT CCAGCCCGAA	780
GACACCTGAT AATGAGTAAA GAAGTACTCT CCTAAAATTC CACAGATTCC CCATATTAAG	840
CCGGATAGGA GCGAATAAAT TTTTCCGTTA ACAATCTTTT TCTGATACTG A	891

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

GAAAGCGTTC AATAGAACAT TGCTTTTSTA TTTTATAGT AAGCTAAGCG CTTGAGCATC	60
TGCGATGATG GTTACATCAG GGTGATTTTG GAGGCTACTT GCAGGTAGGT TCTCAGTCAC	120
TGGGCCAGAT ACTGTTCCGG CAATGGCTTC TGCTTTCGAC TCACCGTAAG CAAAAAGAAT	180
AATAGACTTG GCATCCAAAA TGTTTTSTAAT CCCCATTGAA ATAGCTTGGG TTGGGACGTC	240
TTCAATCTTG GCAAAGAAGC GTGCATTGGC TTCGATAGTA GACTGGTCAA GTTCTACTAG	300

ATGCGTTTGA CTGTCAAATG GAGTG 1368 325

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

CAAGAGCAGT TTGATGATTT TTGATAAGCA TGCGAATTTA AAATACAAAT ATGGCAATCG	60
CAAGTTTGG TGTAGAGGCT ATTATGTAGA TACGGTAGGC CGTAATCAGA AAGTGATAGC	120
TGAATATATT CAGAATCAAT TACAAGAAGA CAGAGTAGCA GACCTAGCTC ACGTTATTCG	180
AGTCAGTAGA TCCGTTTACT GCGGAAATAA ATAAGAGGAA GTAACGTnAA GTGCTTTAGC	240
ACCTGCTCGG GAAAGTGGTG CGCGAGGAAG CTATTTTCAGG ATGCTTTGGC CCTGGCCGGT	300
AGAAGCGTTA TAGCCGCAGA CTACGACACT TCACACTGGT GGTT	344

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CCCTATCCCT GCTATTGGGG CTGCTCTCAT TGCTGCTTTG GCACAAATCA GTCTTCCAAT	60
TGGACCTGTT CCCTTCACTC TGCAAACTT TGCAATCGGC TTGATTCTAC TGTCTTTAGA	120
CCGAGAGAGG CTGTACTTTC TGCTGGACTC TATCTTCTTC TAGGTGCTAT CGGTCTTCCT	180
GTCTTTGCAG GAGGTGGAGC TGGTTTTCAG GCTTTAGTTG GCCCTACTGC AGGCTATCTT	240
TGGTTTTATC TCGTTTACTC TGGACTTACT TCCTCTCTAA CCAACAGCAA GAGTGGTGT	300
GTAAAGATTT TTCTTGCAA CCTCTTGGGT GATGCCCTTG TCTTTGTCGG CGGGATTCTC	360
AGCTTGCATT TCCTAGCTGG AATGGCATTT GAAAAGCTC TTGCTGTGGG GGTTCTTCCC	420
TTTATCATTC CAGACCTTGG CAACTTCTA GCTATTAGTT TTATTAGCCG TCCCCTACTT	480
CAACGCCTTA AAAATCAGGC TTACTTTACT AACTAAAAA GGATATCGAG TTATCATGAC	540
TCAATATCCT TTTCTTTTAT TTTGAAACT TATACTCAAT GAAAATCAA GAGCAAATA	600
GGAAGCTAGC CGCAGGCTnG CAAAACACTG TTTTGAGGTT GTGGATGAAA CTGACGAGTA	660

1369

AnATCTCATA CATACGGCAA GGCAAAGCTG AC

692

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1005 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GTGATGGACT ACTGGTTCAA AACGCATCCA GAAGATTTTT TCGATAATGT CGGACCTCTT	60
GTAGCCAGTA ACTTTTTTCA TACTTACACC GAAGATTTC ACTTGATGAA GGAAATTGGA	120
GTTAATTCTT TCCGCACTTC CATCCAATGG AGTCGACTCA TCAAGAATTT AGAGACAGGT	180
GAGCCTGATC CAAAAGGTAT TGCTTTCTAC AATGCCATCA TTGAAGAAGC TAAAAAGAAC	240
CAGATGGATC TTGTGATGAA TTTACATCAT TTTGATTTAC CAGTGGAAC TCTTCAAAAA	300
TACGGTGGTT GGGAAAGCAA ACATGTAGTG GAGTTATTCG TGAAGTTGC CAAGACTGCT	360
TTACATGCT TTGGAGATAA GGTTCATTAC TGGACAACCT TCAATGAGCC AATGGTCATT	420
CCAGAAGCAG GGTACTTATA TGCTTTCCAT TATCCAAATC TAAAAGGAAA GGGAAAAGAG	480
GCCGTACAAG TCATCTATAA TCTAAACCTT GCTAGTGCAA AAGTGATTCA ACTATATCGC	540
TCATTAGAAC TTGATGGAAA GATTGGGATT ATTTTAAACT TGACACCTGC TTATCCAAGA	600
AGTAATTCTC CAGAAGACTT AGAAGCAAGT CGATTTACAG ATGACTTCTT TAACAAAGTC	660
TTCTTGAATC CAGCTGTAA AGGAACCTTC CCAGAAAGAT TGGTAAAACA GCTAGAGAGA	720
GATGGCGTGT TATGGAGTCA TACCGAAAAA GAGCTTCAAC TGATGAAATC AAATACGGTT	780
GATTTTCTTG GAGTAAACTA CTACCATCCA AAACGTGTTT AAGCACAAGC AAATCCTGAG	840
GAATATCAGA CGCCCTGGAT GCCAGACCAA TACTTCAAAG AGTATGAATG GCTGGAGCGT	900
CGCATGAATC CATATCGTGG TTGGGAAATT TTTCCGAAAG CCATTTATGA TATTGCTATG	960
ATTGTGAAGG AAGAATATGG TAATATCCCA TGGTTTATCA GTGAA	1005

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 973 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CCGACAAGCA ATATTAAGAA GAGTAACTA TTAAGTAGTT AATTAACCGG TTTATTACTT	60
TATAGTGAAT CAAATATACT TAAGAAAAGA GGAAAGAATG AAAATTAATA AAAAATATCT	120
AGCAGGTTCA GTGGCAGTCC TTGCCCTAAG TGTTTGTTCC TATGAGCTTG GACGTTACCA	180
AGCTGGTCAG GATAAGAAAG AGTCTAATCG AGTTGCTTAT ATAGATGGTG ATCAGGCTGG	240
TCAAAAGGCA GAAAACTTGA CACCAGATGA AGTCAGTAAG AGGGAGGGGA TCAACGCCGA	300
ACAAATTGTT ATCAAGATTA CGGATCAAGG TTATGTGACC TCTCATGGAG ACCATTATCA	360
TTACTATAAT GGCAAGGTTT CTTATGATGC CATCATCAGT GAAGAGCTCC TCATGAAAGA	420
TCCGAATTAT CAGTTGAAGG ATTCAGACAT TGTCAATGAA ATCAAGGGTG GTTATGTCAT	480
TAAGGTAAAC GGTAAATACT ATGTTTACCT TAAGGATGCA GCTCATGCGG ATAATATTCTG	540
GACAAAAGAA GAGATTAAAC GTCAGAAGCA GGAACGCAGT CATAATCATA ACTCAAGAGC	600
AGATAATGCT GTTGCTGCAG CCAGAGCCCA AGGACGTTAT ACAACGGATG ATGGGTATAT	660
CTTCAATGCA TCTGATATCA TTGAGGACAC GGGTGATGCT TATATCGTTC CTCACGGCGA	720
CCATTACCAT TACATTCCTA AGAATGAGTT ATCAGCTAGC GAGTTAGCTG CTGCAGAAGC	780
CTATTGGAAT GGAAGCAGG GATCTCGTCC TTCTTCAAGT TCTAGTTATA ATGCAATCC	840
AGCTCAACCA AGATTGTCAG AGAACCACAA TCTGACTGTC ACTCCAACCT ATCATCAAAA	900
TCAAGGGGGA AACATTTCAA GCCTTTTACG TGAATTGTAT GCTAACCCTT ATCAGAACGC	960
CATGTGGGAT CTG	973

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 843 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GGTCGCATCT GCAATATCTG TCGCCTCCAC ATAAGCGACA CCAGCCTTGT CTGCTGCCCCG	60
TTTGACACGT TCTGCAGATT GACCCAGGAT GACCATCTTC TTGAGTCCAG TAATGTCTGG	120
CACCAATTCTG TCAAACTCAT TGCCACGGTC CAAACCACCT GCAATCAAGA CGACCTTGCT	180
GTTGTCAAAT CCTGACAAGC TTTTGTAGTA GCCAAGATAT TAGTTGATTT ACTGTCGTTA	240
TAGAATTTAA CACsCTTGAT GTCATCCACA AACTGGAGAC GGTGTTTGAC ACCACCGAAG	300
GCTGAAAGAG TTTCTTGAT GGTTTGATTG TCCACATCAC GAAGCTTGGC TACAGCAATA	360

1371

GTCGCAAGGG CATTTCAC ATGTGGCTA CCTGGAACAC CGATTTCATT CGCTGCCATG	420
ACTACTTCAC CACGGAAGTA GAGTTGACCA TCTTCCAGAT AAGCTCCATC AACCTTTTCA	480
AGTGTTGAAA ATGGTACAAC AGTGGCTTCT GTCTTGGAAG TCAAGTCTTT TGCCAAGTCT	540
TGATTAAAGT TCAAGACAAG GAAATCAGCT GCTGTCATCT TGTTCGGAT ATCCACTTG	600
GCTGCTACAT ATTCCGAAAA TGACCCATGG TAGTCGATAT GAGTTGGCAT GAGGTTGGTA	660
ATAACCGCAA TCTCTGGATG GAATTCTTGA ACACCCATGA GTTGGAAGA AGAAAGTTC	720
ATAACAAGCG TGTCCTTATC TGATGCTATT TGAGCAACCT GACTAGCTGG ATAGCCGATA	780
TTCCCTGATA AAAGACCATG TTGGCCAGCA GCAGTCAAAA CTTCCCGGGn TCCTCTAGAG	840
TCG	843

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

TTTTTTTAT ATTTTTTTTA TTTATTATTT TTTGGCAAAA AAGACCAATT TGCTTTGGAG	60
CATTGCTTCT GCATTAAATT GTCTATTTT GTCGTGCTG TTACGCTCTT TGTATCATGT	120
ATTAAGTAGC AAGTGCAACT TGCAAACTAC TAGTAAGAGG AGAAAAACAA AATGGTTATG	180
ACTGACCCAA TCGCAGACTT CCTAACTCGT ATTCGTAATG CTAACCAAGC TAAACACGAA	240
GTACTTGAAG TACCTGCATC AAACATCAAA AAAGGGATTG CTGAAATCCT TAAACGCGAA	300
GGTTTTGTAA AAAACGTTGA AATCATTGAA GATGACAAAC AAGGCGTCAT CCGTGTATTT	360
CTTAAATACG GACCAAATGG TGAGAAAGTT ATCACTAACT TGAAACGTGT TTCTAAACCA	420
GGACTTCGTG TCTACAAAAA ACGTGAAGAC CTTCCAAAAG TTCTTAACGG ACTTGGAATT	480
GCCATCCTTT CAACTTCTGA AGGTTTGCTT ACTGATAAAG AAGCACGCCA AAAGAATGTT	540
GGTGGTGAGG TTATCGCTTA CGTTTGGTAA AATCAAGATA CAAAGCTCGT AAAGAACAAA	600
GCAAAATTAG GAAGTTGGAG AAGTTTGTTT ACAAACAGGC CAACTTATCT ATTTTGCACA	660
GTTCTTAGAG CGTGTTCAGT TCAGCTCTTG AGCTAAGTAA GTATCTGAAC CCCGTGAAAA	720
CTGGCCGTGC TGGCATGTTT GGGTAACAGG AGAaAATAAA CATGTCACGT ATTGGTAATA	780
AGTTCAGCTA AGGCCTTCGT AAAAGTT	807

1372

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 653 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

CCCAGTATTT	TGTCCTCAAGC	ACGACCAGAA	AAGGATGATA	CAGATCTGGA	ATTGGCTCTC	60
TTAACCATCT	tTGAACAAAA	TCCTCAGGCT	CAGGTCACCTA	TTTTCGGTGC	CTTGGGTGGC	120
CGTATTGACC	ATATGTTGGC	CAATGTCTTT	CTGCCTAGCA	ATCCTAAGTT	GGCACCCCTAT	180
ATGCATCAAA	TAGAAATTGA	GGATGGGCAA	AACTTGATTA	CTTATTGTCC	AGAAGGAATC	240
AGTCAGCTAG	AACCTCGTTC	AGACTACGAC	TATCTAGCCT	TTATGCCAGT	TCGGGATAGC	300
CAAGTATGAG	TTGACAGAGG	AAAATTTTTT	CTTTAAAAAA	GTGTACGCTT	CTAACGAATA	360
TATAGATAGG	GAAGTGTCGG	TAACCTGCCC	AGATGGTTAT	GTGGTCGTAC	TGCATAGCAA	420
GGACAGGAGG	TAGGATGGAA	AGTTTACTTA	TTCTATTATT	AATTGCCAAT	CTAGCTGGTC	480
TCTTTCTGAT	TTGGCAAAGG	CAGGATAGGC	AGGAGAAACA	CTTAAGTAAG	AGCTTGGAGG	540
ATCAGGCAGA	TCATTTGTCA	GACCAGCTGG	ATTACCGCTT	TGACCAAGCC	AGACAAGCCA	600
GCCAGTTAGA	CCAAAAAGAT	TTGGAAGTGG	TTGTCAGCGA	CCGTTTGCAA	GAA	653

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CACCATGTGA	TGTGACGCTG	GCCACAGCTG	TCAGAAATCT	GGCGAGCCAT	CGTGTGCAAT	60
GACTCTTCCC	GATGTAATCT	TGTTCATAGT	CCTTTGATGA	ATATGTTCAA	GCTGTAGAAG	120
GTGCGCTTCC	TGAACACTTA	TCAACTGTTA	CAGGCGAGTT	GACCAGTCAG	GAAACAGATG	180
GCTGGTACAC	ACTTGCCAAC	ACTTCTTCAT	CCCGCATTTA	CCTAAAACAA	GCCTTCCAAG	240
AAAATAGCAA	CCTCCTAGAG	CAAGTGGTAG	AACCCTTGAC	TATTATCACT	GGTGGACACA	300
ACCACAAGGA	CCAGTTGACC	TATGCTTGGA	AAACACTTTT	GCAGAATGCG	CCACATGATA	360
GTATCTGTGG	CTGTAGCGTG	GACGAAGTTC	ACCGCGAGAT	GGAAACGCGT	TTTGCCAAGG	420

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TCAACCAAGT AGGAAACTTT GTTAAAAGTA ACTTGCTCAA CGAGTGGAAG GGTAAAATTG	480
CTACGGATAA GGCTCAAAGT GACTATCTCT TTACTGTCAT TAACACAGGC TTGCATGATA	540
AGGTCGATAC TGTCAGCACA GTGATTGATG TGGCGACTTG TGATTTC AAG GAATTGCACC	600
CAACAGAAGG CTACAAAAAG ATGGCTGCTC TTATCTTGCC G	641

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CCTCAAGGCC AATTGAAGG CTCTAAAACA ATGGAAAAGT GCTACACAGA TGTGACAGAA	60
TTTGCCATTC CAGCAAGTAC TCAAAGCCTT TACTTATCAC CAGTTT TAGA TGGCTTTAAT	120
AGCGAAATTA TTGCTTTTAA TCTTTCGACT TCACCCAACT TAGAACAAGT ACAAACAATG	180
TTAGAACAGG CATTCAAAGA GAAGCACTAC GAGAATACGA TTCTCCATAG TGACCAAGGC	240
TGGCAATATC AACACGATTC TTATCATCGG TTCCTAGAGA GTAAGGGAAT TCAAGCATCT	300
ATGTCACGCA AGGGCAACAG CCAAGACAAC GGTATGATGG AATCTTCTT TGGCATTTTA	360
AAATCCGAAA TGTTTTATGG CTATGAGAAA ACATTTAAAT CACTTAACCA ATTGGAACAA	420
GCCATTATAG ACTATATTGA TTACTACAAC AACAAACGAA TTAAGGTAAA ACTAAAAGGA	480
CTTAGTCCTG TGCAGTACAG AACTAAATCC TTTGGATAAA TTAATTGTCT AACTTTTTGG	540
GGTCAGTACA AAACCTCTGC TACTATGCGT TTTATTATTG AAAGACTTAT TGGACTTCT	600
CTCAAATCGA GTTTTACTC AATTTCTTA CTTGATTGGG ATTGAAATC CAATTAATTT	660
CTCTGAGTAG AGTGTCTTGA TATTGGCTTC ATCAACAGAG GCCTTATCAA TTTTACGTTT	720
CAAGAAAAAT TCTTGAATGG TTTGATTTTC AGGCTCACGA ATAGCACGGT GTTTGTTTGA	780
GATGAGGATT TCATAGTGAA GCGGAGCTTG GGTAAAAATA ACATCTGTAT TCCCTGCAGA	840
ATAAACCTCA ACAAGGGTTG CATCGGTACT TTCTAGCTGA CTTTTTACAA GTTGCGAGTG	900
TGAGTTTGTC GTATTGATAA GCTTCATAAT ATTCCTCCG ATTTTCTAAT TCTATTATAG	960
CACTTTTTGA ATAAAGTCGC TTGATTTATA CTCAATGAAA ATCAAAGAGC AAAC TAGGAA	1020
GCTAGCCGCA GGCTATACTT GAGTACGGTA AGGCGACGCT GACGTGGTTT GAATTTTATT	1080
TTCGAAGAGT ATTAGCCAAT CTTATGCTGT TTTTCCAAG ATTCAATGGC CCATTTATGG	1140

1374

CTACCACGTT TAAGGTTTTT GATAGCCTCG TCAATAGGGA ACCAGGCAAT ATGATTAAAG	1200
TTTTCTAGTG GCTTTTGATC TTCTTTGAAA GGAGTTGCTT CATAGAGGTA GGCAGGATTG	1260
TAGTAGTAGG TATCACGATG ACGAGAATAG AAATATTCGT CAGCTTGTCG GTAATAGGTA	1320
CCAATTTCTG CTGTGAAACC AAGCTCTTCA ATCAACTCAT GCTTTAGGGC TTCCTGATGA	1380
TTTTCACCTG CTTCAATTTT TCCACATGGT AGGAACCAAG CACCATTGCG TTCTTGAACA	1440
AGAACAATTT GTTTTTGTTT AGGATTAGGG ATAAGTGCAT ATACGCCATA GCGAGCAATA	1500
TAGTCTGTAT TCACCTTTTT TCTCCGAAAG TTGGGTTTGC CATTGCATTT TCCTCATTAT	1560
CTAGTATCGT TATTATTATA GTGAAATGAA CCAAAAATAG TACACAATGT GGTATAATCT	1620
TCTTATGGCA TATTCAATAG ATTTTCGTAA AAAAGTTCTC TCTTATTGTG AGCGAACAGG	1680
TAGTATAACA GAAGCATCAC ACGTTTTCCT AATCTCACGT AATACCATTT ATGGCTGGTT	1740
AAAGCTAAAA GAGAAAACAG GAGAGCTAAA CCACCAAGTA AAAGGAATAA AACCAAGAAA	1800
GGTTGATAGA GATAGACTTA AAAACTATCT TACTGACAAT CCAGACGCTT ATTTGACTGA	1860
AATAGCTTCT GAATTTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG	1920
tACACTCGAA AAAAAAAGA ACTACACCTA CTATGAAC	1958

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 851 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TATGAAATTA AGTTATGATG ATAAAGTTCA GATCTATGAA CTTAGAAAAC AAGGATATAG	60
CTTAGAGAAG CTTTCAAATA AATTTGGGAT AmACAATTCT AATCTTAGGT ATATGATTAA	120
ATTGATTGAT CGTTACGGAA TAGAGTTCGT CAAAAAAGGA AAAAATCGTT ACTATTCTCC	180
TGATTTAAAA CAAGAAATGA TTAATAAAGT CTGACATGAA GGCTGGACTA AAGATAGAGT	240
TTCTCTTGAA TACGGTCTCC CAAGTCGTAC GATACTTCTT AACTGGCTAG CACAATACAG	300
GAAAAACGGG TATACTATTG TTGAGAAACC AAGAGGGAGA GTACCTGAGA GCGGAGAATG	360
CCATCCTAAA AAAGTTAAGA GAACTCCGAT TGAAGGAGGA AAAAGAGAAA GAAGAAAGAC	420
AGAAATTGTT TAAGAATTAA TGAAGAGTTT TTCGTTAGAT CTTCTTTTAA AAGTCATTAA	480
ACTAGCTCGT TCGACCTACT ACTATCACTT GAAACAGCTA GATAAACCAG ATAAGGACCA	540
AGAGCTTAAA GCTGAAATTC AATCCATTTT TATCGAACAC AAAGGAAATT ATGCTTATCG	600

1375

TCGGATTTAT TTAGAACTAA GAAATCGTGG TTATCTGGTA AATCATAAAA GAGTTCAAGG	660
CTTGATGAAA GTACTCAATt TACAAGCTAA AACGCGACAG AAACGAAAAT ATTCTTCTCA	720
TAAAGGAGAC GTTGGCAAGA AGGCAGAGAA TCTCATTCAA GGCCAATTG AAGGCTCTAA	780
AACAATGGAA CAGTGCTACA CAGATGTGAC AGAATTTGCC ATTCCAGTAA GTACTTAAAA	840
GCTTTACTTA T	851

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

GGGTAGAATC GATATCTCCA ATGAGTTGGT tTAGCTGGTG AAAGTGTAAA AAGATTTCGw	60
CCAATTCAAG GTTGAGGCAT CGCAAATAT GGACTGTTTC CTCGTCAGTT CTGGAAAGAA	120
AACGGGATAA GGTGGCTGT GAAGCAAGCT GCCCTCCTTC CAACAATTTT GGAAAGTAGG	180
CATCAGCTGA CAATTCTTTA CAAGCATAGT CCGTTCCTTA ACCTGTTAAC AGTTGAAAGA	240
GGAAGTGGAC AAGGATATCT GAATCCGAAT AACGACAGTA GCGGCGTTGG TCATTCGTTA	300
CTAAATACTT AGAAATCCGC TCTTTTAGTT TCAACTGGGA AAAAAGTTCC TGAAAAAGA	360
TAAGACCACC ATACTGGGTT AAATGACCTC CATCGAAAGA TAGTTGGTAA AAAGACTTGT	420
TTTGGAAGTG ATGATTTGGT AAAGTGTTC TGTGAGTTTC CTTTCTTTT GTGTTT	480
CTACACTTAT ACCATAAAGG GGAACTCTT TTTGTCTAG TAAAAACAC CCATTGGGTG	540
AAAAAGAAA CCATCCAGGA TCTAAGCTAA GGCAAGGATT CTGGATGGTT TTTAGATTTG	600
GGGTGAATAA TTGGGGTTT AGCTGCTTGC GGCCAATCAG GTTCAGATAC AAAAATTAC	660
TCATCAACCT TTAGTGAAA TCCAATACA TTAACTATC TATTAGACTA TTACGCTGAT	720
AATATAGTCA ATTGAAACAA GAACAAGACA AAAGAGCCTC ATAAAAGGTA TTGCAACTTG	780
GTAATACCTT TTTGAGGTGC TTTTGTGATAT GAGCCCATGT TTTCTCAATA GGATTGACT	840
CAGGTGAGTA GGGAGGAAGA GGTAAAAGTT TATACCCAAA CTCTTCACAC AAGAGTTCTA	900
ACTTACCCAT TCTATGGAAT CTTGCATTAT CCATAATAAT AACCGATGGT GTGTTAATG	960
TTGGTAAGAG AAATTTCTGA AACCAAGCTT CAAAAAGTC GTCGTCATC GTCTCTTCGT	1020
AAGTTATTGG AGCGATTAAC TCACCATTG TTAGACCTGC AACCAAAGAA ATCCTCTGAT	1080

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ATCTTCTTCC AGATACTTTG CCTCTTCTTA ACTGACCTTT TAATGAGCGA CCATATTCTC 1140
 GATAAAAATA AGTATCGAAT CCTGTTTC 1168

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GTCAGCTTCA GCAAGCCCAT CAGCTTCTGA ATCTGCATCA ACCAGTGGT CCGCTTCAGC	60
GTCAACCAGT GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC	120
GTCGGCCTCA GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCGGC	180
TTCAGCAAGC ACAAGTGGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC	240
GAGTGGCTCT GAGTCAGCAT CAACGAGTAC GTCAGCCTCA GCAAGCACAT CAGCTTCTGA	300
ATCTGCATCA ACCAGTGGT CAGCCTCAGC ATCGACAAGC GCCTCAGCTT CAGCAAGTAC	360
CAGTGGCTTCA GCCTCAGCGT CGACAAGTGC GTCGGCCTCA ACCAGTGCAT CTGAATCGGC	420
ATCAACCAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC	480
ATCGGCTTCA GCATCAACCA GTGCCTCGGC TTCAGCGTCA ACCAGTGGT CAGCTTCAGC	540
AAGTACCAGT GCTTCAGTCT CAGCATCAAC AAGTGCTTCA GCCTCAGCAT CGACAAGTGC	600
CTCGGCTTCA GCAAGCACAT CAGCATCTGA ATCAGCGTCG ACAAGCGCCT CAGCTTCAGC	660
AAGTACCAGT GCGTCAGCCT CAGCGTCGAC AAGTGGTCA GCCTCAGCAA GTACTAGTGC	720
ATCAGCTTCA GCATCAACGA GTGCATCGGC TTCGGCGTCA ACCAGTGCAT CAGAGTCAGC	780
AAGTACCAGT GCGTCAGCTT CCGCATCAAC AAGTGCCTCG GCTTCAGCAA GCACCAAGTGC	840
GTCGGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCCTCA ACCAGTGGT CAGCCTCAGC	900
AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGGTCC GCTTCAGCAA GTACTAGCGC	960
CTCAGCCTCA GCGTCAACAA GTGCATCGGC TTCAGCGTCA ACGAGTGGT CTGAATCGGC	1020
ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC	1080
ATCGGCTTCA GCATCAACGA GTGCGTCCG TTCAGCAAGT ACTAGCGCCT CAGCCTCAGC	1140
GTCAACAAGT GCATCGGCTT CAGCGTCAAC GAGTGGTCT GAGTCAGCAT CAACGAGTGC	1200
GTCAGCCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGGT CAGCCTCAGC	1260
ATCGACAAGC GCCTCAGCTT CAGCAAGTAC CAGTGGTCA GcTCAGCGTC GACAAGTGCs	1320

1377

TCrGCTTCAG CAAGTACCAG TGCCTCAGCC TCAGCAAGTA CCAGTGCKTC AGCCTCAGCG	1380
TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG TGCCTCAGCC	1440
TCAGCAAGTA CTAGCGCCTC AGCCTCAGCA TCAACGAGTG CGTCCGCTTC AGCAAGTACT	1500
AGTGCAATCAG CTTCAGCAAG TACTAGCGCC TCAGCCTCAG CGTCGACAAG CGCCTCAGCT	1560
TCAGCAAGTA CCAGTGCGTC AGCCTCAGCG TCGACAAGTG CGTCGGCTTC AGCAAGTACC	1620
TCAGCGTCTG AATCAGCATC AACAAGTGCG TCGGCTTCAG CATCAACGAG TGCATCAGCT	1680
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	1740
AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCCG CATCAACAAG TGCCTCGGCT	1800
TCAGCAAGCA CCAGTGCTTC GGCTTCAGCG TCAACGAGTG CGTCTGAGTC AGCATCAACG	1860
AGTGCGTCAC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCACTTC	1920
CGCATCAACA AGCGCCTCGG CCTCAGCAAG TACAAGTGCT TCAGCCTCAG CATCAACCAG	1980
TGCATCAGCT TCAGCCTCAA CAAGTGCTTC AGCCTCAGCG TCAACCAGTG CCTCGGCTTC	2040
AGCAAGTACC AGTGCGTCAG cTTCAGCAAG CACAAGTGCG TCAGCTTCAG CATCAACCAG	2100
TGCTTCGGCT TCGGCATCAA CAAGTGCTTC AGCATCAGCA TCAACGAGTG CGTCAcCTCA	2160
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACCAGTGATC CAGCCTCAGC AAGTATCTCA	2220
GCGTCTGAAT CGGCATCAAC GAGTGATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA	2280
GCGTCAACCA GTGCATCAGT CTCAGCAAGC ACCAGTGCGT CGGCTTCAGC ATCAACCAGT	2340
GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT CAACGAGTGC GTCAGcCTCA	2400
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACGAGTGATC CGGCTTCAGC AAGTACCAGC	2460
GCCTCAGCTT CAGCAAGCAC CAGTGCGTCA GCCTCAGCAA GTACCAGCGC CTCAGCCTCA	2520
GCAAGCACCA GTGCCTCAGC TTCAGCAAGT ACCAGTGCGT CAGCCTCAGC GTCGACAAGT	2580
GCGTCGGCTT CAGCAAGTAC CTCAGCGTCT GAATCAGCAT CAACGAGTGC ATCAGCTTCA	2640
GCATCAACAA GTGCTTCAGC TTCAGCAAGT ACCAGTGCGT CGGCTTCAGC ATCAACGAGT	2700
GCTTCAGTCT CAGCGTCAAC CAGTGCTCTT GAATCAGCAT CAACAAGTGC CTCGGCTTCA	2760
GCAAGCACCA GTGCGTCGGC TTCAGCAAGT ACTAGTGATC CGGCTTCAGC ATCGACAAGT	2820
GCGTCTGAAT CGGCATCAAC GAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCAGCCTCA	2880
GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CCGCTTCAGC GTCAACCAGT	2940
GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCGGCCTCA	3000
GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCCGC TTCAGCAAGC	3060

1378

ACAAGTGCGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCGTCG	3120
GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCCGCCT CAACCAGTGC GTCGGCTTCA	3180
GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT	3240
GCGTCTGAGT CAGCATCAAC GAGTACGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCG	3300
GCATCAACCA GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT	3360
GCTTCAGCCT CAGCGTCGAC AAGTGCGTCG GCCTCAACCA GTGCATCTGA ATCGGCATCA	3420
ACCAGTGCGT CAGCCTCAGC AAGTACTAGT GCATCAGCTT CAGCATCAAC GAGTGCATCG	3480
GCTTCAGCAT CAACCAGTGC CTCGGCTTCA GCGTCAACCA GTGCGTCAGC TTCAGCAAGT	3540
ACCAGTGCTT CAGTCTCAGC ATCAACAAGT GCTTCAGCCT CAGCATCGAC AAGTGCCTCG	3600
GCTTCAGCAA GCACATCAGC ATCTGAATCA GCGTCGACAA GCGCCTCAGC TTCAGCAAGT	3660
ACCAGTGCGT CAGCCTCAGC GTCGACAAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA	3720
GCTTCAGCAT CAACGAGTGC ATCGGCTTCG GCGTCAACCA GTGCATCAGA GTCAGCAAGT	3780
ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT CAGCAAGCAC CAGTGCGTCG	3840
GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA GTGCGTCAGC CTCAGCAAGT	3900
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA	3960
GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA GTGCGTCTGA ATCGGCATCA	4020
ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT CAGCGTCAAC AAGTGCATCG	4080
GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCGTCA	4140
ACAAGTGCAAT CGGGTTCAGC GTCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTGCGTCA	4200
CCTCAKCAAG CACATCAGCT TCTGAATCTG CATCAACCAG TCGGTCACTT CCGCATCAAC	4260
AAGCGCCTCG GCCTCAGCAA GTACAAGTGC TTCAGCCTCA GCATCAACCA GTGCATCAGC	4320
TTCAGCCTCA ACAAGTGCTT CAGCCTCAGC GTCAGACCAG TGCCTCGGCT TCAGCAAGTA	4380
CCAGTGCGTC ACTTCAGCAA GCACAAGTGC GTCAGCTTCA GCATCAACCA GTGCTTCGCG	4440
TTCCGGCATCA ACAAGTGCCT CAGCATCAGC ATCAACGAGT GCG	4483

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

1379

GTACCTCAGC	GTCCTTCCGC	CTCAACCAGT	GCGTCCGCTT	CAGCAAGCAC	AAGTGCCTCA	60
CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	TGCGTCGGCC	TCAGCAAGCG	120
CAAGTACCTC	AGCGTCACCT	CCGCCTCAAC	CAGTGCCTCG	GCTTCAGCAA	GCACAAGTGC	180
GTCAsCTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCCTC	TGAGTCAGCA	240
TCAACGAGTA	CGTCAGCCTC	AGCAAGCACA	TCAGCTTCTG	AATCGGCATC	AACCAGTGCG	300
TCAGCCTCAG	CATCGACAAG	CGCCTCAGCT	TCAGCAAGTA	CCAGTGCTTC	AGCCTCAGCG	360
TCGACAAGTG	CGTCGGCCTC	AACCAGTGCA	TCTGAATCGG	CATCAACCAG	TGCGTCAGCC	420
TCAGCAAGTA	CTAGTGATC	AGCTTCAGCA	TCAACGAGTG	CATCGGCTTC	AGCATCAACC	480
AGTGCCTCGG	CTTCAGCGTC	AACCAGTGCG	TCAGCTTCAG	CAAGTACCAG	TGCTTCAGTC	540
TCAGCATCAA	CAAGTGCTTC	AGCCTCAGCA	TCGACAAGTG	CCTCGGCTTC	AGCAAGCACA	600
TCAGCATCTG	AATCAGCGTC	GACAAGTGCG	TCGGCCTCAA	CCAGTGATC	TGAATCGGCA	660
TCAACCAGTG	CGTCAGCCTC	AGCAAGTACT	AGTGATCAG	CTTCAGCATC	AACGAGTGCA	720
TCGGCTTCGG	CGTCAACCAG	TGATCAGAG	TCAGCAAGTA	CCAGTGCTC	AGCTTCCGCA	780
TCAACAAGTG	CCTCGGCTTC	AGCAAGCACA	TCAGCATCTG	AATCAGCGTC	AACCAGTGCT	840
TCGGCTTCAG	CAAGTACCAG	TGCTTCAGCT	TCAGCATCAA	CCAGCGCCTC	GGCCTCAGCA	900
AGCACCTCAG	CTTCTGAATC	GGCCTCAACC	AGCGCCTCGG	CCTCAGCAAG	CACCTCAGCT	960
TCTGAATCGG	CCTCAACCAG	CGCCTCAGCC	TCAGCATCAA	CGAGTGCTTC	GGCTTCAGCA	1020
AGCACAAGCG	CCTCGGTTTC	AGCATCAACG	AGTACGTCAG	CTTCAGCGTC	AACCAGTGCT	1080
TCAGCCTCAG	CATCAACAAG	TGCGTCAGCC	TCAGCAAGTA	TCTCAGCGTC	TGAATCGGCA	1140
TCAACGAGTG	CGTCTGAGTC	AGCATCAACG	AGTACGTCAG	CCTCAGCAAG	CACAAGTGCT	1200
TCAGCCTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCTC	CGCTTCAGCA	1260
AGTACTAGCG	CCTCAGCATC	AGCGTCAACA	AGTGCTTCGG	CTTCAGCGTC	AACGAGTGCG	1320
TCTGAGTCAG	CATCAACGAG	TACGTACGCC	TCAGCAAGCA	CATCAGCTTC	TGAATCTGCA	1380
TCAACCAGTG	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	TACCAGTGCG	1440
TCAGCCTCAG	CAAGTACCAG	TGCTTCAGCC	TCAGCGTCGA	CAAGTGCTC	GGCCTCAACC	1500
AGTGATCTG	AATCGGCATC	AACCAGTGCG	TCAGCTCAGC	AAGTACTAGT	GCATCAGCTT	1560
CAGCATCAAC	GAGTGATCG	GCTTCGGCGT	CAACCAGTGC	ATCAGAGTCA	GCAAGTACCA	1620
GTGCGTCACT	TCCGCATCAA	CAAGTGCTC	GGCTTCAGCA	AGCACATCAG	CATCTGAATC	1680
AGCGTCAACC	AGTGCTTCGG	CTTCAGCAAG	TACCAGTGCT	TCAGCTTCAG	CATCAACCAG	1740

1380

CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC TGAATCGGCC TCAACCAGCG CCTCGGCCTC	1800
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGCGCC TCAGCCTCAG CATCAACGAG	1860
TGCTTCGGCT TCAGCAAGCA CAAGCGCCTC GGGTTCAGCA TCAACGAGTA CGTCAGCTTC	1920
AGCGTCAACC AGTGCTTCAG CCTCAGCATC AACAAGTGCG TCAGCCTCAG CAAGTATCTC	1980
AGCGTCTGAA TCGGCATCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC	2040
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGTGCG TCAGCCTCAG CATCGACAAG	2100
CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC	2160
AACCAGTGCA TCTGAATCGG CATCAACCAG TCGCTCAGCC TCAGCAAGTA CTAGTGCATC	2220
GGCTTCAGCA TCAACCAGTG CCTCGGCTTC AGCGTCAACC AGTGCGTCAG CTTAGCAAG	2280
TACCAGTGCT TCAGTCTCAG CATCAACAAG TGCTTCAGCC TCAGCATCGA CAAGTGCCTC	2340
GGCTTCAGCA AGCACATCAG CATCTGAATC AGCGTCGACA AGCGCCTCAG CTTAGCAAG	2400
TACCAGTGCG TCAGCCTCAG CGTCGACAAG TCGCTCAGCT ACAGCAAGTA CTAGTGCATC	2460
AGCTTCAGCA TCAACGAGTG CATCGGCTTC GGCCTCAACC AGTGCATCAG AGTCAGCAAG	2520
TACCAGTGCG TCAGTTCAG CATCAACAAG	2550

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

ACCCAGCAAG TACTAGTGCA TCGGCTTCAG CAAGCACCAG TCGCTCGGCT TCAGCATCAA	60
CCAGTGCCCTC AGCCTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCGTCAC	120
CTCAGCAAGT ACTAGTGCAT CAGCATCAGC ATCAACGAGT GCATCGGCTT CAGCAAGTAC	180
CAGCGCCTCA GCTTCAGCAA GCACCAGTGC GTCA ^s CTCAG CAAGTACCAG CGCCTCAGCC	240
TCAGCAAGCA CCAGTGCCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	300
AGTGCGTCGG CTTAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	360
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG	420
AGTGCGTCCG CTTAGCAAG TACTAGCGCC TCAGCATCAG CGTCAACAAG TGCTTCGGCT	480
TCAGCGTCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC AGCAAGCACA	540
TCAGCTTCTG AATCTGCATC AACCAGTGCG TCAGCCTCAG CATCGACAAG CGCCTCAGCT	600

1381

TCAGCAAGTA CCAGTGCCTC AgCCTCAGCA AGTACCAGTG CTTCAGCCTC AGCGTCGACA	660
AGTGCCTCGG CCTCAACCAG TGCATCTGAA TCGGCATCAA CCAGTGCCTC AGCCTCAGCA	720
AGTACTAGCG CCTCAGCCTC AGCATCAACG AGTGCCTCCG CTTCAGCAAG TACTAGTGCA	780
TCAGCTTCAG CAAGTACTAG CGCCTCAGCC TCAGCGTCGA CAAGCGCCTC AGCTTCAGCA	840
AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGCCTCGG CTTCAGCAAG TACCTCAGCG	900
TCTGAATCAG CATCAACAAG TCGCTCGGCT TCAGCATCAA CGAGTGCATC AGCTTCAGCA	960
TCAACAAGTG CTTCAGCTTC AGCAAGTACC AGTGCCTCGG CTTCAGCATC AACGAGTGCT	1020
TCAGTCTCAG CGTCAACCAG TGCCTCTGAA TCCGCATCAA CAAGTGCCTC GGCTTCAGCA	1080
AGCACCAGTG CTTCGGCTTC AGCGTCAACG AGTGCCTCTG AGTCAGCATC AACGAGTGCG	1140
TCAGCCTCAG CAAGCACATC AGCTTCTGAA TCTGCATCAA CCAGTGCCTC AGCTTCCGCA	1200
TCAACAAGCG CCTCGGCTTC AGCAAGTACA AGTGCTTCAG CCTCAGCATC AACCAGTGCA	1260
TCAGCTTCAG CCTCAACAAG TGCTTCAGCC TCAGCGTCAA CCAGTGCCTC GGCTTCAGCA	1320
AGTACCAGTG CGTCAGCTTC AGCAAGCACA AGTGCCTCAG CTTCAGCATC AACCAGTGCT	1380
TCGGCTTCGG CATCAACAAG TGCCTCAGCA TCAGCATCAA CGAGTGCCTC AGCCGG	1436

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 735 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCAGTTGCCA CACCGTGCTG ACCAGCACCC GTTCCTGCGA TAATTTTCTT TTTACCCATG	60
CGTWTGGCAA GCCAAACTTG TCCTAAGGCA TTGTTAATCT TGTGGGCTCC TGTATGGTTA	120
AGGTCTTCCC GTTTGAGATA AATCTTGCTC CGCCAATATG CTGGGTCAAG TTTT'TGCGT	180
AATAAAGAGG AGTTTCACGT CCTACGTACT GGCAGAAAAG CTGGTTTAAT TCCTCTTGGA	240
AACTTGGGTC TGCCTGACTT TCACGGTAGG CCTTCTCCAA CTCCAAAAC TGTGTCATCA	300
ATGTTTCTGG GACAAAACGT CCGCCGAATT TTCCGTAAAA TCCATCTTTA TTTGGTTCCT	360
GATATGCCAT GCTTTACCCT CTCTATAAAT CTTCTAATCT TTTCATGATC TTTTGTCCA	420
TCTGTCTCCA CTCCGCTCGA TACATCTACT GCATAGGGAG TAAAGTGTG AATTGCTTTT	480
ACTACATTAT CTTCAATAAG GCCACCTGCG ATAAAGAAGG GCTGTGCTAG TCCAGTCGTA	540

1382

TCCAGTTGAC	CCCAATCAAA	GGGCTGGCCA	CTTCCTGCCA	CAGGGGCATC	AAAGAGTAGA	600
TAATCTGCCT	GAGAATTGGG	GACATGCCCA	TTTCCATCTA	CCTGCACAGC	CTGAATACTG	660
GCACAAGGCA	AATTCTCAAA	TAAATCATCT	GCCACCTGAC	CGTGAACCTG	AACCAAGTCC	720
AAGCCGGGGA	TCCTC					735

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

TACTAGCGCC	TCAGCCTCAG	CGTCAACAAG	TGCATCGGCT	TCAGCATCAA	CGAGTGCCTC	60
CGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	AGCGTCAACA	AGTGCATCGG	CTTCAGCGTC	120
AACGAGTGCG	TCTGAGTCAG	CATCAACGAG	TGCGTCAGCC	TCAGCAAGCA	CATCAGCTTC	180
TGAATCTGCA	TCAACCAAGT	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	240
TACCAAGTGCG	TCAGCCTCAG	CGTCGACAAG	TGCGTCCGCT	TCAGCAAGTA	CCAGTGCCTC	300
AGCCTCAGCA	AGTACCAAGT	CGTCAGCCTC	AGCGTCGACA	AGTGCCTCGG	CCTCAACCAG	360
TGCATCTGAA	TCGGCATCAA	CCAGTGCCTC	AGCCTCAGCA	AGTACTAGTG	CATCAGCTTC	420
AGCATCAACG	AGTGCATCGG	CTTCAGCATC	AACCAGTGCA	TCAGAGTCAG	CAAGTACCAG	480
TGCGTCAGCT	TCCGCATCAA	CAAGTGCCTC	GGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	540
AGCGTCAACA	AGTGCTTCAG	CTTCCGCGTC	AACCAGCGCC	TCGGCCTCAG	CAAGTATCTC	600
AGCGTCTGAA	TCGGCATCAA	CAAGTGCCTC	GGCTTCAGCA	TCAACGAGTG	CATCAGTCTC	660
AGCAAGCACC	AGTGCCTCGG	CCTCAGCAAG	CACCAGCGCG	TCTGAATCCG	CATCAACCAG	720
TGCCTCAGCT	TCAGCAAGTA	CCTCAGCATC	TGAATCAGCA	TCAACAAGTG	CATCGGCTTC	780
AGCAAGCACA	AGTGCTTCAG	CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	840
TGCGTCCGCT	TCAGCAAGTA	CTAGCGCCTC	AGCATCAGCG	TCAACAAGTG	CTTCGGCTTC	900
AGCGTCAACG	AGTGCCTCTG	AGTCAGCATC	AACGAGTACG	TCAGCCTCAG	CAAGCACATC	960
AGCTTCTGAA	TCTGCATCAA	CCAGTGCCTC	AGCCTCAGCA	TCGACAAGCG	CCTCAGCTTC	1020
AGCAAGTACC	AGTGCCTCAG	CCTCAGCAAG	TACCAAGTCT	TCAGCCTCAG	CGTCGACAAG	1080
TGCGTCGGCC	TCAACCAAGT	CATCTGAATC	GGCATCAACC	AGTGCCTCAG	CCTCAGCAAG	1140
TACTAGCGCC	TCAGCCTCAG	CATCAACGAG	TGCGTCCGCT	TCAGCAAGTA	CTAGTGCATC	1200

1383

AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC AGCGCCTCAG CTTCAGCAAG	1260
CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC TCAGCAAGCA CCAGTGCCTC	1320
AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGCGTCGG CTTCAGCAAG	1380
TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT TCAGCATCAA CAAGTGCTTC	1440
AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG AGTGCTTCAG TCTCAGCGTC	1500
AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCAAGCA CCAGTGCCTC	1560
GGCTTCAGCA AGTACTAGTG CATCGGCTTC AGCATCGACA AGTGCGTCTG AATCGGCATC	1620
AACGAGTGCT TCGGCTTCAG CATCAACGAG TCGCTCAGCC TCAGCAAGCA CATCAGCTTC	1680
TGAATCTGCA TCAACCAAGTG CG	1702

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAGTGCAT CAGCTTCAGC CTCAACAAGT GCTTCAGCCT CAGCGTCAAC CAGTGCCTCG	60
GCTTCAGCAA GTACCAGTGC GTCACTTCAG CAAGCACAAAG TGCGTCACTT CAGCATCAAC	120
CAGTGCTTCG GCTTCGGCAT CAACAAGTGC CTCAGCATCA GCATCAACGA GTGCGTCACC	180
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACCAAGTG CATCAGCCTC AGCAAGTATC	240
TCAGCGTCTG AATCGGCATC AACGAGTGCA TCAGCATCAG CATCAACGAG TGCATCGGCT	300
TCAGCGTCAA CCAGTGCATC AGTCTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACG	360
AGTGCTTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCGTCAGCC	420
TCAGCAAGTA CTAGTGCATC GGCTTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACC	480
AGTGCTTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCGTCAGCC	540
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC	600
AGCGCCTCAG CTTCAGCAAG CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC	660
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	720
AGTGCGTCGG CTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	780
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	840

1384

AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT	900
TCAGCAAGCA CCAGTGCGTC GGCTTCAGCA AGTACTAGTG C	941

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 869 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC ATCGGCTTCT GCGTCAACCA	60
GTGCATCAGA GTCAGCAAGT ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT	120
CAGCAAGCAC CAGTGCGTCG GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA	180
GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT	240
CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA	300
GTGCGTCTGA ATCGGCATCA ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT	360
CAGCGTCAAC AAGTGCATCG GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA	420
GCGCCTCAGC CTCAGCGTCA ACAAGTGCAT CGGCTTCAGC GTCAACGAGT GCGTCTGAGT	480
CAGCATCAAC GAGTGCGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA	540
GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCGTCAGCCT	600
CAGCGTCGAC AAGTGCGTCG GCTTCAGCAA GTACCAGTGC CTCAGCCTCA GCAAGTACCA	660
GTGCGTCAGC CTCAGCGTCG ACAAGTGCGT CGGCCTCAAC CAGTGCATCT GAATCGGCAT	720
CAACCAAGTGC GTCAGCCTCA GCAAGTACTA GTGCATCAGC TTCAGCATCA ACGAGTGCAT	780
CGGCTTCAGC ATCAACCAGT GCATCAGAGT CAGCAAGTAC CAGTGCGTCA GntTCCGCAT	840
GCAACAAGTG CCTCGGCTTC AGCAAGTAC	869

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAACAAGTG CCTCAGCATC AGCATCAACG AGTGCGTCAG CCTCAGCAAG TACTAGTGCA	60
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1385

TCAGCATCAG CATCAACCAG TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	120
TCAACGAGTG CATCAGCATC AGCATCAACG AGTGCATCGG CTTCAGCGTC AACCAGTGCA	180
TCAGTCTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA	240
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	300
TCGGCTTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA CCAGTGCCTC AGCCTCAGCA	360
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	420
TCAGCATCAG CATCAACGAG TGCATCGGCT TCAGCAAGTA CCAGCGCCTC AGCTTCAGCA	480
AGCACCAGTG CGTCAGCCTC AGCAAGTACC AGCGCCTCAG CCTCAGCAAG CACCAGTGCC	540
TCAGCTTCAG CAAGTACCAG TGCCTCAGCC TCAGCGTCGA CAAGTGCCTC GGCTTCAGCA	600
AGTACCTCAG CGTCTGAATC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAAGTGCT	660
TCAGCTTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCCTC CGCTTCAGCA	720
AGTACTAGCG CCTCAGCATC AGCGTCAACG	750

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

CCGGAACA GCTCTGGCGC TTGGTCTTGC CCAGCGTATT GCTAGTGGTG ACGTGCCTGC	60
GGAAATGGCT AAGATGCGCG TGTTAGAACT TGATTTGATG AATGTCGTTG CAGGGACACG	120
CTTCCGTGGT GACTTTGAAG AACGCATGAA TAATATCATC AAGGATATTG AAGAAGATGG	180
CCAAGTCATC CTCTTTATCG ATGAACTCCA CACCATCATG GGTTCCTGGTA GCGGGATTGA	240
TTCGACTCTG GATGCGGCCA ATATCTTGAA ACCAGCCTTG GCGCGTGGAA CTTTGAGAAC	300
GGTTGGTGCC ACTACTCAGG AAGAATATCA AAAACATATC GAAAAAGATG CGGCACTTTC	360
TCGTCGTTTC GCTAAAGTGA CGATTGAAGA ACCAAGTGTG GCAGATAGTA TGACTATTTT	420
ACAAGGTTTG AAGGCGACTT ATGAGAAACA TCACCGTGTA CAAATCACAG ATGAAGCGGT	480
TGAAACAGCG GTTAAGATGG CTCATCGTTA TTAAACAGT CGTCACTTGC CAGACTCTGC	540
TATCGATCTC TTGGATGAGG CGGCAGCAAC AGTGCAAAAT AAGGCAAAGC ATGTAAAAGC	600
AGACGATTCA GATTTGAGTC CAGCTGACAA GGCCCTGATG GATGGCAAGT GGAAACAGGC	660

1386

AGCCCAGCTA ATCGCAAAAG AAGAGGAAGT ACCTGTCTAC AAAGACTTGG TGACAGAGTC	720
TGATATTTTG ACCACCTTGA GTCGCTTGTC AGGAATCCCA GTTCAAAAAC TGACTCAAAC	780
GGATGCTAAG AAGTATTTAA ATCTTGAAGC AGAACTCCAT AAACGGGTTA TCGGTCAAGA	840
TCAAGCTGTT TCAAGCATTG GCCGTGCCAT TCGCCGCAAC CAGTCAGGGA TTCGCAGTCA	900
TAAGCGTCCG ATTGGTTCCT TTATGTTTCT AGGGCCTACA GGTGTCGGGG TATCCGA	957

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

CAAAGCGCCT CAGCTTCAGC ATCAACAAGT GCGTCGGCTT CAGCATCAAC CAGTGCCTCG	60
GCTTCAGCGT CAACCAAGTGC GTCACATTCA GCAAGTACCA GTGCTTCAGT CTCAGCATCA	120
ACAAGTGCTT CAGCCTCAGC ATCGACAAGT GCCTCGGCTT CAGCAAGCAC ATCAGCATCT	180
GAATCAGCGT CAACCAAGTGC TTCGGCTTCA GCAAGTACCA GTGCTTCAGC TTCAGCATCA	240
ACCAGCGCCT CGGCCTCAGC AAGCACCTCA GCTTCTGAAT CGGCCTCAAC CAGCGCCTCG	300
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GCGCCTCAGC CTCAGCATCA	360
ACGAGTGCTT CGGCTTCAGC AAGCACAAGC GCCTCGGGTT CAGCATCAAC GAGTACGTCA	420
GCTTCAGCGT CAACCAAGTGC TTCAGCCTCA GCATCAACAA GTGCGTCAGC CTCAGCAAGT	480
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA	540
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GTGCGTCAGC CTCAGCATCG	600
ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCTTCAGCCT CAGCGTCGAC AAGTGCCTCG	660
GCCTCAACCA GTGCATCTGA ATCGGCATCA ACCAGTGCGT CAGCCTCAGC AAGTACTAGT	720
GCATCGGCTT CAGCATCAAC CAGTGCCTCG GCTTCAGCGT CAACCAAGTGC GTCAGCTTCA	780
GCAAGTACCA TGTGCTTCAT GTCTCAG	807

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1068 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CATCGGCTTC AGCATCAACG AGTGCCTCCG CTTAGCAAG TACTACCGCC TCAGCCTCAG	60
CGTCAACAAG TGCATCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTG	120
CGTCACCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCT CACCTCAGCA	180
TCGACAAGCG CCTCAGCTTC AGCAAGTACC AGTGCCTCAC CTCAGCGTCG ACAAGTGCCT	240
CGGCTTCAGC AAGTACCAGT GCGTCACTC AGCAAGTACC AGTGCCTCAC CTCAGCGTCG	300
ACAAGTGCCT CGGCTCAAC CAGTGCATCT GAATCGGCAT CAACAGTGC GTCACCTCAG	360
CAAGTACTAG TGCATCAGCT TCAGCATCAA CGAGTGCATC GGCTTCAGCA TCAACAGTG	420
CATCAGAGTC AGCAAGTACC AGTGCCTCAG CTTCGCGATC AACAAGTGCC TCGGCTTCAG	480
CAAGTACTAG CGCCTCAGCC TCAGCGTCAA CAAGTGCTTC AGCTTCGCG TCAACAGCG	540
CCTCGGCTTC AGCAAGTATC TCAGCGTCTG AATCGGCATC AACAAGTGCC TCGGCTTCAG	600
CATCAACGAG TGCATCAGTC TCAGCAAGCA CCAGTGCCTC GGCTTCAGCA AGCACCAGCG	660
CGTCTGAATC CGCATCAACC AGTGCCTCAG CTTAGCAAG TACTCAGCA TCTGAATCAG	720
CATCAACAAG TGCATCGGCT TCAGCAAGCA CAAGTGCTTC AGCTCAGCA AGTATCTCAG	780
CGTCTGAATC GGCATCAACG AGTGCCTCCG CTTAGCAAG TACTAGCGCC TCAGCATCAG	840
CGTCAACAAG TGCTTCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA	900
CGTCAGCCTC AGCAAGCACA TCAGCTTCTG AATCTGCATC AACCAGTGC TCAAGCCTCAG	960
CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCCTC AGCTCAGCA AGTACCAGTG	1020
CTTCAGCCTC AGCGTCGACA AGTGCCTCGG GCTCAACCAG TGCATCTG	1068

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CAGCATCAAC GAGTGCTTCA GTTTCAGCGT CAACAGTGC CTCTGAATCA GCTTCAACAA	60
GTGCCTCGGC TTCAGCAAGC CCCAGTGCCT CGGCTTCAGC AAGTACTAGT GCATCGGCTT	120
CAGCATCGAC AAGTGCCTCT GAATCGGCAT CAACAGTGC TTCGGCTTCA GCATCAACGA	180
GTGCGTCAGC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCCGyTT	240

1388

CAGCGTCAAC CAGTGCCTCG GCTTCAGCGT CGACAAGTGC TTCGGCTTCA GCATCAACGA	300
GTGCGTCGGC CTCAGCAAGC GCAAGTACCT CAGCGTCAGC TTCCGCCTCA ACCAGTGCGT	360
CGGCTTCAGC AAGCACAAGT GCGTCAGCCT CAGCAAGTAT CTCAGCCTCT GAATCGGCAT	420
CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC ACATCAGCTT	480
CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA GCTTCAGCAA	540
GTACCAGTGC TTCAGCCTCA GCGTCGACAA GTGCGTCGGC CTCAACCAGT GCATCTGAAT	600
CGGCATCAAC CAGTGCCTCA	620

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GTATTGGGGC GCCCCAACCT CTATGTGACT ACGGATTATT TCCTAGATTA CATGgGGATA	60
AACCATTTAG AAGAATTACC AGTGATTGAT GAGCTTGAGA TTCAAGCCCA AGAAAGCCAA	120
TTATTTGGTG AAAGGATAGA AGAAGATGAG AATCAATAAG TATATTGCCC ACGCAGGTGT	180
GGCCAGTAGG AGAAAAGCAG AAGAGCTGAT TAAGCAAGGC TTGGTGACGG TTAACGGCCA	240
AGTGGTGCGT GAAC TAGCAA CCACTATCAA GTCAGGCGAC AAGGTCGAAG TTGAAGGTCA	300
ACCTATCTAC AACGAAGAAA AGGTCTACTA TCTGCTTAAC AAACCACGCG GTGTGATTTT	360
CAGTGTGACA GATGATAAGG GTCGCAAGAC GGTGTCGAC CTCTTGCCCA ATGTCAAAGA	420
GCGTATTTAC CCTGTGGGTC GTTTGGACTG GGATACATCA GGTGTCTTGA TTTTGACCAA	480
TGATGGGGAC TTTACAGACG AGATGATTCA CCCTCGTAAT GAGATTGACA AGGTTTATGT	540
CGCGCGTGTT AAAGGTGTGG CCAATAAGGA CAATCTCCGC CCCTTGACCC GTGGTCTTGA	600
GATTGATGGT AAGAAAACCA AGCCATAATA TATAGGTTTT GTAGCCTCTA CACCATAAAT	660
ATTTGCTAAT AAAAATACTG TATTATTACC CTCTTAAGGT GCGAAATTAT TCAAGTTCTT	720

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CGCCATTTCC CATCGTACCG CCGAAAATCC CAGCGCCTCA GCCATCAAAT ATCCTATCAA	60
CGTTCTCAAA AAAAGTGACC GCTCTCTCAT CATGTTTCCA AGTGGTAGCC GCCACTCAAA	120
CGATGTCAAG GGGGGCGCAC ACTskATTGC CAAAATGGCC AAGGTCCGTA TCATGCCGGT	180
TACCTACACC GGTCCCATGA CTTTGAAGGG CTTGATTAGC CGTGAACGTG TCGATATGAA	240
CTTTGGAAAT CCAATCGATA TCTCAGATAT CAAGAAAATG AATGATGAAG GCATTGAAAC	300
AGTCGCCAAT CGTATTCAAA CAGAATTCCA ACGTCTGGAC GAAGAAACGA AACAATGGCA	360
CAATGATAAA AAACCAAATC CACTCTGGTG GTTTATCCGC ATCCCTGCCC TCATCCTTGC	420
TATTATCCTC GCTATCCTAA CCATCATCTT TAGCTTTATC GCAAGCTTCA TCTGGAACCC	480
AGATAAGAAA AGAGAAGAAC TTGCATAGAA GAAATGAACC TTGGCCAAAC AGCTAAGGTT	540
TTTCAATTTATA TAGTAGATTG GwACTAGAAT AGTACACCTC TACTTCTAAA ACATTTTtag	600
AAATCGATTT GACTGTCCTG ATCGATTGT CTAATCTTA TTTCAATT	648

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 690 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

GTGCATCGCT TTCAGCATCG ACAAGTGCCT CTGAATCGGC ATCAACGAGT GCTTCGGCTT	60
CAGCATCAAC GAGTGCGTCA GCTTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA	120
GTGCGTCCGC TTCAGCGTCA ACCAGTGCCT CGGCTTCAGC GTCGACAAGT GCTTCGGCTT	180
CAGCATCAAC GAGTGCGTCG GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCCGCCT	240
CAACCAGTGC GTCCGCTTCA GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT	300
CTGAATCGGC ATCAACGAGT GCGTCGGCCT CAGCAAGCGC AAGTACCTCA GCGTCAGCTT	360
CCGCCTCAAC CAGTGCGTCG GCTTCAGCAA GCACAAGTGC GTCAGCCTCA GCAAGTATCT	420
CAGCGTCTGA ATCGGCATCA ACGAGTGCCT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT	480
CAGCAAGCAC ATCAGCTTCT GAATCGGCAT CAACCAGTGC GTCAGCCTCA GCATCGACAA	540
GCGCCTCAGC TTCAGCAAGT ACCAGTGCTT CAGCCTCAGC GTCGACAAGT GCGTCGGCCT	600
CAACCAGTGC ATCTGAATCG GCATCAACCA GTGCGTCAGC CTCAGCAAGT ACTAGTGCAT	660

CAGCTTCAGC ATCAACGAGT GCATCGGCTT 1390 690

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CGAGATTCTC TGGAGTTATG GATGTCGTTC CAATATGTGC ACGTTGGAAT GTTAGTGCTT 60
ATATGGGGGG AACAGAATCC TCTCTTGATT GAAGACAAGC TAGTCATTAG GCTGGTTTGT 120
CTTTTGTCA ACTGTAGTGG GTTGATATAA TAGTATTAGT GAGTGGGATA AAAGTTTCAT 180
TTAGTTTATT CAGTACAAAT TTAACGGGTC AAGATTTATA TACTAGTGGT GTTTTGGGG 240
CTGAGAGAAG TATCTTGATT TTATGTGTGG TTTTATACT TACAGTTGTT CTGCTCCAAA 300
GAGCTTGTAG AGAAGAATTA GCTCATAAAG GAGATTGATT ATTTTGATAT CAAAAAATG 360
CACAGGATAA CCTGATGCAT TTTTTCGCG ACAATGCTTG CTACTTCCTT CTGTCGAATT 420
TAGACAATTT TAAACCCCAA TTATTCACCC CAAATCTAAA AACCATCCAG AATCCTTGCC 480
TTAGCTTAGA TCCTGGATGG TTTCTTTTTT CACCCAATGG GTGTTTTTTA CTAGACAAAA 540
AAGAGTTTCC CCTTTATGGT ATAAGTGTAG AAAAAACAC AAAAAGAAAG GAAACTCACA 600
TGAACAGTTT ACCAAATCAT CACTTCCAAA ACAAGTCTTT TTACCAACTA TCTTTCGATG 660
GAGGTCATTT AAGCCAGTAT GGTGGTCTTA TCTTTTTC GGAACTTT TCCAGTTGA 720
AACTAAAAGA GCGGATTTCT AAGTATTTAG TAACGAATGA CCAACGCCGC TACTGTCGTT 780
ATTCGGATTC AGATATCCTT GTCCAGTTCC TCTTCAACT GTTAACAGGT TATGGAACGG 840
ACTATGCTTG TAAAGAATTG TCAGCTGATG CCTACTTCC AAAATTATTG GAAGGAGGGC 900
AGCTTGCTTC ACAGCCAACC TTATCCCGTT TTCTTCCAG AACTGACGAG GAAACAGTCC 960
ATAGTTTGCG ATGCCTCAAC CTGAATTGG TCGAATTCTT TTT 1003

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

1391

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CCGATGATTC TGATTGGTTT GCTCTTACT TTGCTGGGAA TTTTGAGGTA GATCTATGAT      60
TGAAATACTA ATTGTTTTAG CTATTATCCT ATCTCTTGCT TTGATTGTAT TGGTAACTAT      120
ACAACCCCGT CAAAATCAAC TATTTTCCAT GGATGCCACT AGTAATATTG GTAAACCAAG      180
CTACTGGCAG AGCAACACCT TGGTCAAGGT GCTCACTTTA TTGGTGAGTT TGGCTTTATT      240
TATCTACTA TTAACCTTTA TGGTGATTAC TTATAAATAA AAGAAAACCT CAGATATTCA      300
CCTTTTGTGG ATTGGTCTGA AGTTTCTTT TTTATACTCA ATGAAAATCA AAGAGCAAAC      360
TAGGAAGCTA GCCGCAcKGC TCAAAACACC GTTTTGAGGT TGTAGATATA ACTGACGAGc      420
GACTCAAAAC ACCGTTTTGA GGTGTAGAT ATAAGTACG AGcGACTCAA AACACCGTTT      480
TGAGGTTGTG GATAGAACTG ACGAGcGACT CAAACACCG TTTTGAGGTT GTGGATAGAA      540
CTGACGAAGT CgCTCAAAAC ACCGTTTTGA GGTGTGGAT AGAACTGACG AAtgctCAAA      600
ACACCGTTTT GAGGTTGTGG ATAGAACTGA CGAAGCgaaC ATATATACAG CAAGGCGACG      660
CTGACGTGCT TGAAGAGTA TTACTGTCTA TATTTTGGT AAAAATCAAC TTTTACTTGG      720
ATGAAGGTTT TTTTTTTT                                     738

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(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 695 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

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CCGTCTTATC AAAGAGGTTA ACAAAGGCAC CAAATTTCTC GATACGAACG ACTTTAGCAC      60
GGTAAACTTC ATCCACTTTG GCTTCACGAA CCAAACCAGC AATAATTTCT TTGGCACGGT      120
TAATAGCATC TTGGTCACTA GAGTAGATAG ACACATTTCC TTCTTCGTCT ATATCAATCT      180
TAACACCTGT TTCAGCGATA ATCTTGTCGA TGGTTTCTCC ACCCTTACCG ATGACAATCT      240
TAATCTTGTC CACATCAATC TTGATCGTAT CAATTTTCGG AGCAGTTGGA GCCAATTCTG      300
GACGAACTTC TGAATGGTT GCTTCAATGA CATCAAGGAT TTCAAAACGC GCTTTCTTGG      360
CTTGAGCAAG AGCCTCCGTC AAGATTTCTG CAGTAATCCC TTGAATCTTG ATATCCATTT      420
GAAGGGCTGT AATCCCATCA CGAGTACCTG CAACCTTGAA GTCCATATCT CCAAAGTGAT      480
CTTCCAAACC TTGGATATCT GTCAATACTG TGTAGTTATT TCCATCTGAG ATAAGCCCCA      540
TAGCAATACC AGCTACTGGC GCCTTGATTG GCACACCACC AGCCATAAGG GCAAGAGTTC      600

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1392

CCGCACAGAT AGAAGCTTGA GATGAAGAAC CGTTTGATTG CAAAACCTCT GCTACTAGAC	660
GGATAGCGTA GGGGAATTCT TCCAAGCTTG GCAGG	695

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACATCTTAT CTAAATACAT GCTAATATAT TTAGATACAA ACATTCCAAC TTGATAATTT	60
TCACTCATCT TTCATCATTC CTTATACAAC TATGCAGTAT AAATAGAATA GTTTTCTCAT	120
CAGAAATGAGA CTATTTTAAT ATTAGATCCC CAATTATTCA CCCCAAATCT AAAAACCATC	180
CAGAAATCCTT GCCTTAGCTT AGATCCTGGA TGGTTTCTTT TTTCACCCAA TGGGTGTTTT	240
TTACTAGACA AAAAAGAGTT TCCCCTTTAT GGTATAAGTG TAGAAAAAA CACAAAAAGA	300
AAGGAAACTC ACATGAACAG TTTACCAAAT CATCACTTCC AAAACAAGTC TTTTACCAA	360
CTATCTTTCG ATGGAGGTCA TTTAACCAG TATGGTGGTC TTATCTTTT TCAGGAAGTT	420
TTTTCCAGT TGAACTAAA AGAGCGGATT TCTAAGTATT TAGTAACGAA TGACCAACGC	480
CGCTACTGTC GTTATTCGGA TTCAGATATC CTTGTCCAGT TCCTCTTTCA ACTGTTAACA	540
GGTTATGGAA CGGACTATGC TTGTAAGAA TTGTCAGCTG ATGCCTACTT TCCAAAATTG	600
TTGGAAGGAG GGCAGCTTGc TTCACAGCCA ACCTTATCCC GwTTTCTTTC CAGAACTGAC	660
GAGGAAACAG TCCATAGTTT GCGATGCCTC A	691

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ATCTCTCTGC GTAATGGTCC TCAGATAACT CTGATGATGT GTGGCGATAT AGAACTGAGC	60
CAAGTTATGC CTAAAGGGCC TTAGGAATAG GAGCTTTCAC AAGCTTATCC AGATGATTAT	120
CTTTTACTCG TTATGGACAA TGCTATATGG CATAAATCAA GTACCTTAAA GATTCCGACT	180
AATATGGCT TTGCATTTAT TCCTCCATAC ACACCAGAGA TGAACCCCAT TGAACAAGTG	240

1393

TGGAAAGAGA TTCGTAAACG TGGATTTAAG AATAAAGCCT TTCGAACTTT GGAAGATGTC	300
ATACAAGGAC TGGAGAAGGA GGTGATAAAG TCCATCGTTA ATCGGAGACG GACTAGAATG	360
CTTTTGTGAAA ACAGATGAGT ATAAAAAGAA AGTCCTCATT TCAATAGAAA TCACGACTTT	420
CTGATGAATT TATAGTAAAA TGAAATAAGA ACAGGATAGT CAAATCGATT TCTAACAATG	480
TTTTTAGAAGC AGAGGTGTAC TATTCTAGTT TAAATCCACT ATATTTGGGG AGTGATAGAA	540
AAGCCCTTCA TCAGCCAATC TACTTGTTCA GGTGCGAGAG CTTTGACATC CTTTCTGTGA	600
CTGGACCAAG TCAGTTTTCG GTTCTCAAAG CGTTTATATA ATATCCAAA TCCTTGACCA	660
TCCCAGTAAA GAACTTTAAA GCGGTCTTTA CGTCCACCAC AAAAGAGAAA GACTTGATCG	720
GAGAAAGGAT CCAATTCAAA GTGGGTTTGG	750

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 738 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TCAAATTCTT CGTGGTCCGC ATATCTnTCT TCGTACACGG CAGTCACTTG GTCTTTCCT	60
ACTCGAGTCG CAGCTTCACG GGCCAATTTC TCTTCTACTT GAACTGCCTT TTGGAGGTCA	120
CTGTTGTAGG CTGCAATGAT TTCAGCTTGC AATTCAGCAT CCACGTGAAG CAATTCCACT	180
TCTGCTTTTT CTTTACCGAC AGCAGCAACG ATTTCTTCTT GGAAGGCAAT CAATCTTTG	240
ACAGCTTCGT GCCCTTTAAG GAGCGCTTCC AACATGATTT CTTCTGACAA TTCTTTGGCA	300
CCAGACTCTA CCATGTTGAT AGCGTGCTTG GTTCCAGCTA CTGTCAATTC AAGAAGAGAT	360
TGCTCTGCTT GTTCTTGA CTGGGTGATG ATGATTTGGC CATCTACATA TCCCACCTGT	420
ACCCCAGCAA TTGGTCCGTC AAATGGAATA TCTGAAATAG ACAGTGCCAA AGATGAACCA	480
AACATAGCAG CCATTGGTGC AGATGCATTT TCATCATAAG AAAGCACTGT ATTGATGACT	540
TGGACTTCAT TACGGAAACC TTCCGCAAAC ATAGGACCAA TCGGACGGTC AATCAAACGC	600
GCTGTCAAGG TCGCATCTGT TGAAGGACGT CCTTCACGTT TCATAAAGCC ACCAGGAAAC	660
TTCCCAGCCG CATACATTTT TTCTTCGTAG TTGACTTGGA GTGGGAAGAA ATCCTCAGTT	720
GCCATTTTCT GGGGATCC	738

(2) INFORMATION FOR SEQ ID NO: 384:

1394

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

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CCCCCTATTT ACCGTGGACT AAAGTTGTAC AAGAAAAGTG CAAATAAGAA ATCTCCAGAT      60
TAGGAACTAT ATATGAGTTC TCTAGTCTGG AGATTTTTCa ATAGACTTCG TTATTGGGCG      120
GTTACTTTTCG AAAC TTGAA AACTTCAAAA AACGGATTTT TATCGCTTTC AAATCTTTT      180
GGGGTCAAAC TCAGTAAC TT ATTCGCCTTG TAGACTTCAT GACGCTCAGG GTATACTTTC      240
AAGGTCCCAA ATAGCCAAGA ATCGTCAGCG ATATTATCTG AATCATCTCC TTCTTGTTCT      300
CCTTTAGTTC GCCTGAGGAC AGCCTTGACA CGCGCCAGAA TTCTCTAGGG CTAAAAGGCT      360
TGGTCAGGTA GTCATCAGCC CCTAATTCCA AGGCCAAAAC CTTATCAAAT TCATCACTTT      420
TCGAGAAAC CATCATAATT GGAGTTTGA CGCCTTTGGC TCTCAGCCGC TTACAAACTT      480
CCATGCCATC TAATTGTGGT AACATGATAT CAAGCAAGAT AAAATCAAAG GGTCTGTTT      540
CTGCCAAAGC TAAGGCCTTC CGTCCATTG TCACCAATTG AGTAGAAAAG CCTTCCTTAC      600
TTAAATGGTA GTCAAGCAAT TTCAGAATGT GTTCTTCATC ATCCACTAAT AAGACTT      657

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(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

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CCGCATCAGC ATCAACGAGT GCATCGGCTT CACGTCAACC AGTGCATCAG TCTCAGCAAG      60
CACCAGTGCG TCGGCTTCAG CATCAACGAG TGCCTCAGCC TCAGCAAGTA TCTCAGCGTC      120
TGAATCGGCA TCAACGAGTG CGTCAGCTCA GCAAGTACTA GTGCATCGGC TTCAGCAAGC      180
ACCAAGTGCGT CGGCTTCAGC ATCAACCAAGT GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT      240
GAATCGGCAT CAACGAGTGC GTCACCTCAG CAAGTACTAG TGCATCAGCA TCAGCATCAA      300
CGAGTGCATC GGCTTCAGCA AGTACCAGCG CCTCAGCTTC AGCAAGCACC AGTGCGTCAC      360
CTCAGCAAGT ACCAGCGCCT CAGCCTCAGC AAGCACCAGT GCCTCAGCTT CAGCAAGTAC      420
CAGTGCGTCA CCTCAGCATC GACAAGTGCG TCGGCTTCAG CAAGTACCTC AGCGTCTGAA      480

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1395

TCAGCATCAA CGAGTGGCTC AGCTTCAGCA TCAACCAGTG CCTCAGCCTC AGCAAGTATC 540
 AGTGGCTCAG CTTCAGCATC AACGAGTGGC TCAGCTGCAG CAAGTA 586

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CGTCGGCTTC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAAGTGCT TCAGCTTCAG 60
 CAAGTACCAG TGCGTCGGCT TCAGCATCAA CGAGTGCTTC AGTCTCAGCG TCAACCAGTG 120
 CCTCTGAATC CGCATCAACA AGTGCTCGG CTTCAGCAAG CACCAGTGCT TCGGCTTCAG 180
 CGTCAACGAG TGCGTCTGAG TCAGCATCAA CGAGTGGCTC ACCTCAGCAA GCACATCAGC 240
 TTCTGAATCT GCATCAACCA GTGCGTCAGC TTCCGCATCA ACAAGCGCCT CGGCCTCAGC 300
 AAGTACAAGT GCTTCAGCCT CAGCATCAAC CAGTGCATCA GCTTCAGCCT CAACAAGTGC 360
 TTCAGCCTCA GCGTCAACCA GTGCCTCGGC TTCAGCAAGT ACCAGTGGCT CAGTTcAGCA 420
 AGCACAAAGTG CGTCAATTTA GCATCAACCA G 451

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCTCAGCAAG CACCATTGCG TCGGCTTCAT CAAGCACCAG CGCGTTTGAA TCCGCATCAA 60
 CCAGTGCTTC AGCTTCAGCC AAGTTACCTC AGCATCTGAA TCAGCATCAA CAAGTGCATC 120
 GGCTTCAGCA AGCACAAAGTG CTTCAGCtCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA 180
 ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCAT CAGCGTCAAC AAGTGCTTCG 240
 GCTTCAGCGT CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC 300
 ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA 360
 GCTTCAGCAA GTACCAAGTGC GTCAGCCTCA GCAAGTACCA GTGCTTCAGC CTCAGCGTCG 420

ACAAG 1396 425

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 572 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AGAGGATCCC CGGATCCTCA GTCGCTGAGA TAACTCCTTT GGGCTTGTTT ATCATGTAGT	60
AGACAAACTC TTCATACTCC AACACTTGCC CATTTTATGC GAATCTCATC TATTTTCTCT	120
TTTTTTTGCA ATTTAGCTGA TTTTCTTTT TTACCATTTA CAGTCACGCG CCCAGCCTTG	180
AGCAAGTTTT TGACCTCAGT CCGACTTCCC ACCGCACAGG CAACTAAAAA TTTATCTAAT	240
CTCATAGAAC TATTATATCA TATCAAAAGG AGGCTAGTAC AATGACCAAC CTCCTTTTCG	300
TTTCATACTC TTCAAAAATC TCTTCAAACC GCGTCAACGT CGCCTTGCCG TATATATGTT	360
ACTGACTTCG TCAGTTCTAT CTGCAACCTC AAAACAGTGT TTTGAGCTGA CTTCGTCAGT	420
TCTATCTGCA ACCTCAAAGC AGTGCTTTGA GCATCCTGCG GCTAGTTTCC kAGTkTGCTC	480
TTTGATTTwC ATTGAGTATC AGATTTAGGA AATTAAGTTC CTCGkCTCCA AAAAAkAGCT	540
AAAACAATCA AGGCTCCTAA AATCGCTGGG AT	572

(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

CAACAAGTGC CTCGGCTTCA GCATGCACAA GTGCTTCAGC TTCAGCATGT ACCTGAGCGT	60
CTGAATCAGC ATCAACGTGT GCGTCCGCTT CAGCATGTAC TGCTGCCTCA GCATCAGCGT	120
CAAcAwGTGC TTCGGCTTCA GCGTCAACGA GTGCGTCTGA GTCAGCATCA ACGAGTACGT	180
CAGCCTCAGC AAGCACATCA GCTTCTGAAT CTGCATCAAC CAGTGCGTCA GCCTCAGCAT	240
CGACAAGCGC CTCAGCTTCA GCAAGTACCA GTGCGTCAGC CTCAGCAAGT ACCAGTGCTT	300
CAGCCTCAGC GTCGACAAGT GCGTCGGCCT CAACCAGTGC ATCTGAATCG GCATCAACCA	360
GTGCGTCAGC CTCAGCAAGT ACTAGCGCCT CAGCCTCAGC ATCAACGAGT GCGTCCGCTT	420

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CAGCAAGTAC TAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA GCAAGTACCA 480
 GCGCCTCAGC TTCAGCAAGC ACCGG 505

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GCTAAGACTA CCTCATTAGG GGCATAGGCT GCTAAAATAA CTGCAGCTGT GGTTAATGAC 60
 AATACTGTAC TTTTTCAT TTTAATTCCT TACATATTTA TATAACTTCC AATAGATAAT 120
 AAACTTAAC TTTGCTAGCC TTTGTTATAA AAAGTTTAC TAAGTATTAT CTAGGAAATA 180
 GAGTAGTACA TTTATATATA ATTGTTATCT CTCTATAAAA ACAGTATATC ATTTAAAAAA 240
 ATTTAAGTCA AAAAAATTAA CATTAGTTAA TTTATTTTTT AGCACACATT AAAAAATAAG 300
 ATTAGTACTC AATGAAAATC AAAGAGCAAA CTAGGAAACT AGCCGCAGAT TGCTCAAAAC 360
 AGTGTTTGA GGTGTAGAT GGAATGACGT AGTCAGCTCA AAACACTGTT TTGAAGTTGT 420
 GGATAGAACT GACGAAGTCG GTACCGA 447

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 572 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

AGCACTTGTC GTTGAATTCT ACAACAAAAT GTTGAATAT TTTATTGAAT AAGATAGGCC 60
 TTGATATTAA GCACTTTGGG ACGTTCTCCC TTAGTGCTTT TTTGATTCT CTAGTATCC 120
 AGCTATAATC GTTGAGACAT AACTAGACCG ATATAGTCCA AAGTGATATA GTAAAATGAA 180
 CCAAAAATAG TACACAATGT GGTATAATCC TTTTATGGCA TATTCAATAG ATTTTCGTAA 240
 AAAAGTTCTC TCTTATTGTG AGCGAACAGG TAGTATAACA GAAGCATCAC ACGTTTCCCA 300
 AATCTCACGT AATACCATTT ATGGCTGGTT AAAGCTAAAA GAGAAAACAG GAGAGCTAAA 360
 CCACCAAGTA TAGTGATTG AATCTATAAC AGTACACCTT GGCTGCTAAA ATATTTCTAT 420

1398
AAATTAATTT GACTTTCCTG ATAGAGATGT TCACATCTTA TTTCAAATA CTATATAAGT 480
TCTATAATCT CTTTATAAGA TTTGCCCATC AGACAAAATA GAACGATTG AAGGCGTTTA 540
TGATATTTAG CTGTACGAGA GTCTTTTAAA AG 572

MISSING UPON TIME OF PUBLICATION

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person approved by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PUT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by the applicant in the individual case.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the International publication of the application.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapse, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever two dates occurs earlier.

SINGAPORE

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

NORWAY

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegians Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

ICELAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected in the art.

What Is Claimed Is:

25 1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-391.

30 2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.

35 3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

40 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

 5. A computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising the following elements:

45 a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391;

 b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and

 c) retrieval means for obtaining said homologous sequence(s) of step (b).

50 6. A method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

55

60 7. A method for identifying an expression modulating fragment of
Streptococcus pneumoniae genome comprising the step of comparing a database
comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a
representative fragment thereof, or a nucleotide sequence at least 95% identical to
the nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a
nucleic acid molecule comprised of a complementary nucleotide sequence to said
65 target sequence, wherein said target sequence comprises sequences known to
regulate gene expression.

70 8. An isolated protein-encoding nucleic acid fragment of the *Streptococcus*
pneumoniae genome, wherein said fragment consists of the nucleotide sequence of
any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3, or a
degenerate variant thereof.

75 9. A vector comprising any one of the fragments of the *Streptococcus*
pneumoniae genome SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a
degenerate variant thereof.

80 10. An isolated fragment of the *Streptococcus pneumoniae* genome,
wherein said fragment modulates the expression of an operably linked open reading
frame, wherein said fragment consists of the nucleotide sequence from about 10 to
200 bases in length which is 5' to any one of the open reading frames depicted in
Tables 2 and 3 or a degenerate variant thereof.

85 11. A vector comprising any one of the fragments of the *Streptococcus*
pneumoniae genome of claim 8.

12. An organism which has been altered to contain any one of the
fragments of the *Streptococcus pneumoniae* genome of claim 8.

90 13. An organism which has been altered to contain any one of the
fragments of the *Streptococcus pneumoniae* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *Streptococcus pneumoniae* genome depicted in SEQ ID NOS:1-391 and Tables 2 and 3 or a degenerate variant thereof.

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-391 and Tables 2 and 3, including fragments thereof;

b) identifying members of said library which contain sequences that hybridize to said target sequence; and

c) isolating the nucleic acid molecules from said members identified in step (b).

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

a) isolating mRNA, DNA, or cDNA produced from an organism;

b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Streptococcus pneumoniae* genome to prime said amplification;

c) isolating said amplified sequences produced in step (b).

17. An isolated polypeptide encoded by any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

19. An antibody which selectively binds to any one of the polypeptides of claim 17.

130

20. A method for producing a polypeptide in a host cell comprising the steps of:

135

a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Tables 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and

b) isolating said protein.

Figure 1

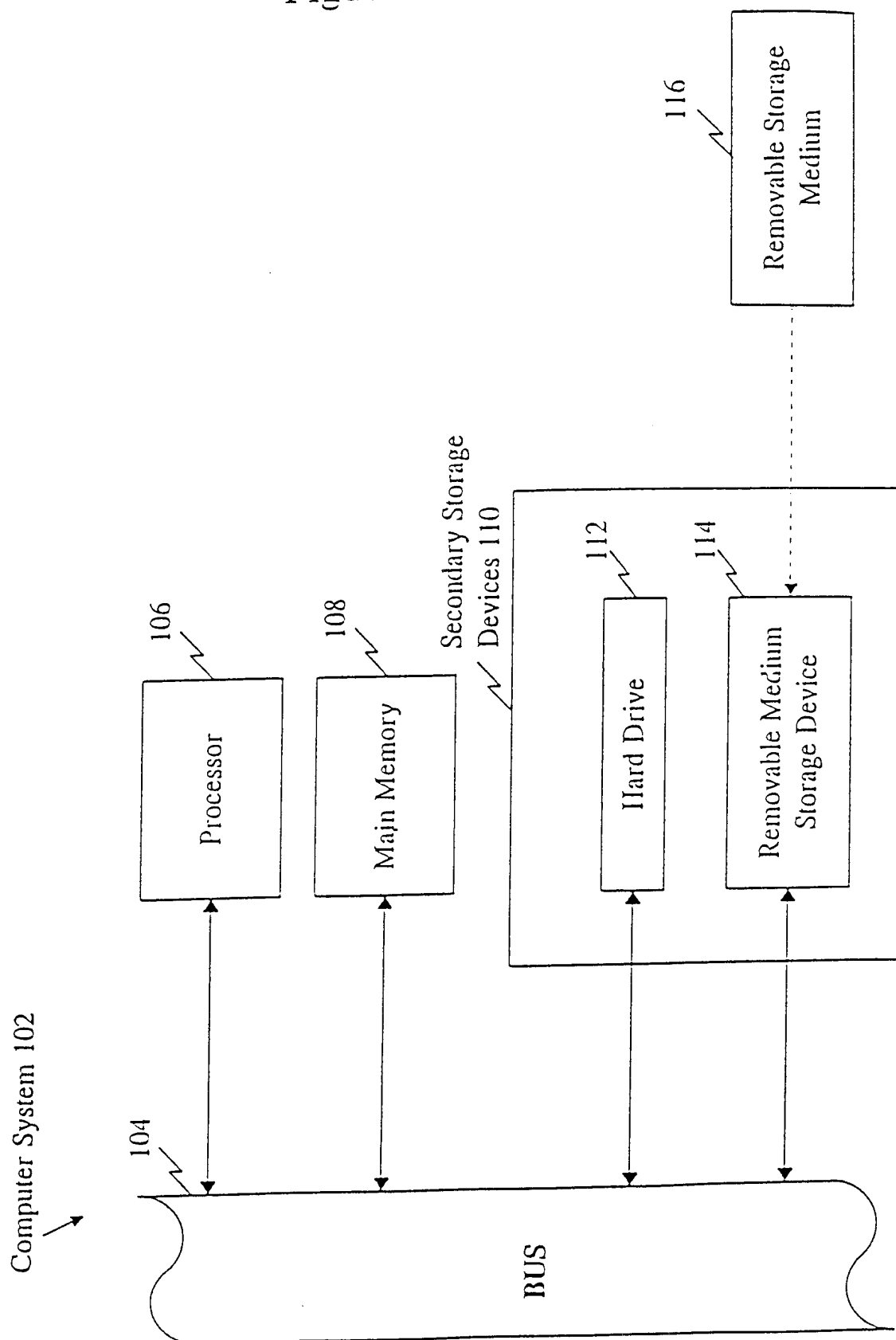
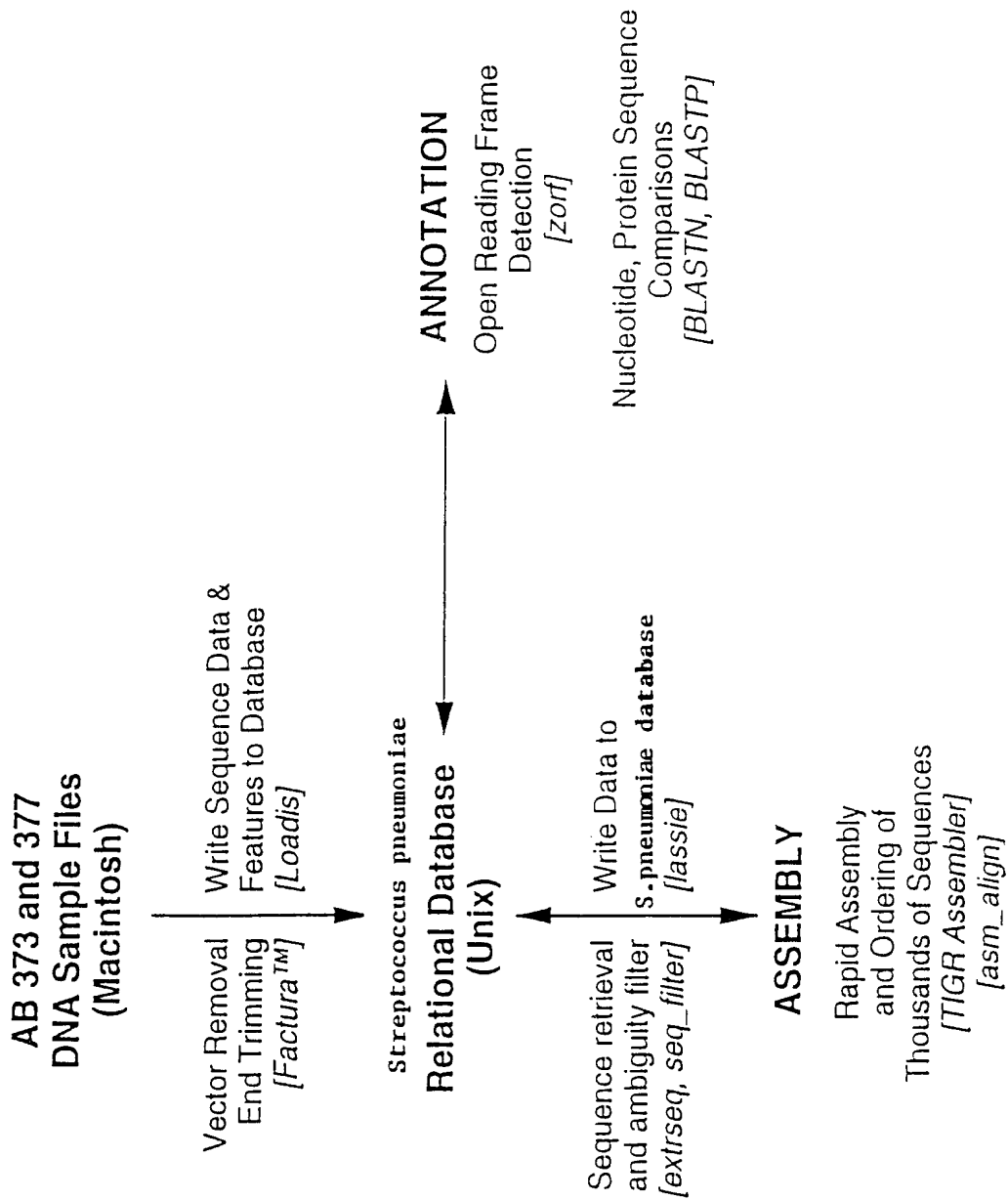


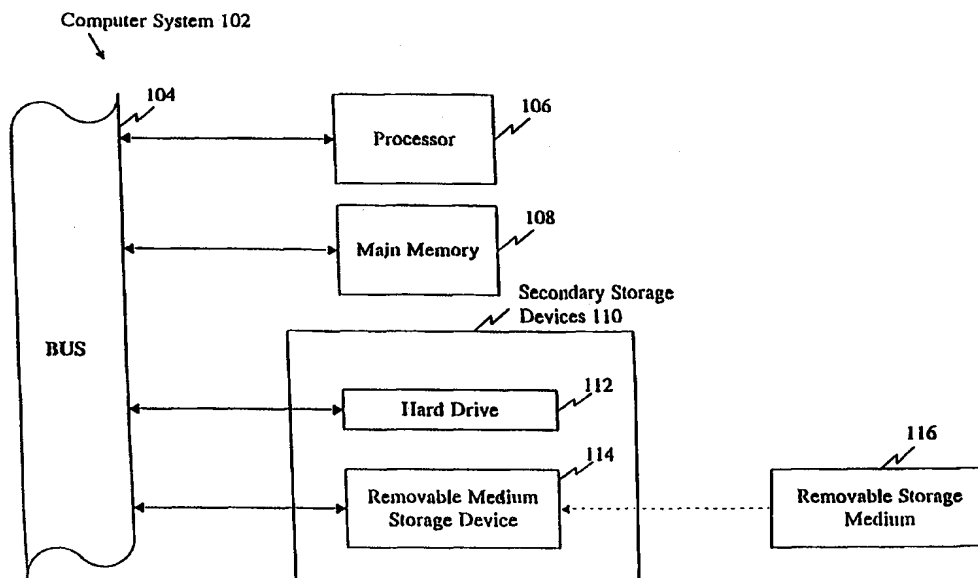
Figure 2





INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/31, C07K 14/315, 16/12, C12Q 1/68		A3	(11) International Publication Number: WO 98/18931
			(43) International Publication Date: 7 May 1998 (07.05.98)
(21) International Application Number: PCT/US97/19588 (22) International Filing Date: 30 October 1997 (30.10.97) (30) Priority Data: 60/029,960 31 October 1996 (31.10.96) US (71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): KUNSCH, Charles, A. [US/US]; 2398B Dunwoody Crossing, Atlanta, GA 30338 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). BARASH, Steven, C. [US/US]; 582 College Parkway #303, Rockville, MD 20850 (US). FANNON, Michael [US/US]; 13501 Rippling Brook Drive, Silver Spring, MD 20850 (US). DOUGHERTY, Brian, A. [US/US]; 708 Meadow Field Court, Mount Airy, MD 21771 (US).		(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 20 August 1998 (20.08.98)	

(54) Title: *STREPTOCOCCUS PNEUMONIAE* POLYNUCLEOTIDES AND SEQUENCES

(57) Abstract

The present invention provides polynucleotide sequences of the genome of *Streptococcus pneumoniae*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

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EE	Estonia	LR	Liberia	SG	Singapore		

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 97/19588

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/31 C07K14/315 C07K16/12 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 33276 A (HUMAN GENOME SCIENCES INC ;UNIV JOHNS HOPKINS (US)) 24 October 1996 see claims 1-7	1-7
A	--- ALTSCHUL S F ET AL: "BASIL LOCAL ALIGNMENT SEARCH TOOL" JOURNAL OF MOLECULAR BIOLOGY, vol. 215, 1990, pages 403-410, XP000604562 cited in the application see the whole document --- -/-	1-7



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

27 March 1998

Date of mailing of the international search report

0 8. 07. 98

Name and mailing address of the ISA

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Authorized officer

HORNIG H.

INTERNATIONAL SEARCH REPORT

Int'l. Application No

PCT/US 97/19588

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	W.R. PEARSON AND D.J. LIPMAN: "Improved tools for biological sequence comparison" PROC. NATL. ACAD. SCI., vol. 85, April 1988, NATL. ACAD. SCI., WASHINGTON, DC, US;, pages 2444-2448, XP002060460 cited in the application see the whole document ---	1-7
A	WO 95 06732 A (UNIV ROCKEFELLER ;MASURE H ROBERT (US); PEARCE BARBARA J (US); TUO) 9 March 1995 see the whole document ---	1-7
A	WO 95 31548 A (UAB RESEARCH FOUNDATION ;YOTHER JANET (US); DILLARD JOSEPH P (US)) 23 November 1995 see the whole document ---	1-7
A	WO 95 14712 A (RES CORP TECHNOLOGIES INC) 1 June 1995 see the whole document ---	1-7
A	WO 96 05859 A (AMERICAN CYANAMID CO) 29 February 1996 see the whole document ---	1-7
A	WO 93 10238 A (US HEALTH) 27 May 1993 see the whole document ---	1-7
A	EP 0 687 688 A (UNIV OVIEDO ;UNIV LEICESTER (GB)) 20 December 1995 see the whole document ---	1-7
A	EP 0 622 081 A (UAB RESEARCH FOUNDATION) 2 November 1994 see the whole document -----	1-7

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 97/ 19588

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 1-4 could be, at least partially be considered as a mere presentation of information Rule 39.1(v), and claims 5-7 at least partially as a computer program, Rule 39.1(vi)PCT, the search has been carried out as far as possible in our systematic documentation.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see continuation-sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-7

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-7

Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID nos. 1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID nos. 1-391; a computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising: a) a data storage means comprising said nucleotide sequence(s); b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and c) retrieval means for obtaining said homologous sequence(s) of step (b); a method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected; a method for identifying an expression modulating fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression;

2. Claims: (8-20) partially

An isolated protein-encoded nucleic acid fragment of the *Streptococcus pneumoniae* genome, wherein said fragment consists of the nucleotide sequence of the fragment of SEQ ID no.1 depicted in Tables 2 and 3, or a degenerate variant thereof; a vector comprising the fragment of the *Streptococcus pneumoniae* genome SEQ ID no.1; an isolated fragment of the *Streptococcus pneumoniae* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frame of SEQ ID no.1 depicted in Tables 2 and 3 or a degenerate variant thereof; a method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the open reading frame of SEQ ID no.1 and Tables 2 and 3 or a degenerate variant thereof; an isolated nucleic acid molecule encoding a homolog of SEQ ID no.1; an isolated polypeptide encoded by SEQ ID no.1 and depicted in Table 2 and 3; an antibody which selectively binds to any one of said polypeptides, a method for producing a polypeptide in a host cell comprising a) incubating a host containing a heterologous nucleic acid

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molecule whose nucleotide sequence consists of SEQ ID no.1 and depicted in Table 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and b) isolating said protein;

3-392. Claims:(8-20) partially

Idem as subject 2 but limited to each of the sequences of SEQ ID no. 2 to 391;

For the sake of conciseness, the second subject matter is explicitly defined, the other subject matters are defined by analogy hereto.